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(54) **RNA INTERFERENCE MEDIATED INHIBITION OF CATENIN (CADHERIN-ASSOCIATED PROTEIN), BETA 1 (CTNNB1) GENE EXPRESSION USING SHORT INTERFERING NUCLEIC ACID (SINA)**

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This patent is subject to a terminal disclaimer.

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Related U.S. Application Data

(63) Continuation of application No. 13/937,412, filed on Aug. 6, 2013, now Pat. No. 8,835,623, which is a continuation of application No. 13/813,465, filed as application No. PCT/US2011/046178 on Aug. 2, 2011, now Pat. No. 8,518,907.

(60) Provisional application No. 61/370,064, filed on Aug. 2, 2010.

(51) **Int. Cl.**

C12N 15/11	(2006.01)
C07H 21/02	(2006.01)
C07H 21/04	(2006.01)
A61K 48/00	(2006.01)
C12N 15/113	(2010.01)

(52) **U.S. Cl.**

CPC ***C12N 15/1138*** (2013.01); ***C12N 15/113*** (2013.01); *C12N 2310/14* (2013.01); *C12N 2320/32* (2013.01)

(58) **Field of Classification Search**

USPC 536/23.1, 24.3, 24.5; 514/44

See application file for complete search history.

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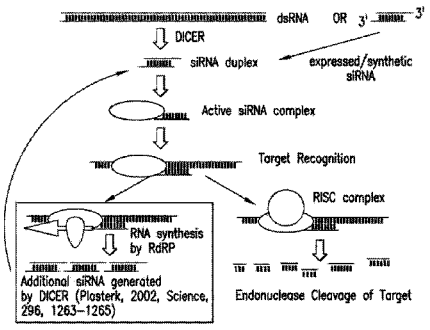
(57) **ABSTRACT**

The present invention relates to compounds, compositions, and methods for the study, diagnosis, and treatment of traits, diseases and conditions that respond to the modulation of CTNNB1 gene expression and/or activity, and/or modulate a beta-catenin gene expression pathway. Specifically, the invention relates to double-stranded nucleic acid molecules including small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules that are capable of mediating or that mediate RNA interference (RNAi) against CTNNB1 gene expression.

39 Claims, 12 Drawing Sheets



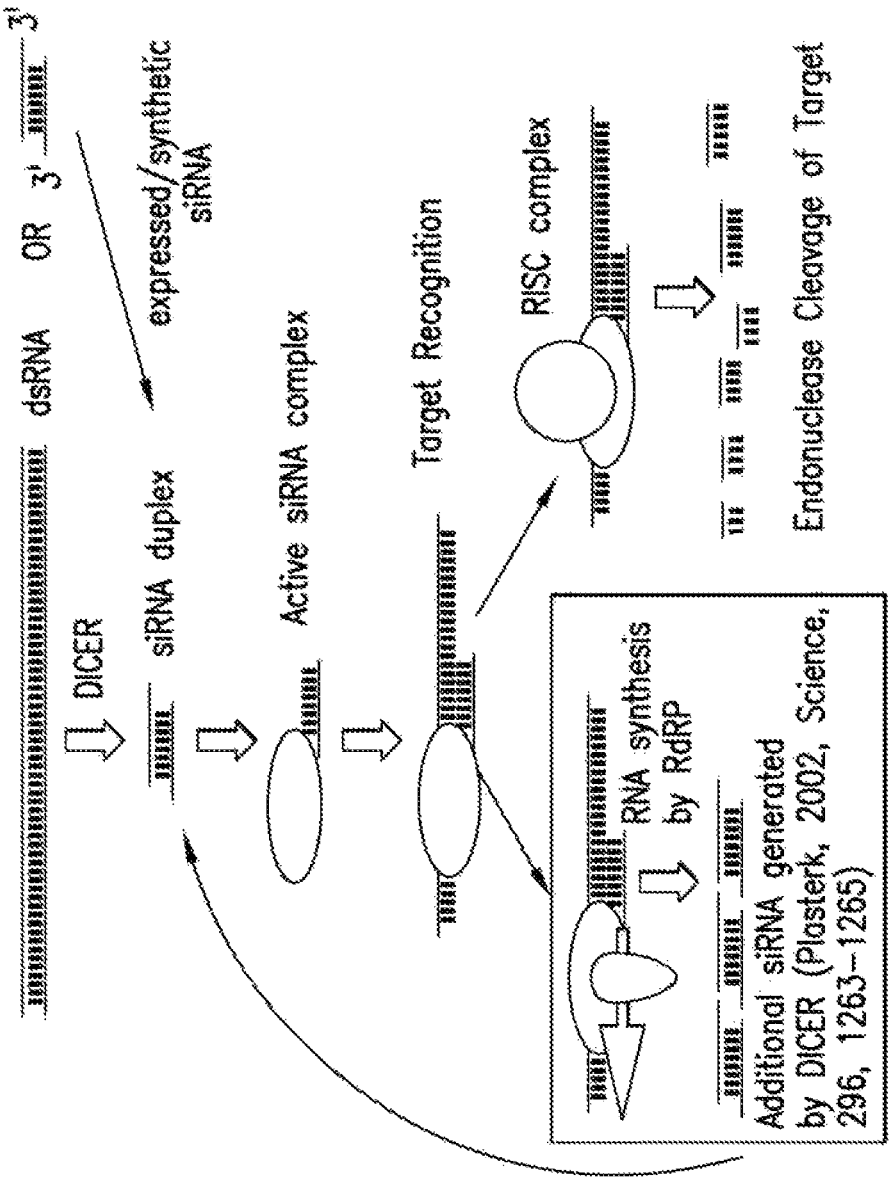
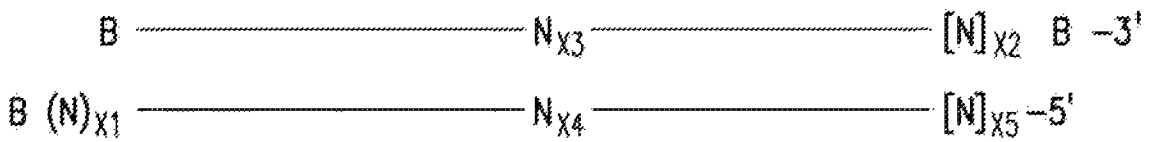

dsRNA OR 3' 3'
DICER
siRNA duplex
expressed/synthetic siRNA
Active siRNA complex
Target Recognition
RISC complex
RNA synthesis by RdRP
Additional siRNA generated by DICER (Plasterk, 2002, Science, 296, 1263–1265)
Endonuclease Cleavage of Target

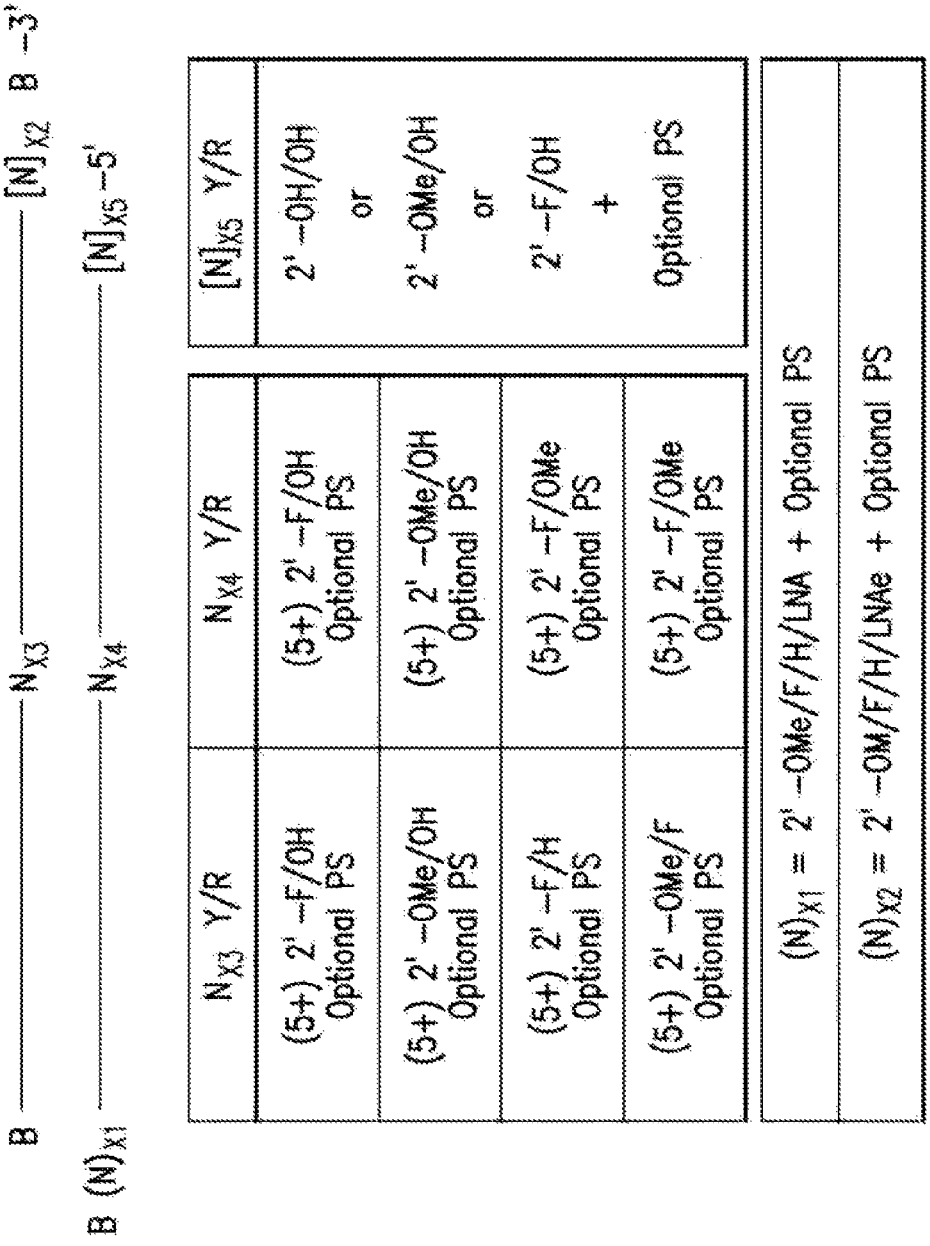
FIG. 1



N = Nucleotide (optionally non-nucleotide)
X1 and X2 are independently integers from 0 to 4
X3 is an integer from 15 to 30
X4 is an integer from 9 to 30
X5 is an integer from 0 to 6; sum of X4 and X5 is 15–30

Each (N) is independently a 2'–OMe, 2'–F, 2'–deoxy or LNA nucleotide or any combination thereof
Each N is independently a 2'–OMe, 2'–F, ribo–, or 2'–deoxy nucleotide or any combination thereof
Each [N] is independently a 2'–OMe, 2'–F, ribo–, or 2'–deoxy nucleotide or any combination thereof
B = an optional CAP
Optional phosphorothioates, *e.g.* between (N), (N); N, N; (N), N; or N, [N] or [N], [N] nucleotides

FIG.2



N_{X3} Y/R	N_{X4} Y/R	$[N]_{X5}$ Y/R
(5+) 2' –F/OH Optional PS	(5+) 2' –F/OH Optional PS	2' –OH/OH or 2' –OMe/OH or 2' –F/OH + Optional PS
(5+) 2' –OMe/OH Optional PS	(5+) 2' –OMe/OH Optional PS	
(5+) 2' –F/H Optional PS	(5+) 2' –F/OMe Optional PS	
(5+) 2' –OMe/F Optional PS	(5+) 2' –F/OMe Optional PS	

$(N)_{X1}$ = 2' –OMe/F/H/LNA + Optional PS

$(N)_{X2}$ = 2' –OM/F/H/LNAe + Optional PS

FIG. 3

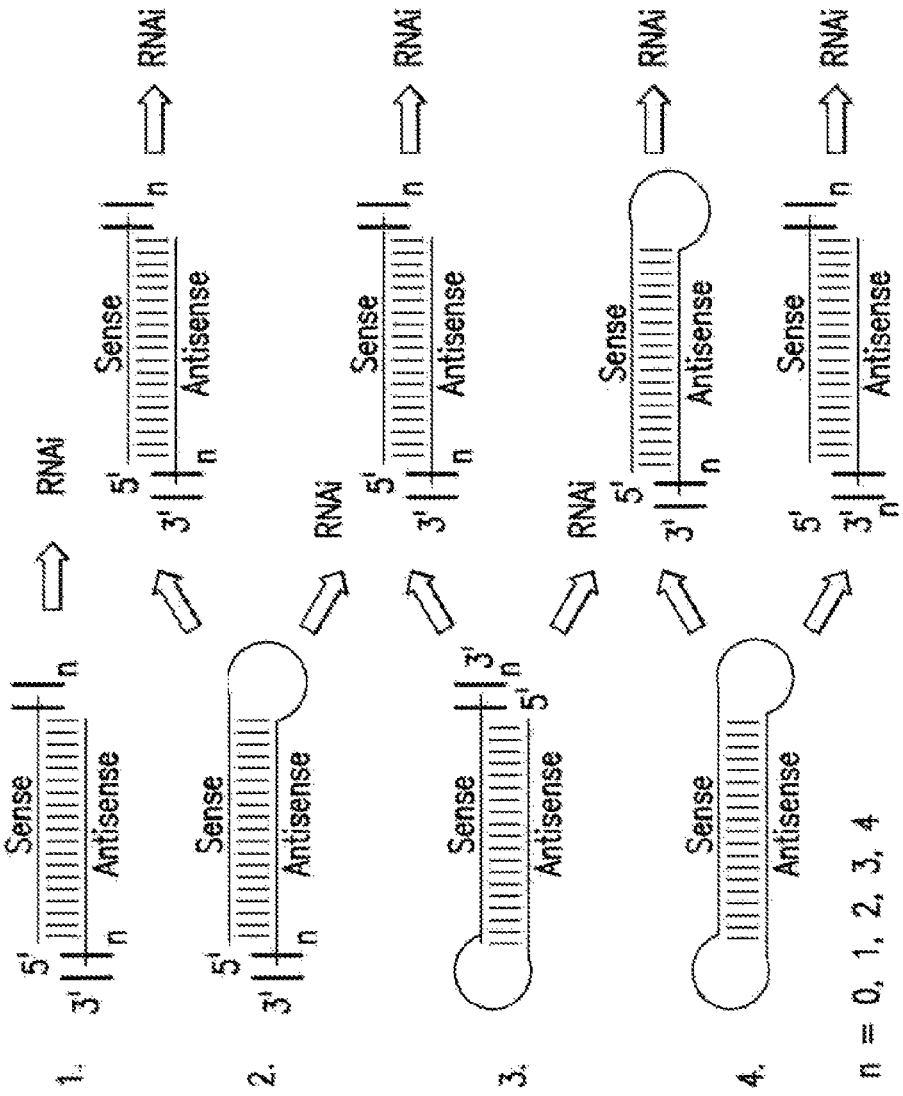


FIG.4A

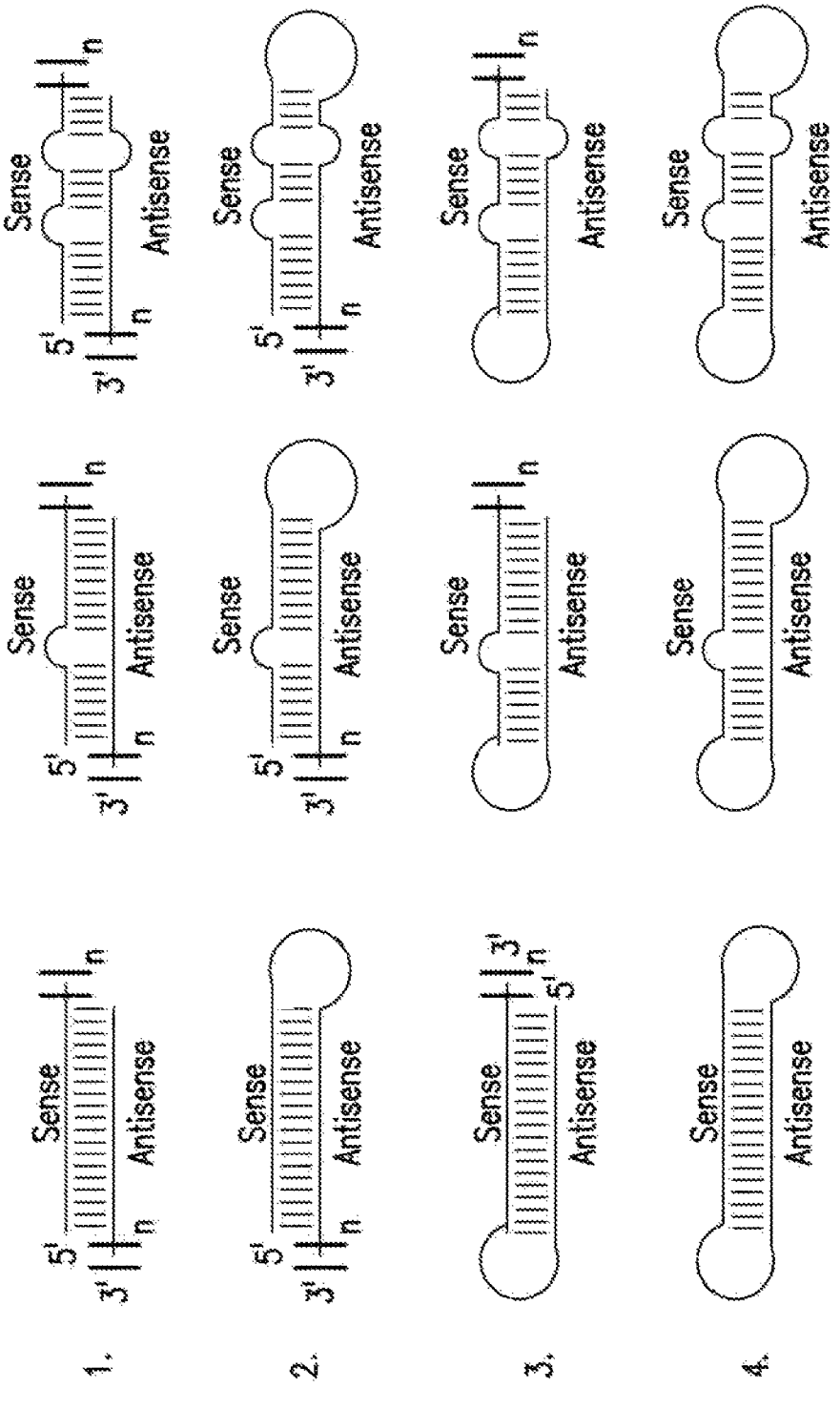
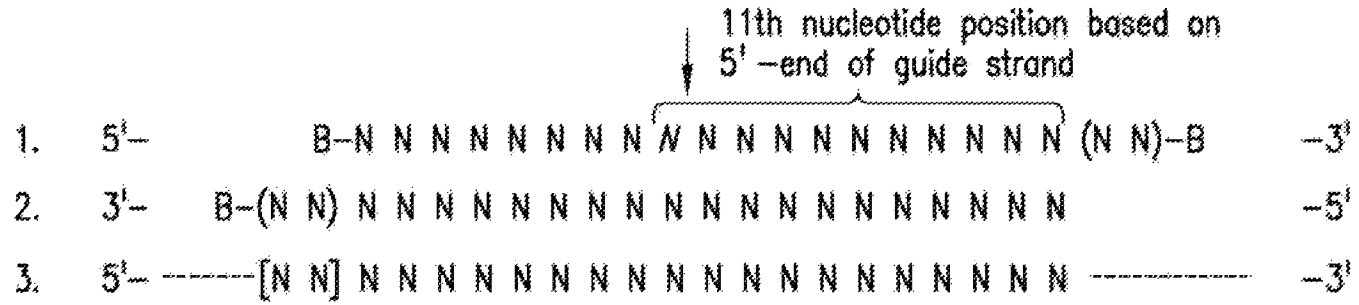


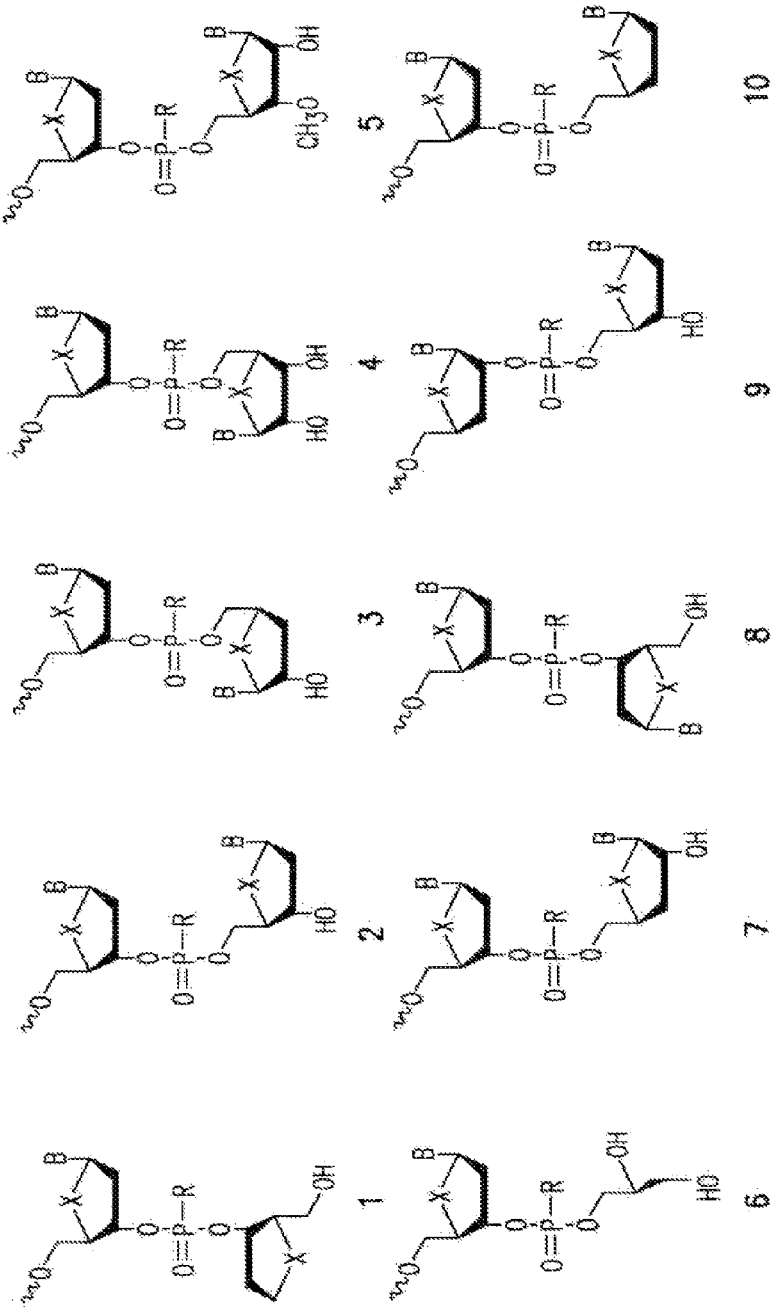
FIG.4B



1. = sense strand (passenger strand)
2. = antisense strand (guide strand)
3. = target polynucleotide sequence

The guide strand is complementary to the target sequence and the passenger strand is complementary to the guide strand.
Overhang nucleotides (NN) in the guide strand can be complementary to nucleotides [NN] in target sequence.
Overhang nucleotides (NN) in the passenger strand can comprise nucleotides [NN] in target sequence.
Position *N* of the passenger strand can comprise a ribonucleotide. For the representative 19 base pair 21 mer duplex shown, position *N* is 9 nucleotides in from the 3' end of the passenger strand. However, in duplexes of differing length, the position *N* is determined based on the 5'-end of the guide strand by counting 11 nucleotide positions in from the 5'-terminus of the guide strand and picking the corresponding base paired nucleotide in the passenger strand. Generally, cleavage by Ago2 takes place between positions 10 and 11 as indicated by the arrow.
Representative 2 nucleotide overhangs are shown, but can vary for example from 0 to about 4 nucleotides.
B = terminal cap which can be present or absent
This generalized motif can be applied to all Stab chemistries herein (see Table 6)

FIG.4C



R = O, S, NH2, N-dialkyl, NH-alkyl, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, or aralkyl
B = independently any nucleotide base, either naturally occurring or chemically modified, or optionally H (abasic)
X = O, S, NH, N-alkyl, alkyl, substituted alkyl, O-alkyl, S-alkyl, sulfone, etc.

FIG. 5

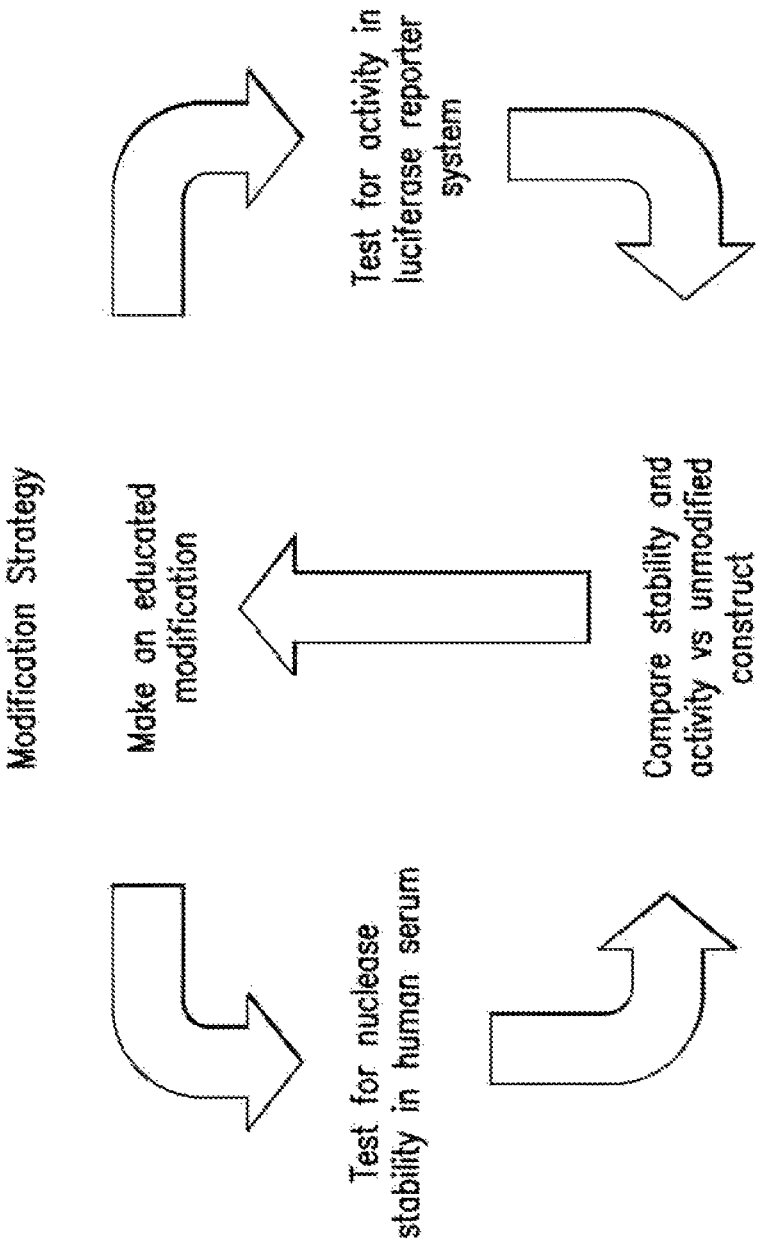

Modification Strategy
Make an educated modification
Test for nuclease stability in human serum
Compare stability and activity vs unmodified construct
Test for activity in luciferase reporter system

FIG.6

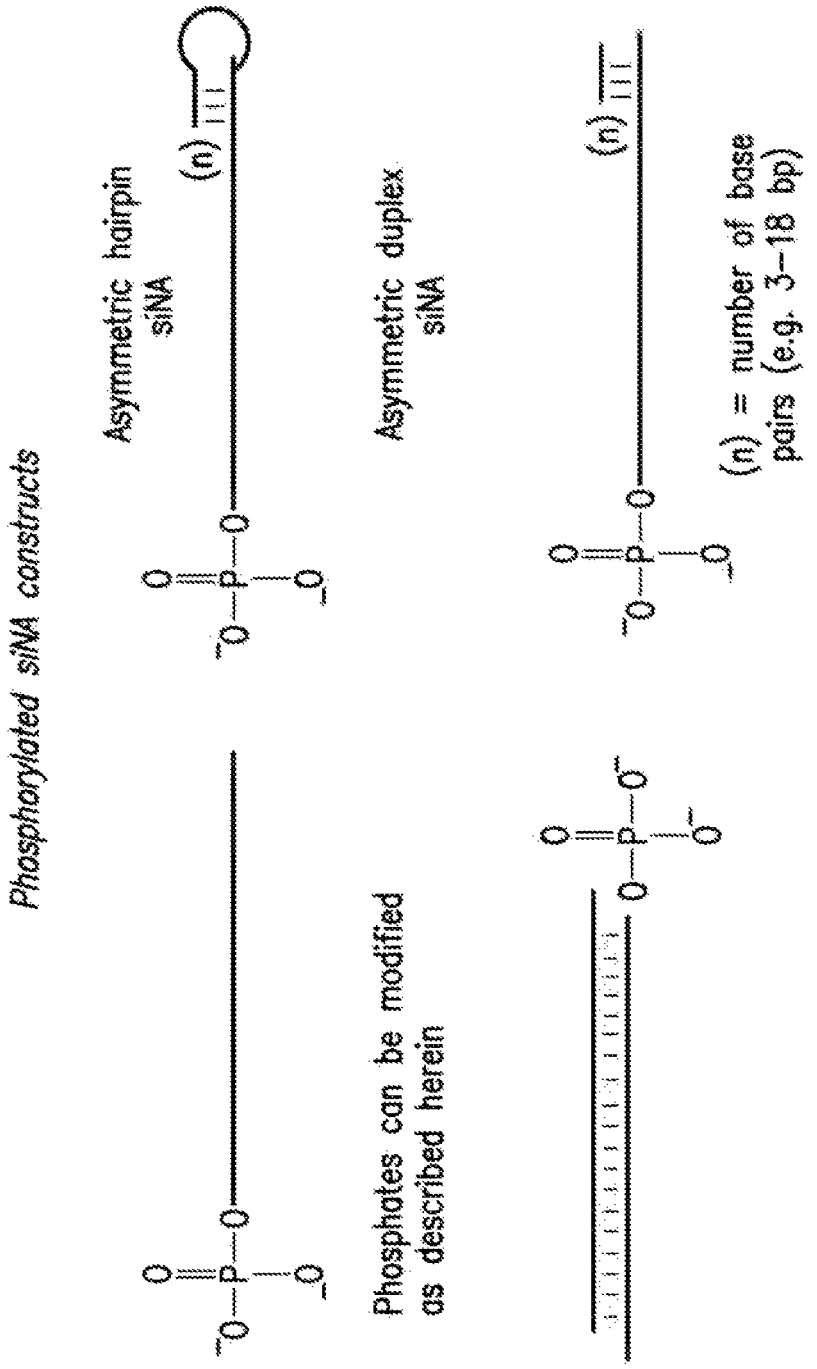

Phosphorylated siNA constructs
Asymmetric hairpin siNA
(n)
Asymmetric duplex siNA
(n)
Phosphates can be modified as described herein
(n) = number of base pairs (e.g. 3–18 bp)

FIG. 7

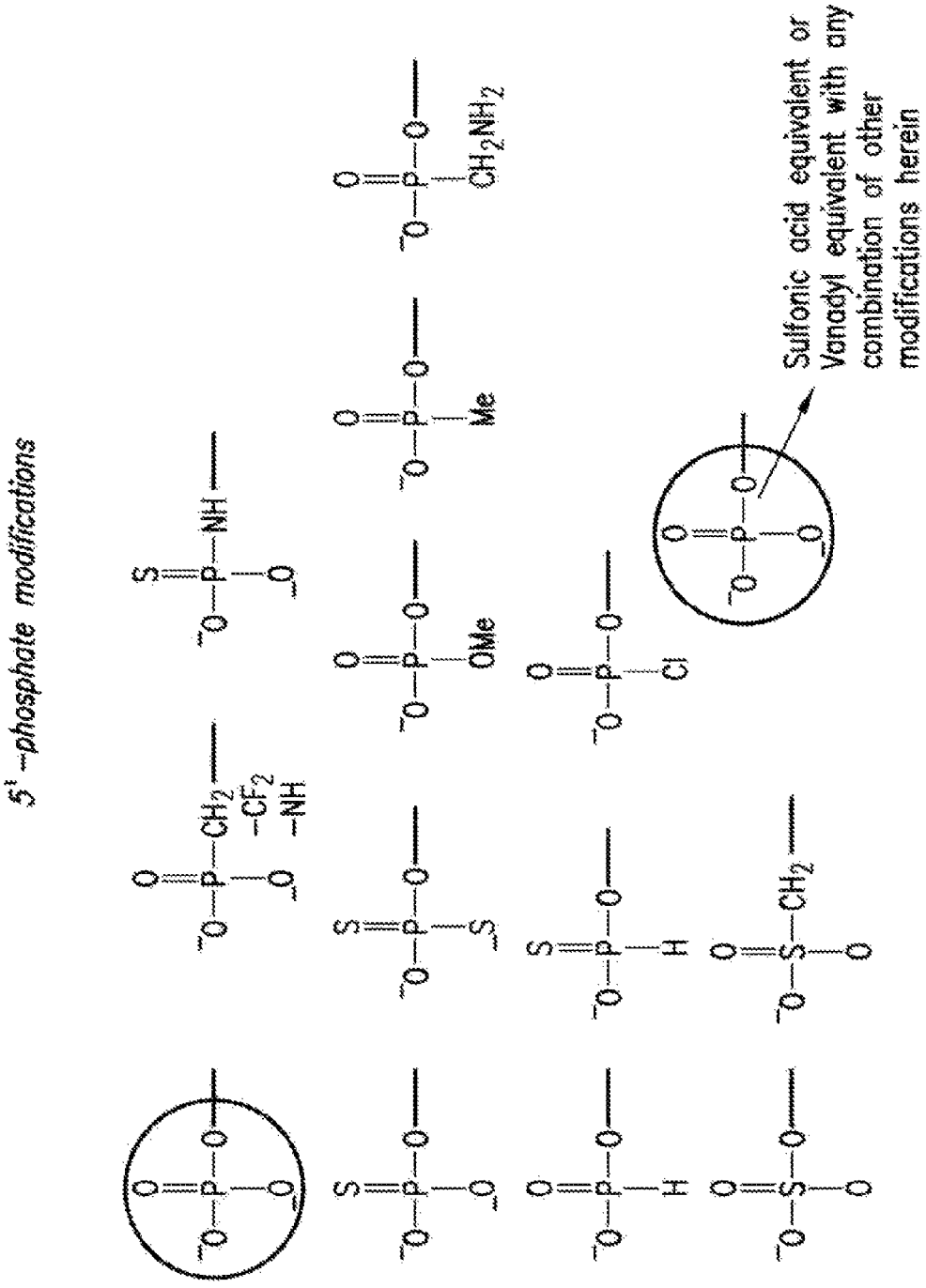
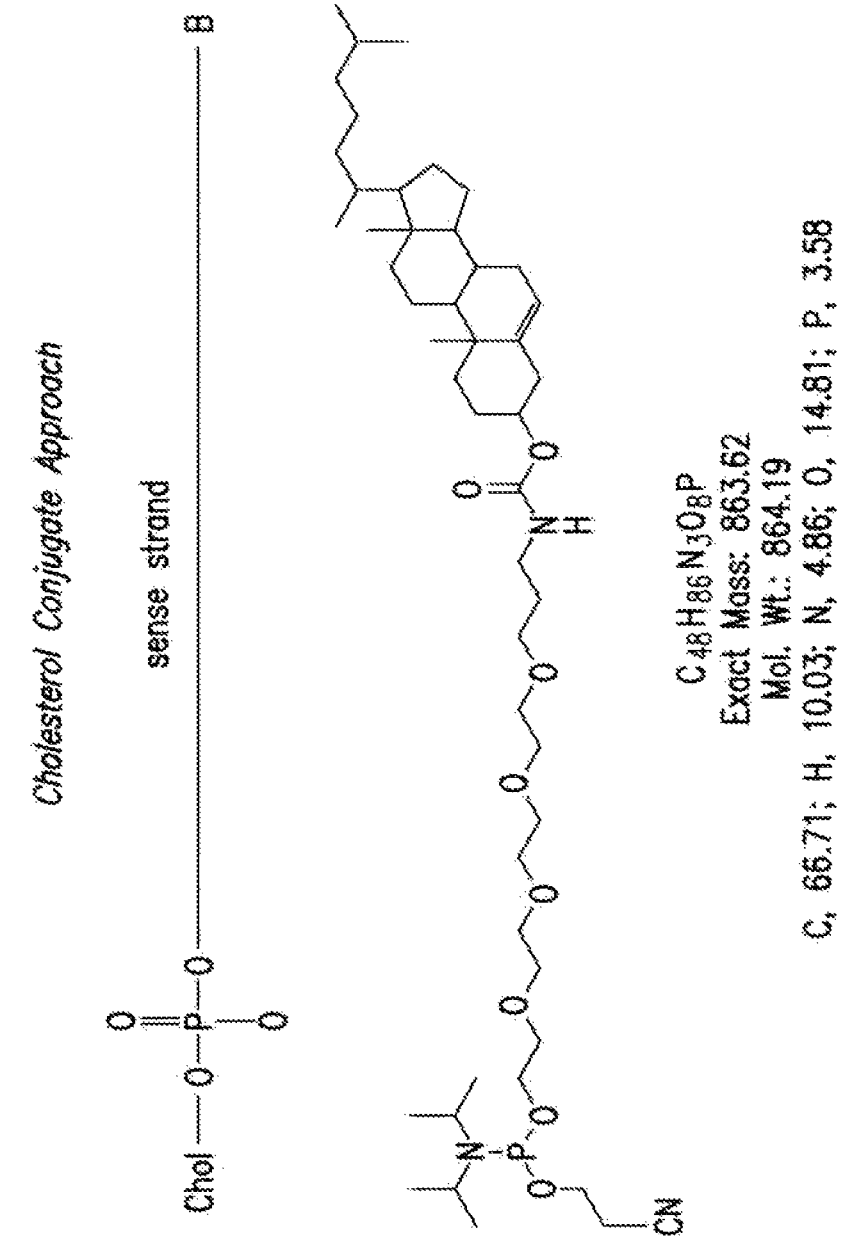

5'-phosphate modifications
Sulfonic acid equivalent or Vanadyl equivalent with any combination of other modifications herein

FIG.8



$C_{48}H_{86}N_3O_8P$
Exact Mass: 863.62
Mol. Wt.: 864.19
C, 66.71; H, 10.03; N, 4.86; O, 14.81; P, 3.58

FIG.9

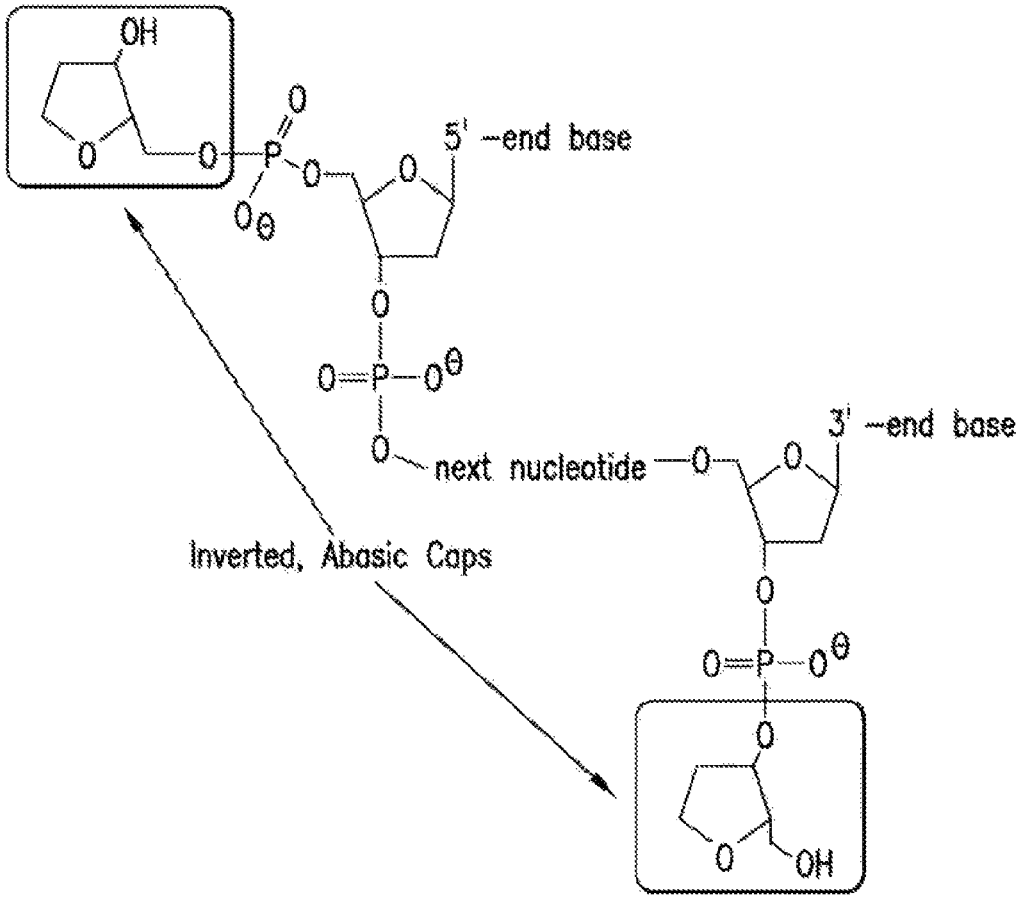

OH
O
O
P
O
O
O
5' -end base
O
O
O
P
O
O
next nucleotide
O
O
3' -end base
Inverted, Abasic Caps
O
O
P
O
O
O
O
OH

FIG. 10

RNA INTERFERENCE MEDIATED INHIBITION OF CATENIN (CADHERIN-ASSOCIATED PROTEIN), BETA 1 (CTNNB1) GENE EXPRESSION USING SHORT INTERFERING NUCLEIC ACID (SINA)

This application is a continuation of application Ser. No. 13/937,412, filed on Aug. 6, 2013, now U.S. Pat. No. 8,835,623, issued on Sept. 16, 2014, which is a continuation of application Ser. No. 13/813,465 filed on Jan. 31, 2013, now U.S. Pat. No. 8,518,907, issued on Aug. 27, 2013, which is a 35 U.S.C. § 371 National Stage filing of International Application No. PCT/US2011/046178, filed on Aug. 2, 2011, which claims the benefit of and priority to U.S. Provisional Patent Application Ser. No. 61/370,064, filed on Aug. 2, 2010. The entire contents of each of the foregoing patent application are incorporated herein by reference.

SEQUENCE LISTING

The sequence listing submitted via EFS, in compliance with 37 CFR §1.52(e)(5), is incorporated herein by reference. The sequence listing text file submitted via EFS contains the file "SIRONC00000USCNT-SEQLIST-27 JUN.2013", created on Jun. 27, 2013, which is 2,174,154 bytes in size.

BACKGROUND OF THE INVENTION

Beta catenin (also known as cadherin-associated protein and β-catenin), is a member of the catenin family of cytosolic proteins, β-catenin is encoded by the CTNNB1 gene.

β-catenin is a pivotal player in the Wnt/Wg signaling pathway, mediators of several developmental processes. In the absence of Wnt, glycogen synthase kinase 3 (GSK-3β), a serine/threonine protein kinase constitutively phosphorylates the β-catenin protein. When Wnt is present and binds to any of the family members of the frizzled receptors (Fz), an intracellular signaling protein known as dishevelled (Dsh) is recruited to the membrane and phosphorylated. GSK-3β is inhibited by the activation of Dsh. As a result, β-catenin levels increase in the cytosol and are translocated into the nucleus to perform a variety of functions. β-catenin acts together with the transcription factors TCF and LEF to activate specific target genes involved in different processes.

β-catenin undergoes phosphorylation upon growth factor stimulation resulting in reduced cell adhesion, thereby functioning as a component of adherin junctions which are multiprotein complexes that mediate cell adhesion, cell-cell communication and cytoskeletal anchoring. (Willert et al., 1998, *Curr. Opin. Genet. Dev.* 8:95-102).

Thompson et al. suggest that β-catenin plays an important role in various aspects of liver biology including liver development (both embryonic and postnatal), liver regeneration following partial hepatectomy, hepatocyte growth factor (HGF)-induced hepatomegaly, liver zonation, and pathogenesis of liver cancer. (Thompson M D., 2007, *Hepatology* May; 45(5):1298-305).

Wang et al. (2008) have shown that β-catenin can function as an oncogene. (Wang et al., 2008, *Cancer Epidemiol. Biomarkers Prev.* 17 (8):2101-8). In patients with basal cell carcinoma an increased level in β-catenin is present and leads to the increase in proliferation of related tumors. Mutations in the β-catenin gene are a cause of colorectal cancer (CRC), pilomatrixoma (PTR), medulloblastoma (MDB), hepatoblastoma, and ovarian cancer.

The role of β-catenin in the development of colorectal cancer has been shown to be regulated by the expression product of the APC (adenomatous polyposis of the colon) gene, a tumor suppressor. (Korinek et al., Science, 1997, 275:1784-1787; Morin et al., Science, 1997, 275:1787-1790). The APC protein normally binds β-catenin in conjunction with TCF/LEF forming a transcription factor complex. Morin et al. (Morin et al., Science, 1997, 275:1787-1790) report that APC protein down-regulates the transcriptional activation mediated by β-catenin and Tcf-4 in colon cancer. Their results indicated that the regulation of β-catenin is critical to APC's tumor suppressive effect and that this regulation can be circumvented by mutations in either APC or β-catenin.

Mutations in the β-catenin gene are either truncations that lead to deletion of part of the N-terminus of β-catenin, or point mutations that affect the serine and threonine residues that are targeted by GSK3α/β or CKIα. These mutant β-catenin proteins are refractory to phosphorylation and thus escape proteasomal degradations. Consequently, β-catenin accumulates within affected cells. Stabilized and nuclear-localized β-catenin is a hallmark of nearly all cases of colon cancer. (Clevers, H., 2006, *Cell* 127:469-480). Morin et al. demonstrated that mutations of β-catenin that altered phosphorylation sites rendered the cells insensitive to APC-mediated down-regulation of β-catenin and that this disrupted mechanism was critical to colorectal tumorigenesis. (Morin et al., 1997, *Science* 275:1787-1790).

Other studies also report on the detection of mutations in β-catenin in various cancer cell lines (see e.g., Chan et al., 1999, *Nature Genet.* 21:410-413; Blaker et al., 1999, *Genes Chromosomes Cancer* 25:399-402; Sagae et al., 1999, *Jpn. J. Cancer Res.* 90:510-515; Wang et al., 2008, *Cancer Epidemiol. Biomarkers Prev.* 17(8):2101-8). Additionally, abnormally high amounts of β-catenin have also been found in melanoma cell lines (see e.g., Rubinfeld et al., 1997, *Science,* 275:1790-1792).

Likewise other cancers, such as hepatocellular carcinoma (HCC), have also been associated with the Wnt/beta-catenin pathway. HCC is a complex and heterogeneous disease accounting for more than 660,000 new cases per year worldwide. Multiple reports have shown that Wnt signaling components are activated in human HCC patients. Activated Wnt signaling and nuclear beta-catenin correlate with recurrence of disease and poor prognosis (Takigawa et al. 2008, *Curr Drug Targets* November; 9 (11):1013-24). Elevated nuclear beta-catenin staining has been documented in 17-66% of HCC patients (Zulehner et al. 2010, *Am J Pathol.* January; 176 (1):472-81; Yu et al. 2009, *J Hepatol.* May; 50 (5):948-57). Merck's internal dataset on ~300 HCC patient tumors generated in collaboration with the Hong Kong University indicates Wnt signaling components are activated in 50% of HCC patients. External data have shown activating beta-catenin mutations in 13-40% of HCC patients, while inactivating Axin 1 or 2 mutations were present in ~10% of HCC patients (Lee et al. 2006, *Frontiers in Bioscience* May 1; 11:1901-1915).

Preclinical studies provide evidence that activation of the Wnt/beta-catenin pathway is important in the generation and maintenance of HCC. Liver-targeted disruption of APC in mice activates beta-catenin signaling and leads to the formation of HCC (Colnot et al. 2004, *Proc Natl Acad Sci USA* December 7; 101 (49):17216-21). Although overexpression of a beta-catenin mutant lacking the GSK-3beta phosphorylation sites alone is not sufficient for hepatocarcinogenesis (Harada et al. 2002, *Cancer Res.* April 1; 62 (7):1971-7.), overexpression of tumorigenic mutant beta-catenin has been

shown to make mice susceptible to HCC induced by DEN (diethylnitrosamine), a known carcinogen (Nejak-Bowen et al. 2010, *Hepatology* 2010 May; 51 (5): 1603-13. Interestingly, 95% of HCC tumors initiated by overexpression of the human Met receptor in mice (Tre-Met transgenic mouse model) harbor beta-catenin activating mutations (Tward et al. 2007, *Proc Natl Acad Sci USA*. September 11; 104 (37): 14771-6). This finding reflects the human disease and suggests that the Wnt pathway cooperates with Met signaling during hepatocarcinogenesis. High rates of beta-catenin activating mutations are also found in other transgenic mouse models for HCC (16% beta-catenin mutations in FGF19, 55% in c-Myc and 41% in H-Ras transgenic mice) (Nicholes et al. 2002, *Am J Pathol*. June; 160 (6):2295-307 de la Coste et al. 1998, *Proc Natl Acad Sci USA*. July 21; 95 (15):8847-51).

Preclinical studies have also shown that beta-catenin is a valid target for HCC. Beta-catenin siRNAs inhibit proliferation and viability of human HCC cell lines (Zeng et al. 2007). Similarly, treatment of human HCC cell lines with an anti-Wnt-1 antibody or TCF4/beta-catenin antagonists induce apoptosis, reduction of c-Myc, cyclin D1 and survivin expression as well as suppress tumor growth in vivo (Wei et al. 2009, *Mol Cancer* September 24; 8:76; Wei et al. 2010, *Int J Cancer*. May 15; 126 (10):2426-36, 2010).

Hepatocellular carcinoma (HCC) is a common and aggressive cancer for which effective therapies are lacking. The Wnt/beta-catenin pathway is activated in a high proportion of HCC cases (~50%), frequently owing to mutations in beta-catenin (i.e. CTNNB1) or in the beta-catenin destruction complex (e.g. Axin1). Moreover, the Wnt pathway as a target has proven to be challenging and is currently undruggable by small molecule inhibitors, making beta-catenin an attractive target for an RNAi-based therapeutic approach (Llovet et al. 2008, *Hepatology* October; 48: 1312-1327).

Alteration of gene expression, specifically CTNNB1 gene expression, through RNA interference (hereinafter "RNAi") is one approach for meeting this need. RNAi is induced by short single-stranded RNA ("ssRNA") or double-stranded RNA ("dsRNA") molecules. The short dsRNA molecules, called "short interfering nucleic acids ("siNA")" or "short interfering RNA" or "siRNA" or "RNAi inhibitors" silence the expression of messenger RNAs ("mRNAs") that share sequence homology to the siNA. This can occur via cleavage of the mRNA mediated by an endonuclease complex containing a siNA, commonly referred to as an RNA-induced silencing complex (RISC). Cleavage of the target RNA typically takes place in the middle of the region complementary to the guide sequence of the siNA duplex (Elbashir et al., 2001, *Genes Dev.,* 15:188). In addition, RNA interference can also involve small RNA (e.g., micro-RNA or miRNA) mediated gene silencing, presumably through cellular mechanisms that either inhibit translation or that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science,* 297:1818-1819; Volpe et al., 2002, *Science,* 297-1833-1837; Jenuwein, 2002, *Science,* 297:2215-2218; and Hall et al., 2002, *Science,* 297:2232-2237). Despite significant advances in the field of RNAi, there remains a need for agents that can inhibit CTNNB1 gene expression and that can treat disease associated with CTNNB1 expression such as cancer.

SUMMARY OF THE INVENTION

The invention provides a solution to the problem of treating diseases that respond to the modulation of the CTNNB1 gene expression using novel short interfering nucleic acid (siNA) molecules to modulate CTNNB1 expression.

The present invention provides compounds, compositions, and methods useful for modulating the expression of CTNNB1 genes, specifically those CTNNB1 genes associated with cancer and for treating such conditions by RNA interference (RNAi) using small nucleic acid molecules.

In particular, the instant invention features small nucleic acid molecules, i.e., short interfering nucleic acid (siNA) molecules including, but not limited to, short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA) and circular RNA molecules and methods used to modulate the expression of CTNNB1 genes and/or other genes involved in pathways of CTNNB1 gene expression and/or activity.

In one aspect, the invention provides double-stranded short interfering nucleic acid (siNA) molecules that inhibit the expression of a CTNNB1 gene in a cell or mammal, wherein the double-stranded siNAs comprise a sense and an antisense stand. The antisense strand comprises a sequence that is complementary to at least a part of an RNA associated with the expression of the CTNNB1 gene. The sense strand comprises a sequence that is complementary to the antisense strand. In various embodiments, at least one strand comprises at least a 15 nucleotide sequence selected from the group of sequences consisting of SEQ ID NOS:1-6374. In certain embodiments, the antisense strand comprises at least 15, 16, 17, 18, or 19 nucleotides having sequence complementarity to a target sequence set forth in Table 1a. In other and/or in the same embodiments, the antisense strand comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of one of the antisense sequences set forth in Table 1b. In some embodiments, the sense strand comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of a sense strand sequence as set forth in Table 1b.

In certain embodiments of this aspect of the invention, double-stranded short interfering nucleic acid (siNA) molecules are provided wherein the antisense stand comprises a modified sequence as set forth in Table 1c that has sequence complementarity to a target sequence of the invention. In some embodiments, the sense strand also comprises a modified sequence as set forth in Table 1c.

In certain embodiments, the present invention provides a double-stranded short interfering nucleic acid (siNA) molecule that modulates the expression of CTNNB1, wherein the siNA comprises a sense strand and an antisense strand; each strand is independently 15 to 30 nucleotides in length; and the antisense strand comprises at least 15, 16, 17, 18, or 19 nucleotides having sequence complementary to any of:

(SEQ ID NO: 5)
5'-CUGUUGGAUUGAUUCGAAA-3';

(SEQ ID NO: 194)
5'-ACGACUAGUUCAGUUGCUU-3';

(SEQ ID NO: 196)
5'-GGAUGAUCCUAGCUAUCGU-3';
or

(SEQ ID NO: 151)
5'-CCAGGAUGAUCCUAGCUAU-3'.

In some embodiments of the invention, the antisense strand of a siNA molecule comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of:

(SEQ ID NO: 4918)
5'-UUUCGAAUCAAUCCAACAG-3';

(SEQ ID NO: 5107)
5'-AAGCAACUGAACUAGUCGU-3';

(SEQ ID NO: 5109)
5'-ACGAUAGCUAGGAUCAUCC-3';
or

(SEQ ID NO: 5064)
5'-AUAGCUAGGAUCAUCCUGG-3';

In some embodiments, the sense strand of a siNA molecule of the invention comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of:

(SEQ ID NO: 5)
5'-CUGUUGGAUUGAUUCGAAA-3';

(SEQ ID NO: 194)
5'-ACGACUAGUUCAGUUGCUU-3';

(SEQ ID NO: 196)
5'-GGAUGAUCCUAGCUAUCGU-3';
or

(SEQ ID NO: 151)
5'-CCAGGAUGAUCCUAGCUAU-3'.

In some embodiments, a siNA molecule of the invention comprises any of:

(SEQ ID NO: 5)
5'-CUGUUGGAUUGAUUCGAAA-3'
and

(SEQ ID NO: 4918)
5'-UUUCGAAUCAAUCCAACAG-3';
or

(SEQ ID NO: 194)
5'-ACGACUAGUUCAGUUGCUU-3'
and

(SEQ ID NO: 5107)
5'-AAGCAACUGAACUAGUCGU-3';
or

(SEQ ID NO: 196)
5'-GGAUGAUCCUAGCUAUCGU-3'
and

(SEQ ID NO: 5109)
5'-ACGAUAGCUAGGAUCAUCC-3';
or

(SEQ ID NO: 151)
5'-CCAGGAUGAUCCUAGCUAU-3'
and

(SEQ ID NO: 5064)
5'-AUAGCUAGGAUCAUCCUGG-3'.

In some embodiments, a siNA molecule of the invention comprises SEQ ID NOS: 6372 AND 6374.

In some embodiments, a siNA molecule of the invention comprises SEQ ID NOS: 6370 AND 6369.

In some embodiments, a siNA molecule of the invention comprises SEQ ID NOS: 2021 AND 2068.

In some embodiments, a siNA molecule of the invention comprises SEQ ID NOS: 6372 AND 6373.

In some embodiments, a siNA molecule of the invention comprises SEQ ID NOS: 2147 and 6368

In some embodiments, the invention features a composition comprising:

(a) a double-stranded short interfering nucleic acid (siNA) of the invention;
(b) a cationic lipid compound having any of compound numbers 1-46 or any combination thereof;
(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

In some embodiments, the invention features a composition comprising:
(a) a double-stranded short interfering nucleic acid (siNA) of the invention;
(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;
(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

In some embodiments, the invention features a composition comprising:
(a) a double-stranded short interfering nucleic acid (siNA) having SEQ ID NOS: 6372 and 6374;
(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;
(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

In some embodiments, the invention features a composition comprising:
(a) a double-stranded short interfering nucleic acid (siNA) having SEQ ID NOS: 6370 and 6369;
(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;
(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

In some embodiments, the invention features a composition comprising:
(a) a double-stranded short interfering nucleic acid (siNA) having SEQ ID NOS: 2021 and 2068;
(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;
(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

In some embodiments, the invention features a composition comprising:
(a) a double-stranded short interfering nucleic acid (siNA) having SEQ ID NOS: 6372 and 6373;
(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;
(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

In some embodiments, the invention features a composition comprising:
(a) a double-stranded short interfering nucleic acid (siNA) having SEQ ID NOS: 2147 and 6368;
(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;
(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

In some embodiments, a composition of the invention comprises any Cationic Lipid having any of the compound numbers 1-46 in the following molar ratios:
Cationic Lipid/Cholesterol/PEG-DMG 56.6/38/5.4;
Cationic Lipid/Cholesterol/PEG-DMG 60/38/2;
Cationic Lipid/Cholesterol/PEG-DMG 67.3/29/3.7;

Cationic Lipid/Cholesterol/PEG-DMG 49.3/47/3.7;
Cationic Lipid/Cholesterol/PEG-DMG 50.3/44.3/5.4;
Cationic Lipid/Cholesterol/PEG-C-DMA/DSPC 40/48/2/10;
Cationic Lipid/Cholesterol/PEG-DMG/DSPC 40/48/2/10; and
Cationic Lipid/Cholesterol/PEG-DMG/DSPC 58/30/2/10.

In some embodiments, a composition of the invention comprises (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine, cholesterol, DSPC, and PEG-DMG, having a molar ration of 50:30:10:2 respectively.

In some embodiments, a composition of the invention further comprises a cryo-protectant. In some embodiments, the cryoprotectant is Sucrose, Trehalose, Raffinose, Stachyose, Verbascose, Mannitol, Glucose, Lactose, Maltose, Maltotriose-heptaose, Dextran, Hydroxyethyl Starch, Insulin, Sorbitol, Glycerol, Arginine, Histidine, Lysine, Proline, Dimethylsulfoxide or any combination thereof. In some embodiments, the cryoprotectant is Sucrose. In some embodiments, the cryoprotectant is Trehalose. In some embodiments, the cryoprotectant is a combination of Sucrose and Trehalose.

In some embodiments of the invention, all of the nucleotides of siNAs of the invention are modified. In other embodiments, one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) of the nucleotide positions independently in either one or both strands of an siNA molecule are modified. Modifications include nucleic acid sugar modifications, base modifications, backbone (internucleotide linkage) modifications, non-nucleotide modifications, and/or any combination thereof. In certain instances, purine and pyrimidine nucleotides are differentially modified. For example, purine and pyrimidine nucleotides can be differentially modified at the 2'-sugar position (i.e., at least one purine has a different modification from at lease one pyrimidine in the same or different strand at the 2'-sugar position). In certain instances the purines are unmodified in one or both strands, while the pyrimidines in one or both strands are modified. In certain other instances, the pyrimidines are unmodified in one or both strands, while the purines in one or both strands are modified. In some instances, at least one modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide, a 2'-deoxy nucleotide, or a 2'-O-alkyl nucleotide. In some instances, at least 5 or more of the pyrimidine nucleotides in one or both stands are either all 2'-deoxy-2'-fluoro or all 2'-O-methyl pyrimidine nucleotides. In some instances, at least 5 or more of the purine nucleotides in one or both stands are either all 2'-deoxy-2'-fluoro or all 2'-O-methyl purine nucleotides. In certain instances, wherein the siNA molecules comprise one or more modifications as described herein, the nucleotides at positions 1, 2, and 3 at the 5' end of the guide (antisense) strand are unmodified.

In certain embodiments, the siNA molecules of the invention have 3' overhangs of one, two, three, or four nucleotide(s) on one or both of the strands. In other embodiments, the siNA molecules lack overhangs (i.e., have blunt ends). Preferably, the siNA molecule has 3' overhangs of two nucleotides on both the sense and antisense strands. The overhangs can be modified or unmodified. Examples of modified nucleotides in the overhangs include, but are not limited to, 2'-O-alkyl nucleotides, 2'-deoxy-2'-fluoro nucleotides, locked nucleic acid (LNA) nucleotides, or 2'-deoxy nucleotides. The overhang nucleotides in the antisense strand can comprise nucleotides that are complementary to nucleotides in the CTNNB1 target sequence. Likewise, the overhangs in the sense stand can comprise nucleotides that are in the CTNNB1 target sequence. In certain instances, the siNA molecules of the invention have two 3' overhang nucleotides on the sense stand that are 2'-deoxy nucleotides. In other instances, the siNA molecules of the invention have two 3' overhang nucleotides that are 2'-O-alkyl (e.g., 2'-O-methyl) nucleotides on both the antisense stand and on the sense stand. In certain embodiments, the 2'-O-alkyl nucleotides are 2'-O-methyl uridine nucleotides. In certain instances, the overhangs also comprise one or more phosphorothioate linkages between nucleotides of the overhang.

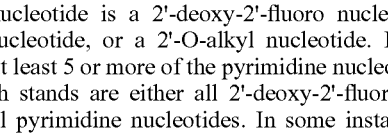
In some embodiments, the siNA molecules of the invention have caps (also referred to herein as "terminal caps." The cap can be present at the 5'-terminus (5'-cap) or at the 3'-terminus (3'-cap) or can be present on both termini, such as at the 5' and 3' termini of the sense strand of the siNA.

In some embodiments, the siNA molecules of the invention are phosphorylated at the 5' end of the antisense strand. The phosphate group can be a phosphate, a diphosphate or a triphosphate.

The siNA molecules of the invention when double stranded can be symmetric or asymmetric. Each strand of these double stranded siNAs independently can range in nucleotide length between 3 and 30 nucleotides. Generally, each strand of the siNA molecules of the invention is about 15 to 30 (i.e., about 19, 20, 21, 22, 23 or 24) nucleotides in length.

The siNa molecules of the invention, which are double stranded or have a duplex structure, independently comprise about 3 to about 30 (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs. Generally, the duplex structure of siNAs of the invention is between 15 and 30, more generally between 18 and 25, yet more generally between 19 and 24, and most generally between 19 and 21 base pairs in length.

In certain embodiments, double-stranded short interfering nucleic acid (siNA) molecules are provided, wherein the molecule has a sense strand and an antisense strand and comprises formula (A):



(A)

wherein, the upper strand is the sense strand and the lower strand is the antisense strand of the double-stranded nucleic acid molecule; wherein the antisense strand comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of SEQ ID NO: 4918, SEQ ID NO: 5107, SEQ ID NO: 5109, or SEQ ID NO: 5064, and the sense strand comprises a sequence having complementarity to the antisense strand:

each N is independently a nucleotide which is unmodified or chemically modified or a non-nucleotide;

each B is a terminal cap that is present or absent;

(N) represents overhanging nucleotides, each of which is independently unmodified or chemically modified;

[N] represents nucleotides that are ribonucleotides;

X1 and X2 are independently integers from 0 to 4;

X3 is an integer from 15 to 30;

X4 is an integer from 9 to 30; and

X5 is an integer from 0 to 6, provided that the sum of X4 and X5 is 15-30.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) of formula (A); wherein

(a) one or more pyrimidine nucleotides in N_{X4} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-alkyl nucleotides, 2'-deoxy nucleotides, ribonucleotides or any combinations thereof;

(b) one or more purine nucleotides in N_{X4} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-alkyl nucleotides, 2'-deoxy nucleotides, ribonucleotides, or any combination thereof;

(c) one or more pyrimidine nucleotides in N_{X3} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-alkyl nucleotides, 2'-deoxy nucleotides, ribonucleotides, or any combination thereof; and

(d) one or more purine nucleotides in N_{X3} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-alkyl nucleotides, 2'-deoxy nucleotides, ribonucleotides.

The present invention further provides compositions comprising the double-stranded nucleic acid molecules described herein with optionally a pharmaceutically acceptable carrier or diluent.

The administration of the composition can be carried out by known methods, wherein the nucleic acid is introduced into a desired target cell in vitro or in vivo.

Commonly used techniques for introduction of the nucleic acid molecules of the invention into cells, tissues, and organisms include the use of various carrier systems, reagents and vectors. Non-limiting examples of such carrier systems suitable for use in the present invention include conjugates, nucleic-acid-lipid particles, lipid nanoparticles (LNP), liposomes, lipoplexes, micelles, virosomes, virus like particles (VLP), nucleic acid complexes, and mixtures thereof.

The compositions of the invention can be in the form of an aerosol, dispersion, solution (e.g., an injectable solution), a cream, ointment, tablet, powder, suspension of the like. These compositions may be administered in any suitable way, e.g. orally, sublingually, buccally, parenterally, nasally, or topcially. In some embodiments, the compositions are aerosolized and delivered via inhalation.

The molecules and compositions of the present invention have utility over a broad range of therapeutic applications. Accordingly another aspect of this invention relates to the use of the compounds and compositions of the invention in treating a subject. The invention thus provides a method for treating a subject, such as a human, suffering from a condition which is mediated by the action, or by the loss of action, of CTNNB1, wherein the method comprises administering to the subject an effective amount of a double-stranded short interfering nucleic acid (siNA) molecule of the invention. In certain embodiments, the condition is cancer.

These and other aspects of the invention will be apparent upon reference to the following detailed description and attached figures. Moreover, it is contemplated that any method or composition described herein can be implemented with respect to any other method or composition described herein and that different embodiments may be combined.

Additionally, patents, patent applications, and other documents are cited throughout the specification to describe and more specifically set forth various aspects of this invention. Each of these references cited herein is hereby incorporated by reference in its entirety, including the drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for example, viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directly into a cell by appropriate means. An active siNA complex forms that recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

FIG. **2** shows non-limiting examples of chemically modified siNA constructs of the present invention using a generalized structure of a representative siNA duplex. The specific modifications shown in the figure can be utilized alone or in combination with other modifications of the figure, in addition to other modifications and features described herein with reference to any siNA molecule of the invention. In the figure, N stands for any nucleotide or optionally a non-nucleotide as described here. The upper strand, having B-N_{X3}-$(N)_{X2}$-B-3' is the sense (or passenger) strand of the siNA, whereas the lower strand, having B$(N)_{X1}$-N_{X4}-$[N]_{X3}$-5' is the antisense (or guide) strand of the siNA. Nucleotides (or optional non-nucleotides) of internal portions of the sense strand are designated N_{X3} and nucleotides (or optional non-nucleotides) of internal portions of the antisense strand are designated N_{X4}. Nucleotides (or optional non-nucleotides) of the internal portions are generally base paired between the two strands, but can optionally lack base pairing (e.g. have mismatches or gaps) in some embodiments. Nucleotides (or optional non-nucleotides) of overhang regions are designated by parenthesis (N). Nucleotides of the 5'-terminal portion of the antisense strand are designated [N]. Terminal caps are optionally present at the 5' and/or 3' end of the sense strand and further optionally present at the 3'-end of the antisense strand. Generally, each strand can independently range from about 15 to about 30 nucleotides in length, but can vary depending on the presence of any overhand nucleotides. In certain embodiments, X1 and X2 are independently integers from 0 to 4; X3 is an integer from 15 to 30; X4 is an integer from 9 to 30; X5 is an integer from 0 to 6, provided that the sum of X4 and X5 is 15-30. Various modifications are shown for the nucleotides of the sense and antisense strands of the siNA constructs. The (N) overhang nucleotide positions can be chemically modified as described herein (e.g., 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-deoxy, LNA, universal bases etc.) and can be either derived from a corresponding target nucleic acid sequence or not. The constructs shown in the figure can also comprise phosphorothioate linkages as described herein. For example, phosphorothioate linkages can exist between any N, (N), and/or [N] positions. Such phosphorothioate incorporation can be utilized between purine "R" and pyrimidine "Y" positions, or for stabilization of pyrimidine linkages in general. Furthermore, although not depicted on the Figure, the constructs shown in the figure can optionally include a ribonucleotide at the 9^{th} position from the 5'-end of the sense strand or the 11^{th} position based on the 5'-end of

the guide strand by counting 11 nucleotide positions in from the 5'-terminus of the guide strand. Similarly, the antisense strand can include a ribonucleotide at the 14^{th} position form the 5'-end, or alternately can be selected or designed so that a 2'-O-alkyl nucleotide (e.g., a 2'-O-methyl purine) is not present at this position. Furthermore, although not shown in the Figure, the 5'-terminal position of the antisense strand can comprise a terminal phosphate group as described herein. The antisense strand generally comprises sequence complementary to any target nucleic acid sequence of the invention, such as those set forth in Table 1a herein.

FIG. **3** shows non-limiting examples of certain combinations of modifications applied to the representative siNA duplex described in FIG. **2**. The table shown below the representative structure provides specific combinations of $(N)_{X1}$. $(N)_{X2}$. N_{X3}. N_{X4}. and/or $[N]_{X5}$ nucleotide (and optional non-nucleotide) positions. For example, combinations of 5 or more (e.g., 5, 6, 7, 8, 9, or 10 or more) N_{X3} and 5 or more (e.g., 5, 6, 7, 8, 9, or 10 or more) N_{X4} pyrimidine "Y" and purine "R" nucleotides are specified, each of which can independently have specific $(N)_{X1}$. and/or $(N)_{X2}$. substitutions as shown in the figure, in addition to optional phosphorothioate substitutions. The 5'-terminal antisense strand [N] nucleotides are generally ribonucleotides, but can also be modified or unmodified depending on if they are purine "R" or pyrimidine "Y" nucleotides.

FIG. **4**A-C shows non-limiting examples of different siNA constructs of the invention. The criteria of the representative structures shown in FIGS. **2** and **3** can be applied to any of the structures shown in FIG. **4**A-C.

The examples shown in FIG. **4**A (constructs 1, 2, and 3) have 19 representative base pairs; however, different embodiments of the invention include any number of base pairs described herein. Bracketed regions represent nucleotide overhangs, for example, comprising about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides. Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 in vivo and/or in vitro. In another example, construct 3 can be used to generate construct 2 under the same principle wherein a linker is used to generate the active siNA construct 2 in vivo and/or in vitro, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 in vivo and/or in vitro. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use in vivo or in vitro and/or in vitro.

The examples shown in FIG. **4**B represent different variations of double-stranded nucleic acid molecule of the invention, such as microRNA, that can include overhangs, bulges, loops, and stem-loops resulting from partial complementarity. Such motifs having bulges, loops, and stem-loops are generally characteristics of miRNA. The bulges, loops, and stem-loops can result from any degree of partial complementarity, such as mismatches or bulges of about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more nucleotides in one or both strands of the double-stranded nucleic acid molecule of the invention.

The example shown in FIG. **4**C represents a model double-stranded nucleic acid molecule of the invention comprising a 19 base pair duplex of two 21 nucleotide sequences having dinucleotide 3'-overhangs. The top strand (1) represents the sense strand (passenger strand), the middle strand (2) represent the antisense (guide strand), and the lower strand (3) represents a target polynucleotide sequence. The dinucleotide overhangs (NN) can comprise a sequence derived from the target polynucleotide. For example, the 3'-(NN) sequence in the guide strand can be complementary to the 5'[NN] sequence of the target polynucleotide. In addition, the 5'-(NN) sequence of the passenger strand can comprise the same sequence as the 5'-[NN] sequence of the target polynucleotide sequence. In other embodiments, the overhangs (NN) are not derived from the target polynucleotide sequence, for example where the 3'-(NN) sequence in the guide strand are not complementary to the 5'-[NN] sequence of the target polynucleotide and the 5'-(NN) sequence of the passenger strand can comprise different sequence from the 5'-[NN] sequence of the target polynucleotide sequence. In additional embodiments, any (NN) nucleotides are chemically modified, e.g., as 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or other modifications herein. Furthermore, the passenger strand can comprise a ribonucleotide position N of the passenger strand. For the representative 19 base pair 21 mer duplex shown, position N can be 9 nucleotides in from the 3' end of the passenger strand. However, in duplexes of differing length, the position N is determined based on the 5'-end of the guide strand by counting 11 nucleotide positions in from the 5'-terminus of the guide strand and picking the corresponding base paired nucleotide in the passenger strand. Cleavage by Ago2 takes place between positions 10 and 11 as indicated by the arrow. In additional embodiments, there are two ribonucleotides, NN, at positions 10 and 11 based on the 5'-end of the guide strand by counting 10 and 11 nucleotide positions in from the 5'-terminus of the guide strand and picking the corresponding base paired nucleotides in the passenger strand.

FIG. **5** shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 5' and/or 3'-ends of siNA sequences of the invention, including (1) [3-3']-inverted deoxyribose; (2) deoxyribonucleotide; (3) [5'-3']-3'-deoxyribonucleotide; (4) [5'-3']-ribonucleotide; (5) [5'-3']-3'-O-methyl ribonucleotide; (6) 3'-glyceryl; (7) [3'-5']-3'-deoxyribonucleotide; (8) [3'-3']-deoxyribonucleotide; (9) [5'-2']-deoxyribonucleotide; and (10) [5'-3']-dideoxyribonucleotide (when X=O). In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different sugar and base nucleotide modifications as described herein.

FIG. **6** shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistant while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on educated design parameters (e.g. introducing 2'-modifications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct is tested in an appropriate system (e.g., human serum for nuclease resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example in a cell culture system such as a luciferase reporter assay and/or against endogenous mRNA). Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

FIG. **7** shows non-limiting examples of phosphorylated siNA molecules of the invention, including linear and duplex constructs and asymmetric derivatives thereof.

FIG. **8** shows non-limiting examples of chemically modified terminal phosphate groups of the invention.

FIG. **9** shows a non-limiting example of a cholesterol linked phosphoramidite that can be used to synthesize cholesterol conjugated siNA molecules of the invention. An example is shown with the cholesterol moiety linked to the 5'-end of the sense strand of an siNA molecule.

FIG. **10** depicts an embodiment of 5' and 3' inverted abasic cap linked to a nucleic acid strand.

DETAILED DESCRIPTION OF THE INVENTION

A. Terms and Definitions

The following terminology and definitions apply as used in the present application.

The term "abasic" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to sugar moieties lacking a nucleobase or having a hydrogen atom (H) or other non-nucleobase chemical groups in place of a nucleobase at the 1' position of the sugar moiety, see for example Adamic et al., U.S. Pat. No. 5,998,203. In one embodiment, an abasic moiety of the invention is a ribose, deoxyribose, or dideoxyribose sugar.

The term "acyclic nucleotide" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to any nucleotide having an acyclic ribose sugar, for example, where any of the ribose carbon/carbon or carbon/oxygen bonds are independently or in combination absent from the nucleotide.

The term "alkyl" as used herein refers to its meanings as is generally accepted in the art. The term generally refers to a saturated or unsaturated hydrocarbons, including straight-chain, branched-chain, alkenyl, alkynyl groups and cyclic groups, but excludes aromatic groups. Notwithstanding the foregoing, alkyl also refers to non-aromatic heterocyclic groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be susbstituted or unsubstituted. When substituted, the substituted group(s) is preferably, hydroxyl, halogen, cyano, C1-C4 alkoxy, =O, =S, NO_2. SH, NH_2. or NR_1R_2. where R_1 and R_2 independently are H or C1-C4 alkyl.

The phrase "agents that interfere with cell cycle checkpoints" refers to compounds that inhibit protein kinases that transduce cell cycle checkpoint signals, thereby sensitizing the cancer cell to DNA damaging agents.

The phrase "agents that interfere with receptor tyrosine kinases (RTKs)" refers to compounds that inhibit RTKs and therefore inhibit mechanisms involved in oncogenesis and tumor progression.

The phrase "androgen receptor modulators" refers to compounds that interfere or inhibit the binding of androgens to the receptor, regardless of mechanism.

The phrase "angiogenesis inhibitors" refers to compounds that inhibit the formation of new blood vessels, regardless of mechanism.

The term "aryl" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which can be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, C1-C4 alkoxy, C1-C4 alkyl, C2-C4 alkenyl, C2-C4 alkynyl, NH_2. and NR_1R_2 groups, where R_1 and R_2 independently are H or C1-C4 alkyl.

The term "alkylaryl" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and examples of heterocyclic aryl groups having such heteroatoms include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. Preferably, the alkyl group is a C1-C4 alkyl group.

The term "amide" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to an —C(O)—NH—R, where R is either alkyl, aryl, alkylaryl or hydrogen.

The phrase "antisense region" as used herein refers to its meanings as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to a nucleotide sequence of an siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of an siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule. In one embodiment, the antisense region of the siNA molecule is referred to as the antisense strand or guide strand.

The phrase "asymmetric hairpin" refers to a linear siNA molecule comprising an antisense region, a loop portion that can comprise nucleotides or non-nucleotides, and a sense region that comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex with loop. For example, an asymmetric hairpin siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 15 to about 30, or about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides) and a loop region comprising about 4 to about 12 (e.g., about 4, 5, 6, 7, 8, 9, 10, 11, or 12) nucleotides, and a sense region having about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides that are complementary to the antisense region. The asymmetric hairpin siNA molecule can also comprise a 5'-terminal phosphate group that can be chemically modified. The loop portion of the asymmetric hairpin siNA molecule can comprise nucleotides, non-nucleotides, linker molecules, or conjugate molecules as described herein.

The term "biodegradable" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to degradation in a biological system, for example, enzymatic degradation or chemical degradation.

The term "biodegradable linker" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to a linker molecule that is designed to connect one molecule to another molecule, and which is susceptible to degradation in a biological system. The linker can be a nucleic acid or non-nucleic acid based linker. For example, a biodegradable linker can be used to attach a ligand or biologically active molecule to an siNA molecule of the invention. Alternately, a biodegradable linker can be sued to connect the sense and antisense strands of an siNA molecule of the invention. The biodegradable linker is

designed such that is stability can be modulated for a particular purpose, such as delivery to a particular tissue or cell type. The stability of a nucleic acid-based biodegradable linker molecule can be modulated by using various chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

The phrase "biologically active molecule" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system and/or are capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules. Examples of biologically active molecules, include siNA molecules alone or in combination with other molecules including, but not limited to therapeutically active molecules such as antibodies, cholesterol, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, polyamines, polyamides, polyethylene glycol, other polyethers, 2-5A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof.

The phrase "biological system" as used herein refers to its meanings as is generally accepted in the art. The term generally refers to material, in a purified or unpurified form, from biological sources including, but not limited to, human or animal, wherein the system comprises the components required for RNAi activity. Thus, the phrase includes, for example, a cell, tissue, subject, or organism, or extract thereof. The term also includes reconstituted material from a biological source.

The phrase "blunt end" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to termini of a double-stranded siNA molecule having no overhanging nucleotides. For example, the two strands of a double-stranded siNA molecule having blunt ends align with each other with matched based-pairs without overhanging nucleotides at the termini. A siNA duplex molecule of the invention can comprise blunt ends at one or both termini of the duplex, such as termini located at the 5'-end of the antisense strand, the 5'-end of the sense strand, or both termini of the duplex.

The term "cap" also referred to herein as "terminal cap," as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to a moiety, which can be a chemically modified nucleotide or non-nucleotide that can be incorporated at one or more termini of one or more nucleic acid molecules of the invention. These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and can help in delivery and/or localization within a cell. The cap can be present at the 5'-terminus (5'-cap) or at the 3'-terminal (3'-cap) or can be present on both termini of any nucleic acid molecule of the invention. A cap can be present at the 5'-end, 3-end and/or 5' and 3'-ends of the sense strand of a nucleic acid molecule of the invention. Additionally, a cap can optionally be present a the 3'-end of the antisense strand of a nucleic acid molecule of the invention. In non-limiting examples, the 5'-cap includes, but is not limited to, LNA; glycerol; inverted deoxy abasic residue (moiety); 4'5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides: alpha-nucleotides; modified basic nucleotide; phosphorodithioate linkage; threo-pentofuranosyl nucleotide; acyclic 3','-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihyroxypentyl nucleotide; 3'-3'-inverted nucleotide moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety. Non-limiting examples of the 3'-cap include, but are not limited to, LNA; glyceryl; inverted deoxy abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide; carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; threo-pentofuranosyl nucleotide; acyclic 3','-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3-5-dihydroxypentyl nucleotide; 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate; phosphorothioate and/or phosphorodithioate; bridging or non bridging methylphosphonate; and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein). FIG. **5** shows some non-limiting examples of various caps.

The term "cell" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human being. The cell can be present in an organism, e.g., birds, plants and mammals, such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (e.g., bacterial cell) or eukaryotic (e.g., mammalian or plant cell). The cell can be of somatic or germ line organ, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

The phrase "chemical modification" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to any modification of the chemical structure of the nucleotides that differs from nucleotides of native siRNA or RNA in general. The term "chemical modification" encompasses the addition, substitution, or modification of native siRNA or RNA at the sugar, base, or internucleotide linkage, as described herein or as is otherwise known in the art. In certain embodiments, the term "chemical modification" can refer to certain forms of RNA that are naturally occurring in certain biological systems, for example 2'-O-methyl modifications or inosine modifications.

The term "CTNNB1" refers to catenin (cadherin-associated protein), beta 1 which is gene that encodes CTNNB1

proteins, CTNNB1 peptides, CTNNB1 polypeptides, CTNNB1 regulatory polynucleotides (e.g., CTNNB1 miRNAs and siNAs), mutant CTNNB1 genes, and splice variants of a CTNNB1 genes, as well as other genes involved in CTNNB1 pathways of gene expression and/or activity. Thus, each of the embodiments described herein with reference to the term "CTNNB1" are applicable to all of the protein, peptide, polypeptide, and/or polynucleotide molecules covered by the term "CTNNB1", as that term is defined herein. Comprehensively, such gene targets are also referred to herein generally as "target" sequences (including the target sequences listed in Table 1a).

The term "complementarity" or "complementary" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the terms generally refer to the formation or existence of hydrogen bond(s) between one nucleic acid sequence and another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types of bonding as described herein. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner et al., 1987, *CSH Symp. Quant. Biol.* LII pp. 123-133; Frier et al., 1986, *Proc. Nat. Acad. Sci.* USA 83:9373-9377; Turner et al., 1987, *J. Am. Chem. Soc,* 109:3783-3785). Perfect complementary means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence. Partial complementarity can include various mismatches or non-based paired nucleotides (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more mismatches, non-nucleotide linkers, or non-based paired nucleotides) within the nucleic acid molecule, which can result in bulges, loops, or overhangs that result between the sense strand or sense region and the antisense strand or antisense region of the nucleic acid molecule or between the antisense strand or antisense region of the nucleic acid molecule and a corresponding target nucleic acid molecule. Such partial complementarity can be represented by a % complementarity that is determined by the number of non-based paired nucleotides, i.e., about 50%, 60%, 70%, 80%, 90% etc. depending on the total number of nucleotides involved. Such partial complementarity is permitted to the extent that the nucleic acid molecule (e.g. siNA) maintains its function, for example the ability to mediate sequence specific RNAi.

The terms "composition" or "formulation" as used herein refer to their generally accepted meaning in the art. These terms generally refer to a composition or formulation, such as in a pharmaceutically acceptable carrier or diluent, in a form suitable for administration, e.g., systemic or local administration, into a cell or subject, including, for example, a human. Suitable forms, in part, depend upon the use or the route of entry, for example, oral, transdermal, inhalation, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (i.e., a cell to which the negatively charged nucleic acid is desirable for delivery). For example, compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that prevent the composition or formulation from exerting is effect. As used herein, pharmaceutical formulations include formulations for human and veterinary use. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: Lipid Nanoparticles (see for example Semple et al., 2010, *Nat Biotechnol.*, February; 28 (2):172-6); P-glycoprotein inhibitors (such as Pluronic P85); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery (Emerich, D F et al, 1999, *Cell Transplant,* 8, 47-58); and loaded nanoparticles, such as those made of polybutylcyanoacrylate. Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado et al., 1998, *J. Pharm Sci.,* 87, 1308-1315; Tyler et al., 1999, *FEBS Lett.,* 421, 280-284; Pardridge et al., 1995, *PNAS USA.,* 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.,* 15, 73-107; Aldrian-Herrada et al., 1998, *Nucleic Acids Res.,* 26, 4910-4916; and Tyler et al., 1999, *PNAS USA.,* 96, 7053-7058. A "pharmaceutically acceptable composition" or "pharmaceutically acceptable formulation" can refer to a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention to the physical location most suitable for their desired activity.

The phrase "cytotoxic/cytostatic agents" refer to compounds that cause cell death or inhibit cell proliferation primarily by interfering directly with the cell's functioning or inhibit or interfere with cell mytosis, including alkylating agents, tumor necrosis factors, intercalators, hypoxia activatable compounds, microtubule inhibitors/microtubule-stabilizing agents, inhibitors of mitotic kinesins, inhibitors of histone deacetylase, inhibitors of kinases involved in mitotic progression, antimetabolites; biological response modifiers; hormonal/anti-hormonal therapeutic agents, hematopoietic growth factors, monoclonal antibody targeted therapeutic agents, topoisomerase inhibitors, proteasome inhibitors and ubiquitin ligase inhibitors.

The phrase "estrogen receptor modulators" refers to compounds that interfere with or inhibit the binding of estrogen to the receptor, regardless of mechanism.

The term "gene" or "target gene" as used herein refers to their meaning as is generally accepted in the art. The terms generally refer a nucleic acid (e.g., DNA or RNA) sequence that comprises partial length or entire length coding sequences necessary for the production of a polypeptide. The target gene can also include the UTR or non-coding region of the nucleic acid sequence. A gene or target gene can also encode a function RNA (fRNA) or non-coding RNA (ncRNA), such as small temporal RNA (stRNA), micro RNA (miRNA), small nuclear RNA (snRNA), short interfering RNA (siRNA), small nucleolar RNA (snRNA), ribosomal RNA (rRNA), transfer RNA (tRNA) and precursor RNAs thereof. Such non-coding RNAs can serve as target nucleic acid molecules for siRNA mediated RNA interference in modulating the activity of fRNA or ncRNA involved in functional or regulatory cellular processes. Aberrant fRNA or ncRNA activity leading to disease can therefore be modulated by siNA molecules of the invention. siNA molecules targeting fRNA and ncRNA can also be used to manipulate or alter the genotype or phenotype of a subject, organism or cell, by intervening in cellular processes such as genetic imprinting, transcription, translation, or nucleic acid processing (e.g., transamination, methylation etc.). The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example, a plant, animal, protozoan, virus, bacte-

rium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates. Non-limiting examples of fungi include molds or yeasts. For a review, see for example Snyder and Gerstein, 2003, Science, 300, 258-260.

The phrase "HMG-CoA reductase inhibitors" refers to inhibitors of 3-hydroxy-3-methylglutaryl-CoA reductase. The term HMG-CoA reductase inhibitor as used herein includes all pharmaceutically acceptable lactone and open-acid forms (i.e., where the lactone ring is opened to form the free acid) as well as salt and ester forms of compounds that have HMG-CoA reductase inhibitory activity, and therefore the use of such salts, esters, open-acid and lactone forms is included within the scope of this invention.

The phrase "homologous sequence" as used herein refers to its meaning as is generally accepted in the art. The term generally refers a nucleotide sequence that is shared by one or more polynucleotide sequences, such as genes, gene transcripts and/or non-coding polynucleotides. For example, a homologous sequence can be a nucleotide sequence that is shared by two or more genes encoding related but different proteins, such as different members of a gene family, different protein epitopes, different protein isoforms or completely divergent genes. A homologous sequence can be a nucleotide sequence that is shared by two or more non-coding polynucleotides, such as noncoding DNA or RNA, regulator sequences, introns, and sites of transcriptional control or regulation. Homologous sequences can also include sequence regions shared by more than one polynucleotide sequence. Homology does not need to be perfect identity (100%), as partially homologous sequences are also contemplated by and within the scope of the instant invention (e.g., at least 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80% etc.). Percent homology is the number of matching nucleotides between two sequences divided by the total length being compared, multiplied by 100.

The phrase "improved RNAi activity" refers to an increase in RNAi activity measured in vitro and/or in vivo, wherein the RNAi activity is reflection of both the ability of the siNA to mediate RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased in vitro and/or in vivo compared to an all RNA siNA or an siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (i.e., less than ten-fold), but the overall activity of the siNA molecule is enhanced in vitro and/or in vivo.

The terms "inhibit," "down-regulate," or "reduce" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term generally refers the reduction in the expression of the gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, below that observed in the absence of the nucleic acid molecules (e.g., siNA) of the invention. Down-regulation can also be associated with post-transcriptional silencing, such as, RNAi mediated cleavage or by alteration in DNA methylation patterns or DNA chromatin structure. Inhibition, down-regulation or reduction with an siNA molecule can be in reference to an inactive molecule, an attenuated molecule, an siNA molecule with a scrambled sequence, or an siNA molecule with mismatches or alternatively, it can be in reference to the system in the absence of the nucleic acid.

The phrase "inhibitors of cell proliferation and survival signaling pathway" refers to pharmaceutical agents that inhibit cell surface receptors and signal transduction cascades downstream of those surface receptors.

The term "integrin blockers" refers to compounds which selectively antagonize, inhibit or counteract binding of a physiological ligand to the $\alpha_\omega\beta_3$ integrin, to compounds which selectively antagonize, inhibit or counteract binding of a physiological ligand to the $\alpha_\omega\beta_5$ integrin, to compounds which antagonize, inhibit or counteract binding of a physiological ligand to both the $\alpha_\omega\beta_3$ integrin and the $\alpha_\omega\beta_5$ integrin, and to compounds which antagonize, inhibit or counteract the activity of the particular integrin(s) expressed on capillary endothelial cells. The term also refers to antagonists of the $\alpha_\omega\beta_6$ $\alpha_\omega\beta_8$ $\alpha_1\beta_1$ $\alpha_2\beta_1$ $\alpha_5\beta_1$ $\alpha_6\beta_1$ and $\alpha_6\beta_4$ integrins. The term also refers to antagonists of any combination of $\alpha_\omega\beta_3$, $\alpha_\omega\beta_5$, $\alpha_\omega\beta_6$, $\alpha_\omega\beta_8$, $\alpha_1\beta_1$, $\alpha_2\beta_1$, $\alpha_5\beta_1$ $\alpha_6\beta_1$ and $\alpha_6\beta_4$ integrins.

The terms "intermittent" or "intermittently" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to periodic stopping and starting at either regular or irregular intervals.

The terms "internucleoside linkage" or "internucleoside linker" or "internucleotide linkage" or "internucleotide linker" are used herein interchangeably and refer to any linker or linkage between two nucleoside units, as is known in the art, including, for example, but not limitation, phosphate, analogs of phosphate, phosphonate, guanidium, hydroxylamine, hydroxythydrazinyl, amide, carbamate, alkyl, and substituted alkyl linkages. The internucleoside linkages constitute the backbone of a nucleic acid molecule.

The terms "mammalian" or "mammal" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to any warm blooded vertebrate species, such as a human, mouse, rat, dog, cat hamster, guinea pig, rabbit, livestock, and the like.

The phrase "metered dose inhaler" or MDI refers to a unit comprising a can, a secured cap covering the can and a formulation metering valve situated in the cap. MDI systems includes a suitable channeling device. Suitable channeling devices comprise for example, a valve actuator and a cylindrical or cone-like passage through which medicament can be delivered from the filled canister via the metering valve to the nose or mouth of a patient such as a mouthpiece actuator.

The term "microRNA" or "miRNA" as used herein refers to its meaning as is generally accepted in the art. The term generally refers a small double-stranded RNA that regulates the expression of target messenger RNAs either by mRNA cleavage, translational repression/inhibition or heterochromatic silencing (see for example Ambros, 2004, Nature, 431, 350-355; Bartel, 2004, Cell, 116, 281-297; Cullen, 2004, Virus Research., 102, 3-9; He et al., 2004, Nat. Rev. Genet. 5, 522-531; Ying et al., 2004, Gene, 342, 25-28; and Sethupathy et al., 2006, RNA, 12:192-197).

The term "modulate" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to when the expression of a gene, or level of one or more RNA molecules (coding or non-coding), or activity of one or more RNA molecules or proteins or protein subunits, is up-regulated or down-regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the molecule that effects modulation. For example, the term "modulate" in some embodiments can refer to inhibition and in other embodiments can refer to potentiation or up-regulation, e.g., of gene expression.

The phrase "modified nucleotide" as used herein refers to its meaning as is generally accepted in the art. The term generally refers a nucleotide, which contains a modification in the chemical structure of the base, sugar and/or phosphate of the unmodified (or natural) nucleotide as is generally known in the art. Non-limiting examples of modified nucleotides are described herein and in U.S. application Ser. No. 12/064,014.

The phrase "NSAIDs that are selective COX-2 inhibitors" for purposes herein, refers to NSAIDs, which possess a specificity for inhibiting COX-2 over COX-1 of at least 100 fold as measured by the ration of IC_{50} for COX-2 over IC_{50} for COX-1 evaluated by cell or microsomal assays.

The phrase "non-base paired" refers to nucleotides that are not base paired between the sense strand or sense region and the antisense strand or antisense region of an double-stranded siNA molecule; and can include for example, but not limitation, mismatches, overhangs, single stranded loops, etc.

The term "non-nucleotide" refers to any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, such as for example but not limitation abasic moieties or alkyl chains. The group or compound is "abasic" in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a nucleobase at the 1'- position.

The term "nucleotide" is used as is generally recognized in the art. Nucleotides generally comprise a nucleobase, a sugar, and an internucleoside linkage, e.g., a phosphate. The base can be a natural base (standard), modified bases, or a base analog, as are well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Additionally, the nucleotides can be unmodified or modified at the sugar, internucleoside linkage, and/or base moiety (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and others; see, for example, U.S. application Ser. No. 12/064,014.

The term "overbang" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary double stranded nucleic acid molecules, the term generally refers to the terminal portion of a nucleotide sequence that is not base paired between the two strands of a double-stranded nucleic acid molecule (see for example, FIG. **4**). Overhangs, when present, are typically at the 3'-end of one or both strands in a siNA duplex.

The term "parenteral" as used herein refers to its meaning as is generally accepted in the art. The term generally refers methods or techniques of administering a molecule, drug, agent, or compound in a manner other than through the digestive tract, and includes epicutaneous, subcutaneous, intravascular (e.g., intravenous), intramuscular, or intrathecal injection or infusion techniques and the like.

The phrase "pathway target" refers to any target involved in pathways of gene expression or activity. For example, any given target can have related pathway targets that can include upstream, downstream, or modifier genes in a biologic pathway. These pathway target genes can provide additive or synergistic effects in the treatment of diseases, conditions, and traits herein.

The term "phosphorothioate" refers to an internucleotide phosphate linkage comprising one or more sulfur atoms in place of an oxygen atom. Hence, the term phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

"Prenyl-protein transferase inhibitor" refers to a compound that inhibits any one or any combination of the prenyl-protein transferase enzymes, including farnesyl-protein transferase (FPTase), geranylgeranyl-protein transferase type I (GGPTase-I), and geranylgeranyl-protein transferase type-II (GGPTase-II, also called Rab GGPTase).

The phrase "retinoid receptor modulators" refers to compounds that interfere or inhibit the binding of retinoids to the receptor, regardless of mechanism.

The term "ribonucleotide" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to a nucleotide with a hydroxyl group at the 2' position of a β-D-ribofuranose moiety.

The term "RNA" as used herein refers to its generally accepted meaning in the art. Generally, the term RNA refers to a molecule comprising at least one ribofuranoside moiety. The term can include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

The phrase "RNA interference" or term "RNAi" refer to the biological process of inhibiting or down regulating gene expression in a cell, as is generally known in the art, and which is mediated by short interfering nucleic acid molecules, see for example Zamore and Haley, 2005, *Science,* 309, 1519-1524; Vaughn and Martienssen, 2005, *Science,* 309, 1525-1526; Zamore et al., 2000, *Cell,* 101, 25-33; Bass, 2001, *Nature,* 411, 428-429; Elbashir et al., 2001, *Nature,* 411, 494-498; and Kreutzer et al., International PCT Publication No. WO 00/44895; Zernicka-Goetz et al., International PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck et al., International PCT Publication No. WO 00/01846; Mello and Fire, International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li et al., International PCT Publication No. WO 00/44914; Allshire, 2002, *Science,* 297, 1818-1819; Volpe et al., 2002, *Science,* 297, 1833-1837; Jenuwein, 2002, *Science,* 297, 2215-2218; and Hall et al., 2002, *Science,* 297, 2232-2237; Hutvagner and Zamore, 2002, *Science,* 297, 2056-60; McManus et al., 2002, *RNA,* 8, 842-850; Reinhart et al., 2002, *Gene & Dev.,* 16, 1616-1626; and Reinhart & Bartel, 2002, *Science,* 297, 1831). Additionally, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, transcriptional inhibition, or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at either the post-transcriptional level or the pre-transcriptional level. In a non-limiting example, epigenetic modulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure or methylation patterns to alter gene expression (see, for example, Verdel et al., 2004, *Science,* 303, 672-676; Pal-Bhadra et al., 2004, *Science,* 303, 669-672; Allshire, 2002, *Science,* 297, 1818-1819; Volpe et al., 2002, *Science,* 297, 1833-1837; Jenuwein, 2002, *Science,*

297, 2215-2218; and Hall et al., 2002, *Science,* 297, 2232-2237). In another non-limiting example, modulation of gene expression by siNA molecules of the invention can result from siNA mediated cleavage of RNA (either coding or non-coding RNA) via RISC, or via translational inhibition, as is known in the art or modulation can result from transcriptional inhibition (see for example Janowski et al., 2005, *Nature Chemical Biology,* 1, 216-222).

The phrase "RNAi inhibitor" refers to any molecule that can down regulate, reduce or inhibit RNA interference function or activity in a cell or organism. An RNAi inhibitor can down regulate, reduce or inhibit RNAi (e.g., RNAi mediated cleavage of a target polynucleotide, translational inhibition, or transcriptional silencing) by interaction with or interfering with the function of any component of the RNAi pathway, including protein components such as RISC, or nucleic acid components such as miRNAs or siRNAs. A RNAi inhibitor can be an siNA molecule, an antisense molecule, an aptamer, or a small molecule that interacts with or interferes with the function of RISC, a miRNA, or an siRNA or any other component of the RNAi pathway in a cell or organism. By inhibiting RNAi (e.g., RNAi mediated cleavage of a target polynucleotide, translational inhibition, or transcriptional silencing), a RNAi inhibitor of the invention can be used to modulate (e.g., up-regulate or down regulate) the expression of a target gene.

The phrase "sense region" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to a nucleotide sequence of an siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of an siNA molecule can comprise a nucleic acid sequence having homology or sequence identity with a target nucleic acid sequence. In one embodiment, the sense region of the siNA molecule is also referred to as the sense strand or passenger strand.

The phrases "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically modified short interfering nucleic acid molecule" refer to any nucleic acid molecule capable of inhibiting or down regulating gene expression or viral replication by mediating RNA interference ("RNAi") or gene silencing in a sequence-specific manner. These terms can refer to both individual nucleic acid molecules, a plurality of such nucleic acid molecules, or pools of such nucleic acid molecules. The siNA can be a double-stranded nucleic acid molecule comprising self-complementary sense and antisense strands, wherein the antisense strand comprises a nucleotide sequence that is complementary to a nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises a nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a polynucleotide with a duplex, asymmetric duplex, hairpin or asymmetric hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region comprises a nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising a self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to a nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region comprises a nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either in vivo or in vitro to generate an active siNA molecule capable of mediating RNAi. The siNA can also comprise a single-stranded polynucleotide having a nucleotide sequence complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of a nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single-stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example, Martinez et al., 2002, *Cell,* 110, 563-574 and Schwarz et al., 2002, *Molecular Cell,* 10, 537-568), or 5',3'-diphosphate.

The term "subject" as used herein refers to its meaning as is generally accepted in the art. The term generally refers an organism to which the nucleic acid molecules of the invention can be administered. A subject can be a mammal or mammalian cells, including a human or human cells. The term also refers to an organism, which is a donor or recipient of explanted cells or the cells themselves.

The phrase "systemic administration" as used herein refers to its meaning as is generally accepted in the art. The term generally refers in vivo systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body.

The term "target" as it refers to CTNNB1 refers to any CTNNB1 target protein, peptide, or polypeptide, such as encoded by Genbank Accession Nos. shown in Table 5. The term also refers to nucleic acid sequences or target polynucleotide sequence encoding any target protein, peptide, or polypeptide, such as proteins, peptides, or polypeptides encoded by sequences having Genbank Accession Nos. shown in Table 5. The target of interest can include target polynucleotide sequences, such as target DNA or target RNA. The term "target" is also meant to include other sequences, such as differing isoforms, mutant target genes, splice variants of target polynucleotides, target polymorphisms, and non-coding (e.g., ncRNA, miRNA, stRNA, sRNA) or other regulatory polynucleotide sequences as described herein.

The phrase "target site" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to a sequence within a target nucleic acid molecule (e.g., RNA) that is "targeted", e.g., for cleavage mediated by an siNA construct, which contains sequences within its antisense region that are complementary to the target sequence.

The phrase "therapeutically effective amount" as used herein refers to its meaning as is generally accepted in the art. The term generally refers to the amount of the compound or composition that will elicit the biological or medical response of a cell, tissue, system, animal or human that is be sought by the researcher, veterinarian, medical doctor or other clinician. For example, if a given clinical treatment is considered effective when there is at least a 25% reduction in a measurable parameter associated with a disease or disorder, a therapeutically effective amount of a drug for the treatment of that disease or disorder is that amount necessary to effect at least a 25% reduction in that parameter.

The phrase "universal base" as used herein refers to its meaning as is generally accepted in the art. The term universal base generally refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little or no discrimination between them. Non-

limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for example, Loakes, 2001, *Nucleic Acids Research,* 29, 2437-2447).

The term "up-regulate" as used herein refers to its meaning as is generally accepted in the art. With reference to exemplary nucleic acid molecules of the invention, the term refers to an increase in the expression of a gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more RNAs, proteins or protein subunits, above that observed in the absence of the nucleic acid molecules (e.g., siNA) of the invention. In certain instances, up-regulation or promotion of gene expression with an siNA molecule is above that level observed in the presence of an inactive or attenuated molecule. In other instances, up-regulation or promotion of gene expression with siNA molecules is above that level observed in the presence of, for example, an siNA molecule with scrambled sequence or with mismatches. In still other instances, up-regulation or promotion of gene expression with a nucleic acid molecule of the instant invention is greater in the presence of the nucleic acid molecule than in its absence. In some instances, up-regulation or promotion of gene expression is associated with inhibition of RNA mediated gene silencing, such as RNAi mediated cleavage or silencing of a coding or non-coding RNA target that down regulates, inhibits, or silences the expression of the gene of interest to be up-regulated. The down regulation of gene expression can, for example, be induced by coding RNA or its encoded protein, such as through negative feedback or antagonistic effects. The down regulation of gene expression can, for example, be induced by a non-coding RNA having regulatory control over a gene of interest, for example by silencing expression of the gene via translational inhibition, chromatin structure, methylation, RISC mediated RNA cleavage, or translational inhibition. As such, inhibition or down regulation of targets that down regulate, suppress, or silence a gene of interest can be used to up-regulate expression of the gene of interest toward therapeutic use.

The term "vector" as used herein refers to its meaning as is generally accepted in the art. The term vector generally refers to any nucleic acid- and/or viral-based expression system or technique used to deliver one or more nucleic acid molecules.

B. siNA Molecules of the Invention

The present invention provides compositions and methods comprising siNAs targeted to CTNNB1 that can be used to treat diseases, e.g., malignancies and/or cancers associated with CTNNB1 expression. In particular aspects and embodiments of the invention, the nucleic acid molecules of the invention comprise at least a 15 nucleotide sequence of the sequences shown in Table 1a and Table 1b. The siNAs can be provided in several forms. For example, the siNA can be isolated as one or more siNA compounds, or it may be in the form of a transcriptional cassette in a DNA plasmid. The siNA may also be chemically synthesized and can include modifications as shown, for example, but not limitation, in Table 1c and Table 6. Thus, in various embodiments, at least one strand or region of the nucleic acids of the invention comprises at least a 15 nucleotide sequence selected from the group of sequences consisting of SEQ ID NOS:1-6374. The siNAs can be administered alone or co-administered with other siNA molecules or with conventional agents that treat a CTNNB1 related disease or condition.

The siNA molecules of the invention can be used to mediate gene silencing, specifically CTNNB1, via interaction with RAN transcripts or alternately by interaction with particular gene sequences, wherein such interaction results in modulation of gene silencing either at the transcriptional level or post-transcriptional level such as, for example, but not limited to, RNAi or through cellular processes that modulate the chromatin structure or methylation patterns of the target and prevent transcription of the target gene, with the nucleotide sequence of the target thereby mediating silencing. More specifically, the target is any of CTNNB1 RNA, DNA, or mRNA.

In one aspect, the invention provides short interfering nucleic acid (siNA) molecules for inhibiting the expression of the CTNNB1 gene in a cell or mammal. The siNA can be single-stranded or double-stranded. When double-stranded, the siNA comprising a sense and an antisense stand. The antisense strand is complementary to at least a part of an mRNA formed in the expression of the CTNNB1 gene. The sense strand comprises a region that is complementary to the antisense strand. In specific embodiments, the antisense strand comprises at least a 15 nucleotide sequence of an antisense sequence listed in Table 1b. Generally, the double-stranded siNA comprises at least a 15 nucleotide sequence of the sense strand in Table 1b and at least a 15 nucleotide sequence of the antisense strand in Table 1b. One or more of the nucleotides of the siNAs of the invention are optionally modified. In further embodiments having modifications, some siNAs of the invention comprises at least one nucleotide sequence selected from the groups of sequences provide in Table 1c. In other embodiments, the siNA comprises at least two sequences selected from the group of sequences provided in Table 1c, wherein one of the at least two sequences is complementary to another of the at least two sequences and one of the at least two sequences is complementary to a sequence of a mRNA generated in the expression of the CTNNB1 gene. Examples of certain modified siNAs of the invention are in Table 1c.

The double stranded RNA molecules of the invention can comprise two distinct and separate strands that can be symmetric or asymmetric and are complementary, i.e., two single-stranded RNA molecules, or can comprise one single-stranded molecule in which two complementary portions, e.g., a sense region and an antisense region, are base-paired, and are covalently linked by one or more single-stranded "hairpin" areas (i.e. loops) resulting in, for example, a single-stranded short-hairpin polynucleotide or a circular single-stranded polynucleotide.

The linker can be polynucleotide liner or a non-nucleotide linker. In some embodiments, the linker is a non-nucleotide linker. In some embodiments, a hairpin or circular siNA molecule of the invention contains one or more loop motifs, wherein at least one of the loop portions of the siNA molecule is biodegradable. For example, a single-stranded hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule in vivo can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising 1, 2, 3 or 4 nucleotides. Or alternatively, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule in vivo can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In symmetric siNA molecules of the invention, each strand, the sense (passenger) strand and antisense (guide) strand, are independently about 15 to about 30 (e.g., about

15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length. Generally, each strand of the symmetric siNA molecules of the invention are 19-24 (e.g., about 19, 20, 21, 22, 23 or 24) nucleotides in length.

In asymmetric siNA molecules, the antisense region or strand of the molecule is about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length, wherein the sense region is about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. Generally, each strand of the asymmetric siNA molecules of the invention is about 19-24 (e.g., about 19, 20, 21, 22, 23 or 24) nucleotides in length.

In yet other embodiments, siNA molecules of the invention comprise single stranded hairpin siNA molecules, wherein siNA molecules are about 25 to about 70 (e.g., about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length.

In still other embodiments, siNA molecules of the invention comprise single-stranded circular siNA molecules, wherein the siNA molecules are about 38 to about 70 (e.g., about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length.

In still other embodiments, siNA molecules of the invention comprise single-stranded non-circular siNA molecules, wherein the siNA molecules are independently about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length.

In various symmetric embodiments, the siNA duplexes of the invention independently comprise about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs. Generally, the duplex structure of siNAs of the invention is between 15 to 30, more generally between 18 to 25, yet more generally between 19 and 24, and most generally between 19 and 21 base pairs in length.

In yet other embodiments, where the duplex siNA molecules of the invention are asymmetric, the siNA molecules comprise about 3 to 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs. Generally, the duplex structure of siNAs of the invention is between 15 and 25, more generally between 18 and 25, yet more generally between 19 and 24, and most generally between 19 and 21 base pairs in length.

In still other embodiments, where the siNA molecules of the invention are hairpin or circular structures, the siNA molecules comprise about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs.

The sense strand and antisense strand, or the sense region and antisense region, of the siNA molecules of the invention can be complementary. Also, the antisense strand or antisense target RNA. The sense strand or sense region of the siNA can comprise a nucleotide sequence of a CTNNB1 gene or a portion thereof. In certain embodiments, the sense region or sense strand of an siNA molecule of the invention is complementary to that portion of the antisense region or antisense strand of the siNA molecule that is complementary to a CTNNB1 target polynucleotide sequence, such as for example, but not limited to, those sequences represented by GENBANK Accession Nos. shown in Table 5.

In some embodiments, siNA molecules of the invention have perfect complementarity between the sense strand or sense region and the antisense strand or antisense region of the siNA molecule. In other or the same embodiments, the antisense strand of the siNA molecules of the invention are perfectly complementary to a corresponding target nucleic acid molecule.

In yet other embodiments, siNA molecules of the invention have partial complementarity (i.e., less than 100% complementarity) between the sense strand or sense region and the antisense strand or antisense region of the siNA molecule or between the antisense strand or antisense region of the siNA molecule and a corresponding target nucleic acid molecule. Thus, in some embodiments, the double-stranded nucleic acid molecules of the invention, have between about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in one strand that are complementary to the nucleotides of the other strand. In other embodiments, the molecules have between about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in the sense region that are complementary to the nucleotides of the antisense region. of the double-stranded nucleic acid molecule. In certain embodiments, the double-stranded nucleic acid molecules of the invention have between about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in the antisense strand that are complementary to a nucleotide sequence of its corresponding target nucleic acid molecule.

In other embodiments, the siNA molecule can contain one or more nucleotide deletions, substitutions, mismatches and/or additions; provided, however, that the siNA molecule maintains its activity, for example, to mediate RNAi. In a non-limiting example, the deletion, substitution, mismatch and/or addition can result in a loop or bulge, or alternately a wobble or other alternative (non Watson-Crick) base pair. Thus, in some embodiments, for example, the double-stranded nucleic acid molecules of the invention, have 1 or more (e.g., 1, 2, 3, 4, 5, or 6) nucleotides, in one strand or region that are mismatches or non-base-paired with the other strand or region. In other embodiments, the double-stranded nucleic acid molecules of the invention, have 1 or more (e.g., 1, 2, 3, 4, 5, or 6) nucleotides in each strand or region that are mismatches or non-base-paired with the other strand or region. In a preferred embodiment, the siNA of the invention contains no more than 3 mismatches. If the antisense strand of the siNA contains mismatches to a target sequence, it is preferable that the area of mismatch not be located in the center of the region of complementarity.

In other embodiments, the siNA molecule can contain one or more nucleotide deletions, substitutions, mismatches and/or additions to a sequence in Table 1b provided, however, that the siNA molecule maintains its activity, for example, to mediate RNAi. In a non-limiting example, the deletion, substitution, mismatch and/or addition can result in a loop or bulge, or alternately a wobble or other alternative (non Watson-Crick) base pair.

The invention also comprises double-stranded nucleic acid (siNA) molecules as otherwise described hereinabove in which the first strand and second strand are complementary to each other and wherein at least one strand is hybridisable to the polynucleotide sequence of a sequence in Table 1b under conditions of high stringency, and wherein any of the nucleotides is unmodified or chemically modified.

Hybridization techniques are well known to the skilled artisan (see for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Preferred stringent hybridization conditions include overnight incubation at 42° C. in a solution comprising: 50% formamide, 5×SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5× Denhardt's solution,

10% dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0.1×SSC at about 65° C.

In one specific embodiment, the first strand has about 15, 16, 17, 18, 19, 20, or 21 nucleotides that are complementary to the nucleotides of the other strand and at least one strand is hybridisable to a polynucleotide sequence in Table 1b. In a more preferred embodiment, the first strand has about 15, 16, 17, 18, 19, 20, or 21 nucleotides that are complementary to the nucleotides of the other strand and at least one strand is hybridisable to SEQ ID NO: 1, SEQ ID NO: 1049, SEQ ID NO: 43, SEQ ID NO: 1091, SEQ ID NO: 51, SEQ ID NO: 1099, SEQ ID NO: 53, or SEQ ID NO:1101; under conditions of high stringency, and wherein any of the nucleotides is unmodified or chemically modified.

In certain embodiments, the siNA molecules of the invention comprise overhangs of about 1 to about 4 (e.g., 1, 2, 3, or 4) nucleotides. The nucleotides in the overhangs can be the same or different nucleotides. In some embodiments, the overhangs occur at the 3'-end at one or both strands of the double-stranded nucleic acid molecule. For example, a double-stranded nucleic acid molecule of the invention can comprise a nucleotide or non-nucleotide overhang at the 3'-end of the antisense strand/region, the 3'-end of the sense strand/region, or both the antisense strand/region and the sense strand/region of the double-stranded nucleic acid molecule.

In some embodiments, the nucleotides comprising the overhang portion of an siNA molecule of the invention comprise sequences based on the CTNNB1 target polynucleotide sequence in which nucleotides comprising the overhang portion of the antisense strand/region of an siNA molecule of the invention can be complementary to nucleotides in the CTNNB1 target polynucleotide sequence and/or nucleotides comprising the overhang portion of the sense strand/region of an siNA molecule of the invention can comprise the nucleotides in the CTNNB1 target polynucleotide sequence. Thus, in some embodiments, the overhang comprises a two nucleotide overhang that is complementary to a portion of the CTNNB1 target polynucleotide sequence. In other embodiments, however, the overhang comprises a two nucleotide overhang that is not complementary to a portion of the CTNNB1 target polynucleotide sequence. In certain embodiments, the overhang comprises a 3'-UU overhang that is not complementary to a portion of the CTNNB1 target polynucleotide sequence. In other embodiments, the overhang comprises a UU overhang at the 3' end of the antisense strand and a TT overhang at the 3' end of the sense strand. In other embodiments, the overhang comprises nucleotides as described in the examples, Tables, and Figures herein.

In any of the embodiments of the siNA molecules described herein having 3'-terminal nucleotide overhangs, the overhangs are optionally chemically modified at one or more nucleic acid sugar, base, or backbone positions. Representative, but not limiting examples of modified nucleotides in the overhang portion of a double-stranded nucleic acid (siNA) molecule of the invention include: 2'-O-alkyl (e.g., 2'-O-methyl), 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-deoxy-2'-fluoroarabino (FANA), 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, universal base, acyclic, or 5-C-methyl nucleotides. In more preferred embodiments, the overhang nucleotides are each independently, a 2'-O-alkyl nucleotide, a 2'-O-methyl nucleotide, a 2'-dexoy-2-fluoro nucleotide, or a 2'-deoxy ribonucleotide. In some instances the overhang nucleotides are linked by a one or more phosphorothioate linkages.

In yet other embodiments, siNA molecules of the invention comprise duplex nucleic acid molecules with blunt ends (i.e., without nucleotide overhangs), wherein both ends are blunt, or alternatively, where one of the ends is blunt. In some embodiments, the siNA molecules of the invention can comprises one blunt end, for example wherein the 5'-end of the antisense strand and the 3'-end of the sense strand do not have any overhanging nucleotides. In another example, the siNA molecule comprises one blunt end, for example, wherein the 3'-end of the antisense strand and the 5'-end of the sense strand do not have any overhanging nucleotides. In other embodiments, siNA molecules of the invention comprise two blunt ends, for example wherein the 3'-end of the antisense strand and the 5'-end of the sense strand as well as the 5'-end of the antisense strand and 3'-end of the sense strand do not have any overhanging nucleotides.

In any of the embodiments or aspects of the siNA molecules of the invention, the sense strand and/or the antisense strand can further have a cap, such as described herein or as known in the art, at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand and/or antisense strand. Or as in the case of a hairpin siNA molecule, the cap can be at either one or both of the terminal nucleotides of the polynucleotide. In some embodiments, the cap is at one of both of the ends of the sense strand of a double-stranded siNA molecule. In other embodiments, the cap is at the 3'-end of antisense (guide) strand. In preferred embodiments, the caps are at the 3'-end of the sense strand and the 5'-end of the sense strand.

Representative, but non-limiting examples of such terminal caps include an inverted abasic nucleotide, an inverted deoxy abasic nucleotide, an inverted nucleotide moiety, a group shown in FIG. **5**, a glyceryl modification, an alkyl or cycloalkyl group, a heterocycle, or any other cap as is generally known in the art.

Any of the embodiments of the siNA molecules of the invention can have a 5' phosphate termini. In some embodiments, the siNA molecules lack terminal phosphates.

Any siNA molecule or construct of the invention can comprise one or more chemical modifications. Modifications can be used to improve in vitro in vivo characteristics such as stability, activity, toxicity, immune response (e.g., prevent stimulation of an interferon response, an inflammatory or pro-inflammatory cytokine response, or a Toll-like Receptor (TIF) response), and/or bioavailability.

Applicants describe herein chemically modified siNA molecules with improved RNAi activity and/or stability compared to corresponding unmodified siNA molecules. Various chemically modified siNA motifs disclosed herein provide the capacity to maintain RNAi activity that is substantially similar to unmodified or minimally modified active siRNA (see for example Elbashir et al., 2001, EMBO J., 20:6877-6888) while at the same time providing nuclease resistance and pharmacokinetic properties suitable for use in therapeutic applications.

In various embodiments, the siNA molecules of the invention comprise modifications wherein any (e.g., one or more or all) nucleotides present in the sense and/or antisense strand are modified nucleotides (e.g., wherein one nucleotide is modified, some nucleotides (i.e., plurality or more than one) are modified, or all nucleotides are modified nucleotides. In some embodiments, the siNA molecules of the invention are partially modified (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55 or 59 nucleotides are modified) with chemical modifications. In some embodi-

ments, an siNA molecule of the invention comprises at least about 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, or 60 nucleotides that are modified nucleotides. In other embodiments, the siNA molecules of the invention are completely modified (e.g., 100% modified) with chemical modifications, i.e., the siNA molecule does not contain any ribonucleotides. In some embodiments, one or more of the nucleotides in the sense strand of the siNA molecules of the invention are modified. In the same or other embodiments, one or more the nucleotides in the antisense strand of the siNA molecules of the invention are modified.

The chemical modification within a single siNA molecule can be the same or different. In some embodiments, at least one strand has at least one chemical modification. In other embodiments, each strand has at least one chemical modifications, which can be the same or different, such as, sugar, base, or backbone (i.e., internucleotide linkage) modifications. In other embodiments, siNA molecules of the invention contain at least 2, 3, 4, 5, or more different chemical modifications.

Non-limiting examples of chemical modifications that are suitable for use in the present invention, are disclosed in U.S. patent application Ser. Nos. 10/444,853; 10/981,966; 12/064,014 and in references cited therein and include sugar, base, and phosphate, non-nucleotide modifications, and/or any combination thereof.

In certain specific embodiments of the invention, at least one modified nucleotide is a 2'-deoxy-2-fluoro nucleotide, a 2'-deoxy nucleotide, a 2'-O-alkyl (e.g., 2'-O-methyl) nucleotide, or a locked nucleic acid (LNA) nucleotide as is generally recognized in the art.

In yet other embodiment of the invention, at least one nucleotide has a ribo-like, Northern or A form helix configuration (see e.g., Saenger, Principles of Nucleic Acid Structure, Springer-Verlag ed., 1984). Non-limiting examples of nucleotides having a Northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2'-O, 4'-O-methylene-(D-riboruranosyl) nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl nucleotides, 2'-deoxy-2'-fluoro nucleotides; 2'-deoxy-2'-chloro nucleotides; 2'-azido nucleotides, 2'-O-trifluoromethyl nucleotides; 2'-O-ethyl-trifluoromethoxy nucleotides; 2'-O-difluoromethoxy-ethoxy nucleotides; 4'-thio nucleotides and 2'-O-methyl nucleotides.

In various embodiments, a majority (e.g., greater than 50%) of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In some of the same and/or other embodiments, a majority (e.g., greater than 50%) of the purine nucleotides present in the double-stranded siNA molecule comprises a sugar modification.

In some embodiments, the pyrimidine nucleotides in the antisense strand are 2'-O-methyl or 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the antisense strand are 2'-O-methyl nucleotides or 2'-deoxy nucleotides. In other embodiments, the pyrimidine nucleotides in the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense strand are 2'-O-methyl or 2'-deoxy purine nucleotides.

In certain embodiments of the invention, all the pyrimidine nucleotides in the complementary region on the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In certain embodiments, all of the pyrimidine nucleotides in the complementary region of the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In certain embodiments, all the purine nucleotides in the complementary region on the sense strand are 2'-deoxy purine nucleotides. In certain embodiments, all of the purines in the complementary region on the antisense strand are 2'-O-methyl purine nucleotides. In certain embodiments, all of the pyrimidine nucleotides in the complementary regions on the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides; all of the pyrimidine nucleotides in the complementary region of the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides; all the purine nucleotides in the complementary region on the sense strand are 2'-deoxy purine nucleotides and all of the purines in the complementary region on the antisense strand are 2'-O-methyl purine nucleotides.

In some embodiments, at least 5 or more of the pyrimidine nucleotides in one or both stands are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In some embodiments, at least 5 or more of the pyrimidine nucleotides in one or both stands are 2'-O-methyl pyrimidine nucleotides. In some embodiments, at least 5 or more of the purine nucleotides in one or both stands are 2'-deoxy-2'-fluoro purine nucleotides. In some embodiments, at least 5 or more of the purine nucleotides in one or both stands are 2'-O-methyl purine nucleotides.

In certain embodiments, the purines and pyrimidines are differently modified at the 2'-sugar position (i.e., at least one purine has a different modification from at least one pyrimidine in the same or different strand at the 2'-sugar position). For example, in some instances, at least 5 or more of the pyrimidine nucleotides in one or both stands are 2'-deoxy-2'-fluoro pyrimidine nucleotides and at least 5 or more purine nucleotides in one or both strands are 2'-O-methyl purine nucleotides. In other instances at least 5 or more of the pyrimidine nucleotides in one or both stands are 2'-O-methyl pyrimidine nucleotides and at least 5 or more purine nucleotides in one or both strands are 2'-deoxy-2'-fluoro purine nucleotides.

Further non-limiting examples of sense and antisense strands of such siNA molecules having various modifications and modifications patterns are shown in FIGS. **2** and **3**.

Any of the above described modifications, or combinations thereof, including those in the references cited, can be applied to any of the siNA molecules of the invention.

The modified siNA molecules of the invention can comprise modifications at various locations within the siNA molecule. In some embodiments, the double-stranded siNA molecule of the invention comprises modified nucleotides at internal base paired positions within the siNA duplex. In other embodiments, a double-stranded siNA molecule of the invention comprises modified nucleotides at non-base paired or overhang regions of the siNA molecule. In yet other embodiments, a double-stranded siNA molecule of the invention comprises modified nucleotides at terminal positions of the siNA molecule. For example, such terminal regions include the 3'-position and/or 5'-position of the sense and/or antisense strand or region of the siNA molecule. Additionally, any of the modified siNA molecules of the invention can have a modification in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. Moreover, with regard to chemical modifications of the siNA molecules of the invention, each strand of the double-stranded siNA molecules of the invention can have one or more chemical modifications, such that each strand comprises a different pattern of chemical modifications.

In certain embodiments each strand or a double-stranded siNA molecule of the invention comprises a different pattern of chemical modifications, such as any Stab modification chemistries described herein (see Table 9) or any combination thereof, i.e., different combinations of defined Stabili-

zation chemistry (Stab) sense and antisense strands. Further, non-limiting examples of modification schemes that could give rise to different patterns of modifications are shown in Table 9. The stabilization chemistries referred to in Table 9 as Stab, can be combined in any combination of sense/antisense chemistries, such as Stab 7/8, Stab 7/11, Stab 8/8, Stab 18/8, Stab 18/11, Stab 12/13, Stab 7/13, Stab 18/13, Stab 7/19, Stab 8/19, Stab 18/19, Stab 7/20, Stab 8/20, Stab 18/20, Stab 7/32, Stab 8/32, or Stab 18/32 or any other combination of Stabilization chemistries.

In any of the siNAs of the invention, one or more (for example 1, 2, 3, 4 or 5) nucleotides at the 5'-end of the guide strand or guide region (also known as antisense strand or antisense region) of the siNA molecule are ribonucleotides.

In certain embodiments, the present invention provides a double-stranded short interfering nucleic acid (siNA) molecule that modulates the expression of CTNNB1, wherein the siNA comprises a sense strand and an antisense strand; each strand is independently 15 to 30 nucleotides in length; and the antisense strand comprises at least 15, 16, 17, 18, or 19 nucleotides having sequence complementary to any of:

(SEQ ID NO: 5)
5'-CUGUUGGAUUGAUUCGAAA-3';

(SEQ ID NO: 194)
5'-ACGACUAGUUCAGUUGCUU-3';

(SEQ ID NO: 196)
5'-GGAUGAUCCUAGCUAUCGU-3';
or

(SEQ ID NO: 151)
5'-CCAGGAUGAUCCUAGCUAU-3'.

In some embodiments, the antisense strand of a siNA molecule of the invention comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of:

(SEQ ID NO: 4918)
5'-UUUCGAAUCAAUCCAACAG-3';

(SEQ ID NO: 5107)
5'-AAGCAACUGAACUAGUCGU-3';

(SEQ ID NO: 5109)
5'-ACGAUAGCUAGGAUCAUCC-3';
or

(SEQ ID NO: 5064)
5'-AUAGCUAGGAUCAUCCUGG-3'.

In some embodiments, the sense strand of a siNA molecule of the invention comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of:

(SEQ ID NO: 5)
5'-CUGUUGGAUUGAUUCGAAA-3';

(SEQ ID NO: 194)
5'-ACGACUAGUUCAGUUGCUU-3';

(SEQ ID NO: 196)
5'-GGAUGAUCCUAGCUAUCGU-3';
or

(SEQ ID NO: 151)
5'-CCAGGAUGAUCCUAGCUAU-3'.

In some embodiments, a siNA molecule of the invention comprises any of:

(SEQ ID NO: 5)
5'-CUGUUGGAUUGAUUCGAAA-3'
and

(SEQ ID NO: 4918)
5'-UUUCGAAUCAAUCCAACAG-3';
or

(SEQ ID NO: 194)
5'-ACGACUAGUUCAGUUGCUU-3'
and

(SEQ ID NO: 5107)
5'-AAGCAACUGAACUAGUCGU-3';
or

(SEQ ID NO: 196)
5'-GGAUGAUCCUAGCUAUCGU-3'
and

(SEQ ID NO: 5109)
5'-ACGAUAGCUAGGAUCAUCC-3';
or

(SEQ ID NO: 151)
5'-CCAGGAUGAUCCUAGCUAU-3'
and

(SEQ ID NO: 5064)
5'-AUAGCUAGGAUCAUCCUGG-3'.

Any of the above described modifications, or combinations thereof, including those in the references cited, can be applied to any of these embodiments.

In certain embodiments, the nucleotides of the at least a 15, 16, 17, 18, or 19 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, or SEQ ID NO: 5064 form a contiguous stretch of nucleotides.

In some embodiments, the siNA molecule can contain one or more nucleotide deletions, substitutions, mismatches and/or additions to the at least 15, 16, 17, 18, or 19 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, or SEQ ID NO: 5064; provided, however, that the siNA molecule maintains its activity, for example, to mediate RNAi. In a non-limiting example, the deletion, substitution, mismatch and/or addition can result in a loop or bulge, or alternately a wobble or other alternative (non Watson-Crick) base pair.

In certain embodiments of the invention, double-stranded siNA molecules are provided, wherein the molecule has a sense strand and an antisense strand and comprises the following formula (A):

$$\begin{array}{l} B\text{—}N_{X3}\text{—}(N)_{X2}\ B\text{-}3' \\ B(N)_{X1}\text{—}N_{X4}\text{—}[N]_{X5}\text{-}5' \end{array} \qquad (A)$$

wherein, the upper strand is the sense strand and the lower strand is the antisense strand of the double-stranded nucleic acid molecule; wherein the antisense strand comprises at least a 15, 16, 17, 18, or 19 nucleotide sequence of SEQ ID NO: 4918, SEQ ID NO: 5107, SEQ ID NO: 5109, or SEQ ID NO: 5064, and the sense strand comprises a sequence having complementarity to the antisense strand;

each N is independently a nucleotide which is unmodified or chemically modified or a non-nucleotide;

each B is a terminal cap that is present or absent;

(N) represents overhanging nucleotides, each of which is independently unmodified or chemically modified;

[N] represents nucleotides that are ribonucleotides;

X1 and X2 are independently integers from 0 to 4;

X3 is an integer from 15 to 30;

X4 is an integer from 9 to 30; and

X5 is an integer from 0 to 6, provided that the sum of X4 and X5 is 15-30.

In certain embodiments, the nucleotides of the at least a 15, 16, 17, 18, or 19 nucleotide sequence of SEQ ID NO: 4918, SEQ ID NO: 5107, SEQ ID NO: 5109, or SEQ ID NO: 5064 form a contiguous stretch of nucleotides.

In some embodiments, the siNA molecule of formula A can contain one or more nucleotide deletions, substitutions, mismatches and/or additions to the at least 15, 16, 17, 18, or 19 nucleotide sequence of SEQ ID NO: 4918, SEQ ID NO: 5107, SEQ ID NO: 5109, or SEQ ID NO: 5064; provided, however, that the siNA molecule maintains its activity, for example, to mediate RNAi. In a non-limiting example, the deletion, substitution, mismatch and/or addition can result in a loop or bulge, or alternately a wobble or other alternative (non Watson-Crick) base pair.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) of formula (A); wherein

(a) one or more pyrimidine nucleotides in N_{X4} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-alkyl nucleotides, 2'-deoxy nucleotides, ribonucleotides, or any combinations thereof;

(b) one or more purine nucleotides in N_{X4} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-nucleotides, 2'-deoxy nucleotides, ribonucleotides, or any combination thereof;

(c) one or more pyrimidine nucleotides in N_{X3} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-alkyl nucleotides, 2'-deoxy nucleotides, ribonucleotides, or any combinations thereof; and

(d) one or more purine nucleotides in N_{X3} positions are independently 2'-deoxy-2'-fluoro nucleotides, 2'-O-alkyl nucleotides, 2'-deoxy nucleotides, ribonucleotides, or any combinations thereof.

In certain embodiments, the invention features a double-stranded short interfering nucleic acid (siNA) molecule of formula (A); wherein

(a) 1, 2, 3, 4, 5 or more pyrimidine nucleotides in N_{X4} positions are 2'-deoxy-2'-fluoro nucleotides;

(b) 1, 2, 3, 4, 5 or more purine nucleotides in N_{X4} positions are 2'-O-alkyl nucleotides;

(c) 1, 2, 3, 4, 5 or more pyrimidine nucleotides in N_{X3} positions are 2'-deoxy-2'-fluoro nucleotides; and

(d) 1, 2, 3, 4, 5 or more purine nucleotides in N_{X3} positions are 2'-deoxy nucleotides.

In certain embodiments, the invention features a double-stranded short interfering nucleic acid (siNA) molecule of formula (A) wherein

(a) 1, 2, 3, 4, 5 or more pyrimidine nucleotides in N_{X4} positions are 2'-O-alkyl nucleotides;

(b) 1, 2, 3, 4, 5 or more purine nucleotides in N_{X4} positions are ribonucleotides;

(c) 1, 2, 3, 4, 5 or more pyrimidine nucleotides in N_{X3} positions are 2'-O-alkyl nucleotides; and

(d) 1, 2, 3, 4, 5 or more purine nucleotides in N_{X3} positions are ribonucleotides.

In certain embodiments, the invention features a double-stranded short interfering nucleic acid (siNA) molecule of formula (A); wherein

(a) 1, 2, 3, 4, 5 or more pyrimidine nucleotides in N_{X4} positions are 2'-deoxy-2'-fluoro nucleotides;

(b) 1, 2, 3, 4, 5 or more purine nucleotides in N_{X4} positions are 2'-O-alkyl nucleotides;

(c) 1, 2, 3, 4, 5 or more pyrimidine nucleotides in N_{X3} positions are 2'-O-alkyl nucleotides; and

(d) 1, 2, 3, 4, 5 or more purine nucleotides in N_{X3} positions are 2'-deoxy-2'-fluoro nucleotides.

In certain embodiments, the invention features a double-stranded short interfering nucleic acid (siNA) molecule of formula (A) further comprising one or more phosphorothioate internucleotide linkages.

In some embodiments, siNA molecules having formula A comprise a terminal phosphate group at the 5'-end of the antisense strand or antisense region of the nucleic acid molecule.

In various embodiments, siNA molecules having formula A comprise X5=0, 1, 2, or 3; each X1 and X2=1 or 2; X3=18, 19, 20, 21, 22, or 23, and X4=17, 18, 19, 20, 21, 22, or 23.

In certain embodiments, siNA molecules having formula A comprise X5=3. In other embodiments siNA molecules having formula A comprise X5=0.

In certain embodiments, siNA molecules having formula A comprise X1=2 and X2=2.

In various embodiments, siNA molecules having formula A comprise X5=0, X1=2, and X2=2. In other embodiments, siNA molecules having formula A comprise X5=3, X1=2, and X2=2.

In one specific embodiment, an siNA molecule having formula A comprises X5=3; each X1 and X2=2; X3=19, and X4=16.

In another specific embodiment, an siNA molecule having formula A comprises X5=0; each X1 and X2=2; X3=19, and X4=19.

In certain embodiments, siNA molecules having formula A comprise caps (B) at the 3' and 5' ends of the sense strand or sense region.

In certain embodiments, siNA molecules having formula A comprise caps (B) at the 3'-end of the antisense strand or antisense region.

In various embodiments, siNA molecules having formula A comprise caps (B) at the 3' and 5' ends of the sense strand or sense region and caps (B) at the 3'-end of the antisense strand or antisense region.

In yet other embodiments, siNA molecules having formula A comprise caps (B) only at the 5'-end of the sense (upper) strand of the double-stranded nucleic acid molecule.

In some embodiments, siNA molecules having formula A further comprise one or more phosphorothioate internucleotide linkages between the nucleotides. In certain embodiments, siNA molecules having formula A comprise one or more phosphorothioate internucleotide linkages between the first terminal (N) and the adjacent nucleotide on the 3'end of the sense strand, antisense strand, or both sense strand and antisense strands of the nucleic acid molecule. For example, a double-stranded nucleic acid molecule can comprise X1 and/or X2=2 having overhanging nucleotide positions with a phosphorothioate internucleotide linkage, e.g., (NsN) where "s" indicates phosphorothioate.

In some embodiments, one or more of the nucleotides of siNA molecules having formula A have a universal base.

In certain embodiments, siNA molecules having formula A have at position 14 from the 5'-end of the antisense strand a ribonucleotide when the nucleotide at that position 14 is a purine. In other embodiments, siNA molecules having formula A have at position 14 from the 5'-end of the antisense

strand a ribonucleotide, a 2'-deoxy-2'-fluoro nucleotide or a 2'-O-methyl nucleotide when the nucleotide at that position 14 is a pyrimidine nucleotide.

In some embodiments, siNA molecules having formula A comprises (N) nucleotides in the antisense strand (lower strand) that are complementary to nucleotides in a CTNNB1 target polynucleotide sequence, which also has complementarity to the N and [N] nucleotides of the antisense (lower) strand.

In certain embodiments, one or more siNA molecules of the invention are modified according to modification criteria as shown and described in U.S. Ser. No. 61/408,428 and U.S. Ser. No. 61,408,303, both of which are incorporated by reference herein.

Any of the above described modifications, or combinations thereof, discussed above as applicable to siNAs of the invention, including those in the references cited, can be applied to any of the embodiments to siNA molecules of the present invention.

C. Generation/Synthesis of siNA Molecules

The siNAs of the invention can be obtained using a number of techniques known to those of skill in the art. For example the siNA can be chemically synthesized or may be encoded by plasmid (e.g., transcribed as sequences that automatically fold into duplexes with hairpin loops.). siNA can also be generated by cleavage of longer dsRNA (e.g., dsRNA greater than about 25 nucleotides in length) by the *E coli* RNase II or Dicer. These enzymes process the dsRNA into biologically active siNA (see, e.g., Yang et al., PNAS USA 99:9942-9947 (2002); Calegari et al. *PNAS USA* 99:14236 (2002) Byron et al. Ambion Tech Notes; 10 (1):4-6 (2009); Kawaski et al., *Nucleic Acids Res.,* 31:981-987 (2003), Knight and Bass, *Science,* 293:2269-2271 (2001) and Robertson et al., *J. Biol. Chem* 243:82 (1969).

1. Chemical Synthesis

Preferably, siNA of the invention are chemically synthesized. Oligonucleotides (e.g., certain modified oligonucleotides or portions of oligonucleotides lacking ribonucleotides) are synthesized using protocols known in the art, for example as described in Caruthers et al., 1992, *Methods in Enzymology* 211, 3-19, Thompson et al., International PCT Publication No. WO 99/54459, Wincott et al., 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott et al., 1997, *Methods Mol. Bio.,* 74, 59, Brennan et al., 1998, *Biotechnol Bioeng.,* 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end.

siNA molecules without modifications are synthesized using procedures as described in Usman et al., 1987, *J. Am. Chem. Soc.,* 109, 7845; Scaringe et al., 1990, *Nucleic Acids Res.,* 18, 5433. These syntheses makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end that can be used for certain siNA molecules of the invention.

In certain embodiments, the siNA molecules of the invention are synthesized, deprotected, and analyzed according to methods described in U.S. Pat. Nos. 6,995,259, 6,686,463, 6,673,918, 6,649,751, 6,989,442, and U.S. patent application Ser. No. 10/190,359.

In a non-limiting synthesis example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 second coupling step for 2'-deoxy nucleotides or 2'-deoxy-2'-fluoro nucleotides. Table 10 outlines the amounts and the contact times of the reagents used in the synthesis cycle.

Alternatively, the siNA molecules of the present invention can be synthesized separately and jointed together post-synthetically, for example, by ligation (Moore et al., 1992, *Science* 256, 9923; Draper et al., International PCT Publication No. WO 93/23569; Shabarova et al., 1991, *Nucleic Acids Research* 19, 4247; Bellon et al., 1997, *Nucleosides & Nucleotides,* 16, 951; Bellon et al., 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

Various siNA molecules of the invention can be synthesized using the teachings of Scaringe et al., U.S. Pat. Nos. 5,889,136; 6,008,400; and 6,111,086.

2. Vector Expression

Alternatively, siNA molecules of the invention interact with and down-regulate gene encoding target CTNNB1 molecules can be expressed and delivered from transcription units (see for example Couture et al., 1996, *TIG.,* 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus.

In some embodiments, pol III based constructs are used to express nucleic acid molecules of the invention. Transcription of the siNA molecule sequences can be driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). (see for example, Thompson, U.S. Pat. Nos. 5,902,880 and 6,146,886). (See also, Izant and Weintraub, 1985, *Science,* 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci.*, USA 83, 399; Scanlon et al., 1991, *Proc. Natl. Acad. Sci., USA,* 88, 10591-5; Kashani-Sabet et al., 1992, *Antisense Res. Dev.,* 2, 3-15; Dropulic et al., 1992, *J. Virol.,* **66**, **1432**-41; Weerasinghe et al., 1991, *J. Virol,* 65, 5531-4; Ojwang et al., 1992, *Proc. Natl. Acad. Sci. USA,* 89, 10802-6; Chem et al., 1992, *Nucleic Acids Res.,* 20, 4581-9; Sarver et al., 1990 *Science,* 247, 1222-1225; Thompson et al., 1995, *Nucleic Acids Res.,* 23, 2259; Good et al., 1997, *Gene Therapy,* 4, 45. Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, *Proc. Natl. Acad. Sci. USA,* 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.,* 21, 2867-72; Lieber et al., 1993, *Methods Enzymol.,* 217, 47-66; Zhou et al., 1990, *Mol. Cell. Biol.,* 10, 4529-37). Several investigators have demonstrated that nucleic acid molecules expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet et al., 1992, *Antisense Res. Dev.,* 2, 3-15; Ojwang, et al., 1992, *Proc. Natl. Acad. Sci. USA,* 89, 10802-6; Chen et al., 1992, *Nucleic Acids Res.,* 20, 4581-9; Yu et al., 1993, *Proc. Natl. Acad. Sci. USA,* 90, 6340-4; L'Huillier et al., 1992, *EMBO J.,* 11, 4411-8; Lisziewicz et al., 1993, *Proc. Natl. Acad, Sci. U.S.A.,* 90, 8000-4; Thompson et al., 1995, *Nucleic Acids Res.,* 23, 2259; Sullenger & Cech, 1993, *Science,* 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus. VA RNA are useful in generating high concentrations of desired RNA molecules such as siNA in cells (Thopmson et al., supra; Couture and Stinchcomb, 1996, supra; Noonberg et al., 1994, *Nucleic Acid Res.,* 22, 2830; Noonberg et al., U.S. Pat. No. 5,624,803; Good et al., 1997, *Gene Ther.,* 4, 45: Beigelman et al., International PCT

Publication No. WO 96/18736. The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, supra).

Vectors used to express the siNA molecules of the invention can encode one or both strands of an siNA duplex, or a single self-complementary strand that self hybridizes into an siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul et al., 2002, *Nature Biotechnology.* 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology.* 19, 497; Lee et al., 2002, *Nature Biotechnology,* 19, 500; and Novina et al., 2002, *Nature Medicine*, advance online publication doi; 10.1038/nm725).

D. Carrier/Delivery Systems

The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or as a recombinant plasmid or viral vectors which express the siNA molecules, or otherwise delivered to target cells or tissues. Methods for the delivery of nucleic acid molecules are described in Akhtar et al., 1992, *Trends Cell Bio.,* 2, 139; *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995, Maurer et al., 1999, *Mol. Membr. Biol.,* 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.,* 137, 165-192; and Lee et al., 2000, *ACS Symp. Ser.,* 752, 184-192. Beigelman et al., U.S. Pat. No. 6,395,713 and Sullivan et al., PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as biodegradable polymers, hydrogels, cyclodextrins, (see for example, Gonzalez et al., 1999, *Bioconjugate Chem.,* 10, 1068-1074; Wang et al., International PCT Publication Nos. WO 03/47518 and WO 03/46185), poly (lactic-co-glycolic)acid (PLGA) and PLGA microspheres (see for example U.S. Pat. No. 6,447,796 and US Patent Application Publication No. US 2002130430), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722).

In one aspect, the present invention provides carrier systems containing the siNA molecules described herein. In some embodiments, the carrier system is a lipid-based carrier system, cationic lipid, or liposome nucleic acid complexes, a liposome, a micelle, a virosome, a lipid nanoparticle or a mixture thereof. In other embodiments, the carrier system is a polymer-based carrier system such as a cationic polymer-nucleic acid complex. In additional embodiments, the carrier system is a cyclodextrin-based carrier system such as a cyclodextrin polymer-nucleic acid complex. In further embodiments, the carrier system is a protein-based carrier system such as a cationic peptide-nucleic acid complex. Preferably, the carrier system is a lipid nanoparticle ("LNP") formulation.

In certain embodiments, the siNA molecules of the invention are formulated with a lipid nanoparticle composition such as is described in U.S. patent application Ser. Nos. 11/353,630, 11/586,102, 61/189,925, 61/204,878, 61/235,476, 61/249,807, 61/298,022, 61/351,373, 61/347,640, 61/345,754, 61/322,054, 12/640,342, and 12/617,079, and PCT Applications Nos. PCT/US10/020013 and PCT/US09/053336. In certain preferred embodiments, the siNA molecules of the invention are formulated with a lipid nanoparticle composition comprising a cationic lipid/Cholesterol/PEG-C-DMA/DSPC in a 40/48/2/10 ratio or a cationic lipid/Cholesterol/PEG-DMG/DSPC in a 40/48/2/10 ratio. In more certain embodiments, the cationic lipid is DLinDMA (see Table 12), the PEG is PEG-DMG, and the N/P ratio of the formulation is 2.8. In more preferred embodiments, the cationic lipid is DLinDMA (see Tables 11 & 12).

In various embodiments, lipid nanoparticle formulations described in Table 11 are applied to any siNA molecule or combination of siNA molecules herein. In some embodiments, the invention features a composition comprising an siNA molecule of the invention formulated as any of formulation LNP-051; LNP-053; LNP-04; LNP-069; LNP-073; LNP-077; LNP-080; LNP-082; LNP-083; LNP-060; LNP-061; LNP-086; LNP-097; LNP-098; LNP-099; LNP-100; LNP-101; LNP-102; LNP-103; OR LNP-104 (see Table 11).

In certain other embodiments, the invention features a composition comprising an siNA molecule of the invention formulated with any of the cationic lipid formulations described in U.S. patent application Nos. 61/189,295, 61/204,878, 61/235,476, 61/249,807, and 61/298,022.

In other embodiments, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. Non-limiting, examples of such conjugates are described in U.S. Publication Nos. US2008/0152661 A1 and US 2004/0162260 A1 (e.g., CDM-LBA, CDM-Pip-LBA, CDM-PEG, CDM-NAG, etc.) and U.S. patent application Ser. Nos. 10/427,160 10/201,394, 61/322,422, and 61/315,223; and U.S. Pat. Nos. 6,528,631; 6,335,434; 6,235,886; 6,153,737; 5,214,136; and 5,138,045.

In various embodiments, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular weight, preferably from about 100 to about 50,000 daltons (Da).

In yet other embodiments, the invention features compositions or formulations comprising surface-modified liposomes containing poly(ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes) and siNA molecules of the invention, such as is disclosed in for example, International PCT Publication No. WO 96/10391; Ansell et al., International PCT Publication No. WO 96/10390; Holland et al., International PCT Publication No. WO 96/10392.

In some embodiments, the siNA molecules of the invention can also be formulated or complexed with polyethyleneimine and derivatives thereof, such as polyethyleneimine-polyethyleneglycol-N-acetylgalactosamine (PEI-PEG-GAL) or polyethyleneimine-polyethyleneglycol-tri-N-acetylgalactosamine (PEI-PEG-triGAL) derivatives. In one embodiment, the nucleic acid molecules of the invention are formulated as described in U.S. Patent Application Publication No. 20030077829.

In other embodiments, siNA molecules of the invention are complexed with membrane disruptive agents such as those described in U.S. Patent Application Publication No.

20010007666. In still other embodiments, the membrane disruptive agent or agents and the siNA molecule are also complexed with a cationic lipid or helper lipid molecule, such as those lipids described in U.S. Pat. No. 6,235,310.

In certain embodiments, siNA molecules of the invention are complexed with delivery systems as described in U.S. Patent Application Publication Nos. 2003077829; 20050287551; 20050164220; 20050191627; 20050118594; 20050153919; 20050085486; and 20030158133; and International PCT Publication Nos. WO 00/03683 and WO 02/087541.

In some embodiments, a liposomal formulation of the invention comprises an siNA molecule of the invention (e.g., siNA) formulated or complexed with compounds and compositions described in U.S. Pat. Nos. 6,858,224; 6,534,484; 6,287,591; 6,835,395; 6,586,410; 6,858,225; 6,815,432; 6,586,001; 6,120,798; 6,977,223; 6,998,115; 5,981,501; 5,976,567; 5,705,385; and U.S. Patent Application Publication Nos. 2006/0019912; 2006/0019258; 2006/0008909; 2005/0255153; 2005/0079212/ 2005/0008689; 2003/0077829, 2005/0064595, 2005/0175682, 2005/0118253; 2004/00071654; 2005/0244504; 2005/0265961 and 2003/0077829.

Alternatively, recombinant plasmids and viral vectors, as discussed above, which express siNAs of the invention can be used to deliver the molecules of the invention. Delivery of siNA molecules expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture et al., 1996, TIG., 12, 510). Such recombinant plasmids can also be administered directly or in conjunction with a suitable delivery reagents, including, for example, the Mirus Transit LT1 lipophilic reagent; lipofectin, lipofectamine; cellfectin, polycations (e.g., polylysine) or liposomes lipid-based carrier system, cationic lipid, or liposome nucleic acid complexes, a micelle, a virosome, a lipid nanoparticle.

E. Kits

The present invention also provides nucleic acids in kit form. The kit may comprise a container. The kit typically contains a nucleic acid of the invention with instructions for its administration. In certain instances, the nucleic acids may have a targeting moiety attached. Methods of attaching targeting moieties (e.g. antibodies, proteins) are known to those of skill in the art. In certain instances, the nucleic acids are chemically modified. In other embodiments, the kit contains more than one siNA molecule of the invention. The kits may comprise an siNA molecule of the invention with a pharmaceutically acceptable carrier or diluent. The kits may further comprise excipients.

F. Therapeutic Users/Pharmaceutical Compositions

The present body of knowledge in CTNNB1 research indicates the need for methods to assay CTNNB1 activity and for compounds that can regulate CTNNB1 expression for research, diagnostic, and therapeutic use. As described infra, the nucleic acid molecules of the present invention can be used in assays to diagnose disease state related of CTNNB1 levels. In addition, the nucleic acid molecules and pharmaceutical compositions can be used to treat disease states related to CTNNB1 RNA levels.

1. Disease States Associated with CTNNB1

Particular disease states that can be associated with CTNNB1 expression modulation include various cancers including solid tumors. Non-limiting examples of such cancers include: bilary tract cancer, bladder cancer, transitional cell carcinoma, urothelial carcinoma, osteosarcoma, brain cancer, gliomas, astrocytomas, breast carcinoma, metaplastic carcinoma, cervical cancer, cervical squamous cell carcinoma, rectal cancer, colorectal carcinoma, colon cancer, hereditary nonpolyposis colorectal cancer, colorectal adenocarcinomas, gastrointestinal stromal tumors (GISTs), endometrial carcinoma, endometrial stromal sarcomas, esophageal cancer, esophageal squamous cell carcinoma, esophageal adenocarcinoma, ocular melanoma, uveal melanoma, gallbladder carcinomas, gallbladder adenocarcinoma, renal cell carcinoma, clear cell renal cell carcinoma, transitional cell carcinoma, urothelial carcinomas, wilms tumor, leukemia, acute lymocytic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic (CLL), chronic myeloid (CML), chronic myelomonocytic (CMML), liver cancer, liver carcinoma, hepatoma, hepatocellular carcinoma, cholangiocarcinoma, hepatoblastoma, Lung cancer, non-small cell lung cancer (NSCLC), mesothelioma, B-cell lymphomas, non-Hodgkin lymphoma, diffuse large B-cell lymphoma, Mantle cell lymphoma, T-cell lymphomas, non-Hodgkin lymphoma, precursor T-lymphoblastic lymphoma/leukemia, peripheral T-cell lymphomas, multiple myeloma, nasopharyngeal carcinoma (NPC), neuroblastoma, oropharyngeal cancer, oral cavity squamous cell carcinomas, osteosarcoma, ovarian carcinoma, pancreatic cancer, pancreatic ductal adenocarcinoma, pseudopapillary neoplasms, acinar cell carcinomas, Prostate cancer, prostate adenocarcinoma, skin cancer, melanoma, malignant melanoma, cutaneous melanoma, small intestine carcinomas, stomach cancer, gastric carcinoma, gastrointestinal stromal tumor (GIST), uterine cancer, and uterine sarcoma.

It is understood that the siNA molecules of the invention can degrade the target CTNNB1 mRNA (and thus inhibit the diseases stated above). Inhibition of a disease can be evaluated by directly measuring the progress of the disease in a subject. It can also be inferred through observing a change or reversal in a condition associated with the disease. Additionally, the siNA molecules of the invention can be used as a prophylaxis. Thus, the use of the nucleic acid molecules and pharmaceutical compositions of the invention can be used to ameliorate, treat, prevent, and/or cure these diseases and others associated with regulation of CTNNB1 gene expression.

2. Pharmaceutical Compositions

The siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, prophylactic, cosmetic, veterinary, diagnostic, target validation, genomic discovery, genetic engineering, and pharmacogenomic applications.

a. Formulations

Thus, the present invention, in one aspect, also provides for pharmaceutical compositions of the siNA molecules described, i.e., compositions in a pharmaceutically acceptable carrier or diluent. These pharmaceutical compositions include salts, esters, or salts of such esters, of the above compounds, e.g., acid addition salts, for example, salts of hydrochloric, hydrobromic, hydroiodic, acetic acid, and benzene sulfonic acid. Other salts include for example, sodium potassium, manganese, ammonium, and calcium salts. These formulations or compositions can comprise a pharmaceutically acceptable carrier or diluent as is generally known in the art.

In one embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 5. In another embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising at

least a 15 nucleotide sequence of SEQ ID NO: 4918. In yet another embodiment the invention features a pharmaceutical composition comprising an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 194. In still another embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 5107. In another embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 196. In another embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 5109. In another embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 151. In yet another embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 5064. In still another embodiment, the invention features a pharmaceutical composition comprising an siNA molecule comprising formula (A).

The siNA molecules of the invention are preferably formulated as pharmaceutical compositions prior to administering to a subject, according to techniques known in the art. Pharmaceutical compositions of the present invention are characterized as being at least sterile and pyrogen-free. Methods for preparing pharmaceutical compositions of the invention are within the skill in the art for example as described in *Remington's Pharmaceutical Science,* 17th ed., Mack Publishing Company, Easton, Pa. (1985).

In some embodiments, pharmaceutical compositions of the invention (e.g. siNA and/or LNP formulations thereof) further comprise conventional pharmaceutical excipients and/or additives. Suitable pharmaceutical excipients include preservatives, flavoring agents, stabilizers, antioxidants, osmolality adjusting agents, buffers, and pH adjusting agents. Suitable additives include physiologically biocompatible buffers (e.g., trimethylamine hydrochloride), addition of chelants (such as, for example, DTPA or DTPA-bisamide) or calcium chelate complexes (as for example calcium DTPA, CaNaDTPA-bisamide), or, optionally, additions of calcium or sodium salts (for example, calcium chloride, calcium ascorbate, calcium gluconate or calcium lactate). In addition, antioxidants and suspending agents can be used.

Non-limiting examples of various types of formulations for local administration include ointments, lotions, creams, gels, foams, preparations for delivery by transdermal patches, powders, sprays, aerosols, capsules or cartridges for use in an inhaler or insufflator or drops (for example eye or nose drops), solutions/suspensions for nebulization, suppositories, pessaries, retention enemas and chewable or suckable tablets or pellets (for example for the treatment of aphthous ulcers) or liposome or microencapsulation preparations.

Ointments, creams and gels, can, for example, can be formulated with an aqueous or oily base with the addition of suitable thickening and/or gelling agent and/or solvents. Non limiting examples of such bases can thus, for example, include water and/or an oil such as liquid paraffin or a vegetable oil such as arachis oil or castor oil, or a solvent such as polyethylene glycol. Various thickening agents and gelling agents can be used depending on the nature of the base. Non-limiting examples of such agents include soft paraffin, aluminum stearate, cetostearyl alcohol, polyethylene glycols, woolfat, beeswax, carboxypolymethylene and cellulose derivatives, and/or glyceryl monostearate and/or non-ionic emulsifying agents.

In one embodiment lotions can be formulated with an aqueous or oily base and will in general also contain one or more emulsifying agents, stabilizing agents, dispersing agents, suspending agents or thickening agents.

In one embodiment powders for external application can be formed with the aid of any suitable powder base, for example, talc, lactose or starch. Drops can be formulated with an aqueous or non-aqueous base also comprising one or more dispersing agents, solubilizing agents, suspending agents or preservatives.

Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agent, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a time delay material such as glyceryl monosterate or glyceryl distearate can be employed.

Formulations for oral use can also presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropyl-methylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate; or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example, arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be

added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid

Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

Syrups and elixirs can be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents that have been mentioned above. The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The nucleic acid molecules of the invention can also be administered in the form of suppositories, e.g., for rectal administration of the drug. These compositions can be prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

In other embodiments, the siNA and LNP compositions and formulations provided herein for use in pulmonary delivery further comprise one or more surfactants. Suitable surfactants or surfactant components for enhancing the uptake of the compositions of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoyl-phosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid, ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycero-3-phosphocoline, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitinic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants can be used either as single or part of a multiple component surfactant in a formulation, or as covalently bound additions to the 5' and/or 3' ends of the nucleic acid component of a pharmaceutical composition herein.

b. Combinations

The siNAs and pharmaceutical formulations according to the invention can be administered to a subject alone or used in combination with or include one or more other therapeutic agents, for example, anticancer agents. Thus, combinations of the presently disclosed compounds with other anti-cancer or chemotherapeutic agents are within the scope of the invention. Examples of such agents can be found in *Cancer Principles and Practice of Oncology* by V. T. Devita and S. Hellman (editors), 6^{th} edition (Feb. 15, 2001), Lippincott Williams & Wilkins Publishers. A person of ordinary skill in the art would be able to discern which combinations of agents would be useful based on the particular characteristics of the drugs and the cancer involved. Such anti-cancer agents include, but are not limited to, the following: estrogen receptor modulators, androgen receptor modulators, retinoid receptor modulators, cytotoxic/cytostatic agents, antiproliferative agents, prenyl-protein transferase inhibitors, HMG-CoA reductase inhibitors and other angiogenesis inhibitors, inhibitors of cell proliferation and survival signaling, apoptosis inducing agents and agents that interfere with cell cycle checkpoints. The siNAs of the invention are also useful in combination with any therapeutic agent used in the treatment of HCC, for example, but not limitation sorafenib. The instant compounds are particularly useful when co-administered with radiation therapy.

In a further embodiment, therefore, the invention provides a combination comprising an siNA molecule of the invention, such as for example, but not limitation, an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, or SEQ ID NO: 5064; or formula (A) or a pharmaceutically acceptable salt, solvate or physiologically functional derivative thereof together with one or more anti-cancer or chemotherapeutic agents.

In certain embodiments, the instant siNA molecules of the invention are useful in combination with known anti-cancer agents including the following: estrogen receptor modulators, androgen receptor modulators, retinoid receptor modulators, cytotoxic agents, antiproliferative agents, prenyl-protein transferase inhibitors, HMG-CoA reductase inhibitors, HIV protease inhibitors, reverse transcriptase inhibitors, and other angiogenesis inhibitors.

Examples of estrogen receptor modulators that can be used in combination with the compounds of the invention include, but are not limited to, tamoxifen, raloxifene, idoxifene, LY353381, LY117081, toremifene, fulvestrant, 4-[7-(2,2-dimethyl-1-oxopropoxy-4-methyl-2-[4-[2-(1-piperidinyl)ethoxy]phenyl]-2H-1-benzopyran-3-yl]phenyl-2,2-dimethylpropanoate, 4,4'-dihydroxybenzophenone-2,4-dinitrophenyl-hydrazone, and SH646.

Examples of androgen receptor modulators that can be used in combination with the compounds of the invention include, but are not limited to, finasteride and other 5α-re-

ductase inhibitors, nilutamide, flutamide, bicalutamide, liarozole, and abiraterone acetate.

Examples of such retinoid receptor modulators that can be used in combination with the compounds of the invention include, but are not limited to, bexarotene, tretinoin, 13-cis-retinoic acid, 9-cis-retinoic acid, α-difluoromethylornithine, ILX23-7553, trans-N-(4'-hydroxyphenyl)retinamide, and N-4-carboxyphenyl retinamide.

Examples of cytotoxic agents that can be used in combination with the compounds of the invention include, but are not limited to, sertenef, cachectin, ifosfamide, tasonermin, lonidamine, carboplatin, altretamine, prednimustine, dibromodulcitol, ranimustine, fotemustine, nedaplatin, oxaliplatin, temozolomide, heptaplatin, estramustine, improsulfan tosilate, trofosfamide, nimustine, dibrospidium chloride, pumitepa, lobaplatin, satraplatin, profiromycin, cisplatin, irofulven, dexifosfamide, cis-aminedichloro(2-methyl-pyridine)platinum, benzylguanine, glufosfamide, GPX100, (trans,trans,trans)-bis-mu-(hexane-1,6-diamine)-mu-[diamine-platnium(II)]bis[diamine(chloro)platinum(II)]tetrachloride, diarizidinylspermine, arsenic trioxide, 1-(11-dodecylamino-10-hydroxyundecyl)-3,7-dimethylxanthine, zorubicin, idarubicin, daunorubicin, bisantrene, mitoxantrone, pirarubicin, pinafide, valrubicin, amrubicin, antineoplaston, 3'-deamino-3'-morpholino-13-deoxo-10-hydroxycarminomycin, annamycin, galarubicin, elinafide, MEN10755, and 4-demethoxy-3-deamino-3-aziridinyl-4-methylsulphonyl-daunorubicin (see WO 00/50032).

An example of a hypoxia activatable compound that can be used in combination with the compounds of the invention is tirapazamine.

Examples of proteasome inhibitors that can be used in combination with the compounds of the invention include, but are not limited to, lactacystin and bortezomib.

Examples of microtubule inhibitors/microtubule-stabilising agents that can be used in combination with the compounds of the invention include, but are not limited to, paclitaxel, vindesine sulfate, 3',4'-didehydro-4'-deoxy-8'-norvincaleukoblastine, docetaxol, rhizoxin, dolastatin, mivobulin isethionate, auristatin, cemadotin, RPR109881, BMS184476, vinflunine, cryptophycin, 2,3,4,5,6-pentafluoro-N-(3-fluoro-4-methoxyphenyl)benzene sulfonamide, anhydrovinblastine, N,N-dimethyl-L-valyl-L-valyl-N-methyl-L-valyl-L-prolyl-L-proline-t-butylamide, TDX258, the epothilones (see for example U.S. Pat. Nos. 6,284,781 and 6,288,237) and BMS188797.

Some examples of topoisomerase inhibitors that can be used in combination with the compounds of the invention include, but are not limited to, are topotecan, hycaptamine, irinotecan, rubitecan, 6-ethoxypropionyl-3',4'-O-exo-benzylidene-chartreusin, 9-methoxy-N,N-dimethyl-5-nitropyrazolo[3,4,5-kl]acridine-2-(6H)propanamine, 1-amino-9-ethyl-5-fluoro-2,3-dihydro-9-hydroxy-4-methyl-1H,12H-benzo[de]pyrano[3',4':b,7]-indolizino[1,2b]quinoline-10,13(9H,15H)dione, lurtotecan, 7-[2-(N-isopropylamiono)ethyl]-(20S)camptothecin, BNP1350, BNP11100, BN80915, BN80942, etoposide, phosphate, teniposide, sobuzoxane, 2'-dimethylamino-2'-deoxy-etoposide, GL331, N-[2-(dimethylamino)ethyl]-9-hydroxy-5,6-dimethyl-6H-pyrido[4,3-b]carbazole-1-carboxamide, asulacrine, (5a,5aB,8aa,9b)-9-[2-[N-[2-dimethylamino)ethyl]-N-methylamino]ethyl]-5-[4-hydro0xy-3,5-dimethoxyphenyl]-5,5a,6,8,8a,9-hexohydrofuro(3',4';6,7)naphtho(2,3-d)-1,3-dioxol-6-one, 2,3-(methylenedioxy)-5-methyl-7-hydroxy-8-methoxybenzo[c]-phenanthridinium, 6,9-bis[(2-aminoethyl)amino]benzo[g]isoguinoline-5,10-dione, 5-(3-aminopropylamino)-7,10-dihydroxy-2-(2-hydroxyethylaminomethyl)-6H-pyrazolo[4,5,1-de]acridin-6-one, N-[1-[2(diethylamino)ethylamino]-7-methoxy-9-oxo-9H-thioxanthen-4-ylmethyl]formamide, N-(2-(dimethylamino)ethyl)acridine-4-carboxamide, 6-[[2-(dimethylamino)ethyl]amino]-3-hydroxy-7H-indeno[2,1-c]quinolin-7-one, and dimesna.

Examples of inhibitors of mitotic kinesins, and in particular the human mitotic kinesin KSP, that can be used in combination with the compounds of the invention include, but are not limited to, inhibitors described in PCT Publications WO 01/30768, WO 01/98278, WO 03/050,064, WO 03/050,122, WO 03/049,527, WO 03/049,679, WO 03/049,678, WO04/039774, WO03/079973, WO03/099211, WO03/105855, WO03/106417, WO04/037171, WO04/058148, WO04/058700, WO04/126699, WO05/018638, WO05/109206, WO05/019205, WO05/018547, WO05/017190, US2005/0176776. In an embodiment inhibitors of mitotic kinesins include, but are not limited to inhibitors of KSP, inhibitors of MKLP1, inhibitors of CENP-E, inhibitors of MCAK, inhibitors of Kif14, inhibitors of Mphosph1 and inhibitors of Rab6-KIFL.

Examples of "histone deacetylase inhibitors" that can be used in combination with the compounds of the invention include, but are not limited to, TSA, oxamflatin, PXD101, MG98, valproic acid and scriptaid. Further reference to other histone deacetylase inhibitors may be found in the following manuscript; Miller, T. A. et al. J. Med. Chem. 46 (24):5097-5116 (2003).

Inhibitors of kinases involved in mitotic progression that can be used in combination with the compounds of the invention include, but are not limited to, inhibitors of aurora kinase, inhibitors of Polo-like kinases (PLK) (in particular inhibitors of PLK-1), inhibitors of but-1 and inhibitors of bub-R1.

Antiproliferative agents that can be used in combination with the compounds of the invention include, but are not limited to, antisense RNA and DNA oligonucleotides such as G3139, ODN698, RVASKRAS, GEM231, and INX3001, and antimetabolites such as enocitabine, carmofur, tegafur, pentostatin, doxifluridine, trimetrexate, fludarabine, capecitabine, galocitabine, cytarabine ocfosfate, fosteabine sodium hydrate, raltitrexed, paltitrexid, emitefur, tiazofurin, decitabine, nolatrexed, pemetrexed, nelzarabine, 2'-deoxy-2'-methylidenecytidine, 2'-fluoromethylene-2'-deoxycytidine, N-[5-(2,3-dihydro-benzofuryl)sulfonyl]-N'-(3,4-dichlorophenyl)urea, N6-[4-deoxy-4-[N2-[2(E),4(E)-tetradecadienoyl]glycylamino]-L-glycero-B-L-manno-heptopyranosyl]adenine, aplidine, ecteinascidin, troxacitabine, 4-[2-amino-4-oxo-4,6,7,8-tetrahydro-3H-pyrimidino[5,4-b][1,4]thiazin-6-yl-(S)-ethyl]-2,5-thienoyl-L-glutamic acid, aminopterin, 5-flurouracil, alanosine, 11-acetyl-8-(carbamoyloxymethyl)-4-formyl-6methoxy-14-oxa-1,11-diazatetracyclo(7,4,1,0,0)-tetradeca-2,4,6-trien-9-yl acetic acid ester, swainsonine, lometrexol, dexrazoxane, methioninase, 2'-cyano-2'-deoxy-N4-palmitoyl-1-B-D-arabino furanosyl cytosine and 3-aminopyridine-2-carboxyldehyde thiosemicarbazone.

Examples of monoclonal antibody targeted therapeutic agents that can be used in combination with the compounds of the invention include those therapeutic agents which have cytotoxic agents or radioisotopes attached to a cancer cell specific or target cell specific monoclonal antibody, such as, for example, Bexxar.

Examples of HMG-CoA reductase inhibitors that may be used that can be used in combination with the compounds of the invention include, but are not limited to, lovastatin (MEVACOR®; see U.S. Pat. Nos. 4,231,938, 4,294,926 and 4,319,039), simvastatin (ZOCOR®; see U.S. Pat. Nos. 4,444,784, 4,820,850 and 4,916,239), pravastatin (PRAVA-

CHOL®; see U.S. Pat. Nos. 4,346,227, 4,537,859, 4,410,629, 5,030,447 and 5,180,589), fluvastatin (LESCOL®; see U.S. Pat. Nos. 5,354,772, 4,911,165, 4,929,437, 5,189,164, 5,118,853, 5,290,946 and 5,356,896) and atorvastatin (LIPITOR®; see U.S. Pat. Nos. 5,273,995, 4,681,893, 5,489,691, and 5,342,952). The structural formulas of these and additional HMG-CoA reductase inhibitors that may be used in the instant methods are described at page 87 of M. Yalpani, "Cholesterol Lowering Drugs", *Chemistry & Industry*, pp. 85-89 (5 Feb. 1996) and U.S. Pat. Nos. 4,782,084 and 4,885,314.

Examples of prenyl-protein transferase inhibitors that can be used in combination with the compounds of the invention include, but are not limited to, can be found in the following publications and patents: WO 96/30343, WO 97/18813, WO 97/21701, WO 97/23478, WO 97/38665, WO 98/28980, WO 98/29119, WO 95/32987, U.S. Pat. Nos. 5,420,245, 5,523,430, 5,532,359, 5,510,510, 5,589,485, 5,602,098, European Patent Publ. 0 618 221, European Patent Publ 0 675 112, European Patent Publ. 0 604 181, European Patent Publ. 0 696 593, WO 94/19357, WO 95/08542, WO 95/11917, WO 95/12612, WO 95/12572, WO 95/10514, U.S. Pat. No. 5,661,152, WO 95/10515, WO 95/10516, WO 95/24612, WO 95/34535, WO 95/25086, WO 96/05529, WO 96/06138, WO 96/06183, WO 96/16443, WO 96/21701, WO 96/21456, WO 96/22278, WO 96/24611, WO 96/24612, WO 96/05168, WO 96/05169, WO 96/00736, U.S. Pat. No. 5,571,792, WO 96/17861, WO 96/33159, WO 96/34850, WO 06/34851, WO 96/30017, WO 96/30018, WO 96/30362, WO 96/30363, WO 96/3111, WO 96/31477, WO 96/31478, WO 96/31501, WO 97/00252, WO 97/03047, WO 97/03050, WO 97/04785, WO 97/02920, WO 97/17070, WO 97/23478, WO 97/26246, WO 97/30053, WO 97/44350, WO 98/02436, and U.S. Pat. No. 5,532,359. For an example, of the role of a prenyl-protein transferase inhibitor on angiogenesis see *European J. of Cancer*, Vol. 35, No. 9, pp. 1394-1401 (1999).

Examples of angiogenesis inhibitors that can be used in combination with the compounds of the invention include, but are not limited to, tyrosine kinase inhibitors, such as inhibitors of the tyrosine kinase receptors Flt-1 (VEGFR1) and Flk-1/KDR (VEGFR2), inhibitors of epidermal-derived, fibroblast-derived, or platelet derived growth factors, MMP (matrix metalloprotease) inhibitors, integrin blockers, interferon-α, interleukin-12, pentosan polysulfate, cyclooxygenase inhibitors, including nonsteroidal anti-inflammatories (NSAIDs) like aspirin and ibuprofen as well as selective cyclooxy-genase-2 inhibitors like celecoxib and rofecoxib (*PNAS*, vol. 89, p. 7384 (1992); *JNCI*, Vol. 69, p. 475 (1982); *Arch. Opthalmol.*, Vol. 108, p. 573 (1990); *Anat. Rec.*, Vol. 238, p. 68 (1994); *FEBS Letters*, Vol. 372, p. 83 (1995); *Clin. Orthop.* Vol. 313, p. 76 (1995); *J. Mol. Endocrinol.*, Vol. 16, p. 107 (1996); *Jpn. J. Pharmacol.*, Vol. 75, p. 105 (1997); *Cancer Res.*, Vol. 57, p. 1625 (1997); *Cell*, Vol. 93, p. 705 (1998); *Intl. J. Mol. Med.*, Vol. 2, p. 715 (1998); *J. Biol. Chem.*, Vol. 274, p. 9116 (1999)), steroidal anti-inflammatories (such as corticosteroids, mineralocorticoids, dexamethasone, prednisone, prednisolone, methylpred, betamethasone), carboxyamidotriazole, combretastatin A-4, squalamine, 6-O-chloroacetyl-carbonyl)-fumagillol, thalidomide, angiostatin, troponin-1, angiotensin II antagonists (see Fernandez et al., *J. Lab. Clin. Med.* 105:141-145 (1985)), and antibodies to VEGF (see, *Nature Biotechnology*, Vol. 17, pp. 963-968 (October 1999); Kim et al., *Nature*, 362, 841-844 (1993); WO 00/44777; and WO 00/61186).

Other therapeutic agents that modulate or inhibit angiogenesis may also be used in combination with the compounds of the instant invention and include agents that modulate or inhibit the coagulation and fibrinolysis systems (see review in *Clin. Chem. La. Med.* 38:679-692 (2000)). Examples of such agents that modulate or inhibit the coagulation and fibrinolysis pathways that can be used in combination with the compounds of the invention include, but are not limited to, heparin (see *Thromb. Haemost.* 80:10-23 (1998)), low molecular weight heparins and carboxypeptidase U inhibitors (also known as inhibitors of active thrombin activatable fibrinolysis inhibitor [TAFIa]) (see *Thrombosis Res.* 101:329-354 (2001)). TFAIa inhibitors have been described in PCT Publication WO 03/013,526 and U.S. Ser. No. 60/349,925 (filed Jan. 18, 2002).

Agents that interfere with cell cycle checkpoints that can be used in combination with the compounds of the invention include, but are not limited to, inhibitors of ATR, ATM, the Chk1 and Chk2 kinases and cdk and cdc kinase inhibitors and are specifically exemplified by 7-hydroxystaurosporin, flavopiridol, CYC202 (Cyclacel) and BMS-387032.

Agents that interfere with receptor tyrosine kinases (RTKs) that can be used in combination with the compounds of the invention include, but are not limited to, inhibitors of c-Kit, Eph, PDGF, Flt3 and CTNNB1. Further agents include inhibitors of RTKs as described by Bume-Jensen and Hunter, *Nature,* 411:355-365, 2001.

Inhibitors of cell proliferation and survival signaling pathway that can be used in combination with the compounds of the invention include, but are not limited to, inhibitors of EGFR (for example gefitinib and erlotinib), inhibitors or ERB-2 (for example trastuzumab), inhibitors of IGFR, inhibitors of cytokine receptors, inhibitors of CTNNB1, inhibitors of P13K (for example LY294002), serine/threonine kinases (including but not limited to inhibitors of Akt such as described in WO 02/083064, WO 02/083139, WO 02/083,140, US 2004-0116432, WO 02/083138, US 2004-0102360, WO 03/086404, WO 03/086279, WO 03/086394, WO 03/084473, WO 03/086403, WO 2004/041162, WO 2004/096,131, WO 2004/096129, WO 2004/096135, WO 2004/096130, WO 2005/100356, WO 2005/100344), inhibitors of Raf kinase (for example BAY-43-9006), inhibitors of MEK (for example C1-1040 and PD-098059) and inhibitors of mTOR (for example Wyeth CCI-779). Such agents include small molecule inhibitor compounds and antibody antagonists.

Apoptosis inducing agents that can be sued in combination with the compounds of the invention include, but are not limited to, activators of TNF receptor family members (including the TRAIL receptors).

NSAIDs that are selective COX-2 inhibitors that can be used in combination with the compounds of the invention include, but are not limited to, those NSAIDs disclosed in U.S. Pat. Nos. 5,474,995, 5,861,419, 6,001,843, 6,020,343, 5,409,944, 5,436,265, 5,536,752, 5,550,142, 5,604,260, 5,698,584, 5,710,140, WO 94/15932, U.S. Pat. Nos. 5,344,991, 5,134,142, 5,380,738, 5,393,790, 5,466,823, 5,633,272, and 5,932,598, all of which are hereby incorporated by reference.

Inhibitors of COX-2 that are particularly useful in combination with the compound of the invention include: 3-phenyl-4-(4-(methylsulfonyl)phenyl)-2-(5H)-furanone; and 5-chloro-3-(4-methylsulfonyl)-phenyl-2-(2-methyl-5-pyridinyl)pyridine; or a pharmaceutically acceptable salt thereof.

Compounds that have been described as specific inhibitors of COX-2 and are therefore useful in the present

invention include, but are not limited to: parecoxib, CELEBREX® and BEXTRA® or a pharmaceutically acceptable salt thereof.

Angiogenesis inhibitors that can be used in combination with the compounds of the invention include, but are not limited to, endostatin, ukrain, ranpirnase, 1M862, 5-methoxy-4-[2-methyl-3-(3-methyl-2-butenyl)oxiranyl]-1-oxaspiro[2,5]oct-6-yl(chloroacetyl)carbamate, acetyldinanaline, 5-amino-1-[[3,5-dichloro-4-(4-chlorobenzoyl)-phenyl]methyl]-1H-1,2,3-triazole-4-carboxamide, CM101, squalamine, combretastatin, RPI4610, NX31838, sulfated mannopentaose phosphate, 7,7-(carbonyl-bis[imino-N-methyl-4,2-pyrrolocarbonylimino[N-methyl-4,2-pyrrole]-carbonylimino]-bis (1,3-naphthalene disulfonate), and 3-[(2,4-dimethylpyrrol-5-yl)methylene]-2-indolinone (SU5416).

Tyrosine kinase inhibitors that can be used in combination with the compounds of the invention include, but are not limited to, N-(trifluoromethylphenyl)-5-methylisoxazol-4-carboxamide, 3-[(2,4-dimethylpyrrol-5-yl)methylidenyl)indolin-2-one, 17-(allylamino)-17-demethoxygeldanamycin, 4-(3-chloro-4-fluorophenylamino)-7-methoxy-6-[3-(4-morpholinyl)propoxy]quinazoline, N-(3-ethynylphenyl)-6,7-bis (2-methoxyethoxy)-4-quinazolinamine, BIBX1382, 2,3,9,10,11,12-hexahydro-10-(hydroxymethyl)-10-hydroxy-9-methyl-9,12-epoxy-1H-diindolo[1,2,3-fg:3',2',1'-kl]pyrrolo [3,4-i][1,6]benzodiazocin-1-one, SH268, genistein, imatinib (STI571), CEP2563, 4-(3-chlorophenylamino)-5,6-dimethyl-7H-pyrrolo[2,3-d]pyrimidinemethane sulfonate, 4-(3-bromo-4-hydroxyphenyl)amino-6,7-dimethoxyquinazoline, 4-(4'-hydroxyphenyl)amino-6,7-dimethoxyquinazoline, SU6668, STI571A, N-4-chlorophenyl-4-(4-pyridylmethyl)-1-phthalazinamine, and EMD121974.

Combinations with compounds other than anti-cancer compounds are also encompassed in the instant compositions and methods. For example, combinations of the instantly claimed compounds with PPAR-γ (i.e., PPAR-gamma) agonists and PPAR-δ (i.e., PPAR-delta) agonists are useful in the treatment of certain malignancies. PPAR-γ and PPAR-δ are the nuclear peroxisome proliferator-activated receptors γ and δ. The expression of PPAR-γ on endothelial cells and its involvement in angiogenesis has been reported in the literature (see *J. Cardiovasc. Pharmacol.* 31:909-913 (1998); J. Biol. Chem. 274:9116-9121 (1999); Invest. *Ophthalmol Vis. Sci.* 41:2309-2317 (2000)). More recently, PPAR-γ agonists have been shown to inhibit the angiogenic response to VEGF in vitro; both troglitazone and rosiglitazone maleate inhibit the development of retinal neovascularization in mice. (*Arch. Ophthamol.* 119:709-717 (2001)). Examples of PPAR-γ agonists and PPAR-γ/α agonists that can be used in combination with the compounds of the invention include, but are not limited to, thiazolidinediones (such as DRF2725, CS-011, troglitazone, rosiglitazone, and pioglitazone), fenofibrate, gemfibrozil, clofibrate, GW2570, SB219994, AR-H039242, JTT-501, MCC-555, GW2331, GW409544, NN2344, KRP297, NP0110, DRF4158, NN622, GI262570, PNU182716, DRF552926, 2-[(5,7-dipropyl-3-trifluoromethyl-1,2-benzisoxazol-6-yl)oxy]-2-methylpropionic acid (disclosed in U.S. Ser. No. 09/782,856), and 2(R)-7-(3-(2-chloro-4-(4-fluorophenoxy) phenoxy)propoxy)-2-ethylchromane-2-carboxylic acid (disclosed in U.S. Ser. No. 60/235,708 and 60/244,697).

Another embodiment of the instant invention is the use of the presently disclosed compounds in combination with gene therapy for the treatment of cancer. For an overview of genetic strategies to treating cancer see Hall et al. (*Am J Hum Genet* 61:785-789 (1997)) and Kufe et al. (*Cancer Medicine,* 5th Ed. pp 876-889, B C Decker, Hamilton, 2000). Gene therapy can be used to deliver any tumor suppressing gene. Examples of such genes include, but are not limited to p53, which can be delivered via recombinant virus-mediated gene transfer (see U.S. Pat. No. 6,069,134, for example), a uPA/uPAR antagonist ("Adenovirus-Mediated Delivery of a uPA/uPAR Antagonist Suppresses Angiogenesis-Dependent Tumor Growth and Dissemination in Mice." *Gene Therapy*, August 5 (8):1105-13 (1998)), and interferon gamma (*J Immunol* 164:217-222 (2000)).

The compounds of the instant invention may also be administered in combination with an inhibitor of inherent multidrug resistance (MDR), in particular MDR associated with high levels of expression of transporter proteins. Such MDR inhibitors include inhibitors of p-glycoprotein (P-gp), such as LY335979, XR9576, OC144-093, R101922, VX853 and PSC833 (valspodar).

A compound of the present invention may be employed in conjunction with anti-emetic agents to treat nausea or emesis, including acute, delayed, late-phase, and anticipatory emesis, which may result from the use of a compound of the present invention, alone or with radiation therapy. For the prevention or treatment of emesis, a compound of the present invention may be used in conjunction with other anti-emetic agents, especially neurokinin-1 receptor antagonists, 5H53 receptor antagonists, such as ondansetron, granisetron, tropisetron, and zatisetron, GABAB receptor agonists, such as baclofen, a corticosteriod such as Decadron (dexamethasone), Kenalog, Aristocort, Nasalide, Preferid, Benecorten or others such as disclosed in U.S. Pat. Nos. 2,789,118, 2,990,401, 3,048,581, 3,126,375, 3,929,768, 3,996,359, 3,928,326 and 3,749,712, an antidopaminergic, such as the phenothiazines (for example prochlorperazine, fluphenazine, thioridazine and mesoridazine), metoclopramide or dronabinol. In an embodiment, an anti-emesis agent selected from a neurokinin-1 receptor antagonist, a 5HT3 receptor antagonist and a corticosteroid is administered as an adjuvant for the treatment or prevention of emesis that may result upon administration of the instant compounds.

Neurokinin-1 receptor antagonists of use in conjunction with the compounds of the present invention are fully described, for example, in U.S. Pat. Nos. 5,162,339, 5,232,929, 5,242,930, 5,373,003, 5,387,595, 5,459,270, 5,494,926, 5,496,833, 5,637,699, 5,719,147; European Patent Publication Nos. EP 0 360 390, 0 394 989, 0 428 434, 0 429 366, 0 430 771, 0 436 334, 0 443 132, 0 482 539, 0 498 069, 0 499 313, 0 512 901, 0 512 902, 0 514 273, 0 514 274, 0 514 275, 0 514 276, 0 515 681, 0 517 589, 0 520 555, 0 522 808, 0 528 495, 0 532 456, 0 533 280, 0 536 817, 0 545 478, 0 558 156, 0 577 394, 0 585 913, 0 590 152, 0 599 538, 0 610 793, 0 634 402, 0 686 629, 0 693 489, 0 694 535, 0 699 655, 0 699 674, 0 707 006, 0 708 101, 0 709 375, 0 709 376, 0 714 891, 0 723 959, 0 733 632 and 0 776 893; PCT International Patent Publications Nos. WO 90/05525, 90/05729, 91/098444, 01/18899, 92/01688, 92/06079, 92/12151, 92/15585, 92/17449, 92/20661, 92/20661, 92/20676, 92/21677, 92/22569, 93/00330, 93/00331, 93/01159, 93/01165, 93/01169, 93/01170, 93/06099, 93/09116, 93/10073, 93/14084, 93/14113, 93/18023, 93/19064, 93/21155, 93/21181, 93/23380, 93/24465, 94/00440, 94/01402, 94/02461, 94/02595, 94/03429, 94/03445, 94/04494, 94/04496, 94/05625, 94/07843, 94/08997, 94/10165, 94/10167, 94/10168, 94/10170, 94/11368, 94/13639, 94/13663, 94/14767, 94/15903, 94/19320, 94/19323, 94/20500, 94/26735, 94/26740, 94/29309, 95/02595, 95/04040, 95/04042, 95/06645, 95/07886, 95/07908, 95/08549, 95/11880, 95/14017,

95/15311, 95/16679, 95/17382, 95/18124, 95/18129, 95/19344, 95/20575, 95/21819, 95/22525, 95/23798, 95,26338, 95/28418, 95/30674, 95/30687, 95/33744, 96/05181, 96/05193, 96/05203, 96/06094, 96/07649, 96/10562, 96/16939, 96/18643, 96/20197, 96/21661, 96/29304, 96/29317, 96/29326, 96/29328, 96/31214, 96/32385, 96/37489, 97/01553, 97/01554, 96/03066, 96/08144, 97/14671, 07/17362, 97/18206, 97/19084, 97/19942 and 97/21702; and in British Patent Publication Nos. 2 266 529, 2 268 931 2 269 170, 2 269 590, 2 271 774, 2 292 144, 2 293 168, 2 293 169, and 2 302 689. The preparation of such compounds is fully described in the aforementioned patents and publications, which are incorporated herein by reference.

In an embodiment, the neurokinin-1 receptor antagonist for use in conjunction with the compounds of the present invention is selected from: 2-(R)-(1-(R)-(3,5-bis(trifluoromethyl)-phenyl)ethoxy)-3-(S)-(4-fluorophenyl)-4-(3-(5-oxo-1H,4H,-1,2,4-triazolo)methyl)morpholine, or a pharmaceutically acceptable salt thereof, which is described in U.S. Pat. No. 5,719,147.

A compound of the instant invention may also be useful for treating or preventing cancer, including bone cancer, in combination with bisphosphonates (understood to include bisphosphonates, diphosphonates, bisphosphonic acids and diphosphonic acids). Examples of bisphosphonates include but are not limited to: etidronate (Didronel), pamidronate (Aredia), alendronate (Fosamax), risedronate (Acetonel), zoledronate (Zometa), ibandronate (Boniva), incadronate or cimadronate, clodronate, EB-1053, minodronate, neridronate, piridronate and tiludronate including any and all pharmaceutically acceptable salts, derivatives, hydrates and mixtures thereof.

A compound of the instant invention may also be administered with an agent useful in the treatment of anemia. Such an anemia treatment agent is, for example, a continuous eythropoiesis receptor activator (such as epoetin alfa).

A compound of the instant invention may also be administered with an agent useful in the treatment of neutropenia. Such a neutropenia treatment agent is, for example, a hematopoietic growth factor which regulates the production and function of neutrophils such as a human granulocyte colony stimulating factor, (G-CSF). Examples of a G-CSF include filgrastim and PEG-filgrastim.

A compound of the instant invention may also be administered with an immunologic-enhancing drug, such as levamisole, isoprinosine and Zadaxin.

A compound of the instant invention may also be useful for treating or preventing breast cancer in combination with aromatase inhibitors. Examples of aromatase inhibitors include but are not limited to: anastrozole, letrozole and exemestane.

A compound of the instant invention may also be useful for treating or preventing cancer in combination with other siNA therapeutics.

The compounds of the instant invention may also be administered in combination with γ-secretase inhibitors and/or inhibitors of NOTCH signaling. Such inhibitors include compounds described in WO 01/90084, WO 02/30912, WO 01/70677, WO 03/013506, WO 02/36555, WO 03/093252, WO 03/093264, WO 03/093251, WO 03/093253, WO 23004/039800, WO 2004/039370, WO 2005/030731, WO 2005/014553, U.S. Ser. No. 10/957,251, WO 2004/089911, WO 02/081435, WO 02/081433, WO 03/018543, WO 2004/031137, WO 2004/031139, WO 2004/031138, WO 2004/101538, WO 2004/101539 and WO 02/47671 (including LY-450139).

A compound of the instant invention may also be useful for treating or preventing cancer in combination with PARP inhibitors.

A compound of the instant invention may also be useful for treating cancer in combination with the following therapeutic agents: abarelix (Plenaxis depot®); aldesleukin (Prokine®); Aldesleukin (Proleukin®); Alemtuzumabb (Campath®); alitretinoin (Panretin®); allopurinol (Zyloprim®); altretamine (Hexalen®); amifostine (Ethyol®); anastrozole (Arimidex®); arsenic trioxide (Trisenox®); asparaginase (Elspar®); azacitidine (Vidaza®); bendamustine hydrochloride (Treanda®); bevacuzimab (Avastin®); bexarotene capsules (Targretin®); bexarotene gel (Targretin®); bleomycin (Blenoxane®); bortezomib (Velcade®); brefeldin A; busulfan intravenous (Bisulfex®); busulfan oral (Myleran®); calusterone (Methosarb®); capecitabine (Xeloda®); carboplatin (Paraplatin®); carmustine (BCNU®); BiCNU®); carmustine (Gliadel®); carmustine with Polifeprosan 20 Implant (Gliadel Wafer®); celecoxib (Celebrex®); cetuximab (Erbitux®); chlorambucil (Leukeran®); cisplatin (Platinol®); cladribine (Leustatin®, 2-CdA®); clofarabine (Clolar®); cyclophosphamide Cytoxan®, Neosar®); cyclophosphamide (Cytoxan Injection®); cyclophosphamide (Cytoxan Tablet®); cytarabine (Cytosar-U®); cytarabine liposomal (DepoCyt®); decarbazine (DTIC-Dome®); dactinomycin, actinomycin D(Cosmegen®); dalteparin sodium injection (Fragmin®); Darbepoetin alfa (Aranesp®); dasatinib (Sprycel®); daunorubicin liposomal (DanuoXome®); daunorubicin, daunomycin (Daunorubicin®); daunorubicin, daunomycin (Cerubidine®); degarelix (Firmagon®); Denileukin diftitox (Ontak®); dexrazoxane (Zinecard®); dexrazoxane hydrochloride (Totect®); didemnin G; 17-DMAG; docetaxel (Taxotere®); doxorubicin (Adriamycin PFS®); doxorubicin (Adriamycin®, Rubex®); doxorubicin (Adriamycin PFS Injection®); doxorubicin liposomal (Doxil®); dromostanolone propionate (Dromostanolone®); dromostanolone propionate (Masterone Injection®); eculizumab injection (Soliris®); Elliott's B Solution (Elliott's B Solution®); eltrombopag (Promacta®); epirubicin (Ellence®); Epoetin alfa (epogen®); erlotinib (Tarceva®); estramustine (Emcyt®); ethinyl estradiol; etoposide phosphate (Etopophos®); etoposide, VP-16 (Vepesid®); everolimus tablets (Afinitor®); exemestane (Aromasin®); ferumoxytol (Feraheme Injection®); Filgrastim (Neupogen®); floxuridine (intraarterial) (FUDR®); fludarabine (Fludata®); fluorouracil, 5-FU (Adrucil®); fulvestrant (Faslodex®); gefitinib (Iressa®); geldanamycin; gemcitabine (Gemzar®); gemtuzumab ozogamicin (Mylotarg®); goserelin acetate (Zoladex Implant®); goserelin acetate (Zoladex®); histrelin acetate (Histrelin implant®); hydroxyurea (Hydrea®); Ibritumomab Tiuxetan (Zevalin®); idarubicin (Idamycin®); ifosfamide (IFEX®); imatinib mesylate (Gleevec®); interferon alfa 2a (Roferon A®); Interferon alfa-2b (Intron A®); iobenguane I 123 injection (AdreView®); irinotecan (Camptosar®); ixabepilone (Ixempra®); lapatinib tablets (Tykerb®); lenalidomide (Revlimid®); letrozole (Femara®); leucovorin (Wellcovorin®, Leucovorin®); Leuprolide Acetate (Eligard®); levamisole (Ergamisol®); lomustine, CCNU (CeeBU®); mechlorethamine, nitrogen mustard (Mustargen®); megestrol acetate (Megace®); melphalan, L-PAM (Alkeran®); mercaptopurine, 6-MP (Purinethol®); mesna (Mesnex®); mesna (Mesnex tabs®); methotrexate (Methotrexate®); methoxsalen (Uvadex®); 8-methoxypsoralen; mitomycin C (Mutamycin®); mitotane (Lysodren®); mitoxantrone (Novantrone®); mitramycin; nandrolone phenpropionate (Durabolin-50®); nelarabine (Arranon®); nilotinib (Ta-

signa®); Nofetumomab (Verlum®); ofatumumab (Arzerra®); Oprelvekin (Neumega®); oxaliplatin (Eloxatin®); paclitaxel (Paxene®); paclitaxel (Taxol®); paclitaxel protein-bound particles (Abraxane®); palifermin (Kepivance®); pamidronate (Aredia®); panitumumab (Vectibix®); pazopanib tablets (Votrienttm®); pegademase (Adagen (Pegademase Bovine)®); pegaspargase (Oncaspar®); Pegfilgrastim (Neulasta®); pemetrexed disodium (Alimta®); pentostatin (Nipent®); pipobroman (Vercyte®); plerixafor (Mozobil®); plicamycin, mithramycin (Mithracin®); porfimer sodium (Photofrin®); pralatrexate injection (Folotyn®); procarbazine (Matulane®); quinacrine (Atabrine®); rapamycin, Rasburicase (Elitek®); raloxifene hydrochloride (Evista®); Rituximab (Rituxan®); romidepsin (Istodax®); romiplostim (Nplate®); sargramostim (Leukine®); Sargramostim (Prokine®); sorafenib (Nexavar®); streptozocin (Zanosar®); sunitinib maleate (Sutent®); talc (Sclerosol®); tamoxifen (Nolvadex®); temozolomide (Temodar®); temsirolimus (Torisel®); teniposide, VM-26 (Vumon®); testolactone (Teslac®); thioguanine, 6-TG (Thioguanine®); thiopurine; thiotepa (Thioplex®); topotecan (Hycamtin®); toremifene (Fareston®); Tositumomab (Bexxar®); Tositumomab/I-131 tositumomab (Bexxar®); trans-retinoic acid; Trastuzumab (Herceptin®); tretinoin, ATRA (Vesanoid®); triethylenemelamine; Uracil Mustard (Uracil Mustard Capsules®); valrubicin (Valstar®); vinblastine (Velban®); vincristin (Oncovin®); vinorelbine (Navelbine®); vorinostat (Zolinza®); wortmannin; and zoledronate (Zometa®).

The invention also provides a combination comprising an siNA molecule of the invention comprising at least a 15 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, or SEQ ID NO: 5064; or formula (A) and/or a pharmaceutically acceptable salt, solvate or physiologically functional derivative thereof together with another CTNNB1 inhibitor.

The combinations referred to above can conveniently be presented for use in the form of a pharmaceutical formulation and thus pharmaceutical compositions comprising a combination as defined above together with a pharmaceutically acceptable diluent or carrier represent a further aspect of the invention.

The individual compounds of such combinations can be administered either sequentially or simultaneously in separate or combined pharmaceutical formulations. In one embodiment, the individual compounds will be administered simultaneously in a combined pharmaceutical formulation.

Thus, the described molecules could be used in combination with one or more known compounds, treatments, or procedures to prevent or treat diseases, disorders, conditions, and traits described herein in a subject or organism as are known in the art, such as other CTNNB1 inhibitors.

3. Therapeutic Applications

The present body of knowledge in CTNNB1 research indicates the need for methods that can regulate CTNNB1 expression for therapeutic use.

Thus, one aspect of the invention comprises a method of treating a subject including, but not limited to, a human suffering from a condition which is mediated by the action, or by loss of action, of CTNNB1 gene expression, which method comprises administering to said subject an effective amount of a double-stranded siNA molecule of the invention. In one embodiment of this aspect, the siNA molecules comprises at least a 15 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, or SEQ ID NO: 5064; or formula (A). In another embodiment of this aspect, the condition is or is caused by cancer. Thus, in certain embodiments the molecules and compositions of the instant invention are useful in a method for treating cancer. Cancers treatable according to this aspect of the invention include bilary tract cancer, bladder cancer, transitional cell carcinoma, urothelial carcinoma, osteosarcoma, brain cancer, gliomas, astrocytomas, breast carcinoma, metaplastic carcinoma, cervical cancer, cervical squamous cell carcinoma, rectal cancer, colorectal carcinoma, colon cancer, hereditary nonpolyposis colorectal cancer, colorectal adenocarcinomas, gastrointestinal stromal tumors (GISTs), endometrial carcinoma, endometrial stromal sarcomas, esophageal cancer, esophageal squamous cell carcinoma, esophageal adenocarcinoma, ocular melanoma, uveal melanoma, gallbladder carcinomas, gallbladder adenocarcinoma, renal cell carcinoma, clear cell renal cell carcinoma, transitional cell carcinoma, urothelial carcinomas, wilms tumor, leukemia, acute lymocytic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic (CLL), chronic myeloid (CML), chronic myelomonocytic (CMML), liver cancer, liver carcinoma, hepatoma, hepatocellular carcinoma, cholangiocarcinoma, hepatoblastoma, lung cancer, non-small cell lung cancer (NSCLC), mesothelioma, B-cell lymphomas, non-Hodgkin lymphoma, diffuse large B-bell lymphoma, Mantle cell lymphoma, T-cell lymphomas, non-Hodgkin lymphoma, precursor T-lymphoblastic lymphoma/leukemia, peripheral T-cell lymphomas, multiple myeloma, nasopharyngeal carcinoma (NPC), neuroblastoma, oropharyngeal cancer, oral cavity squamous cell carcinomas, osteosarcoma, ovarian carcinoma, pancreatic cancer, pancreatic ductal adenocarcinoma, pseudopapillary neoplasms, acinar cell carcinomas, prostate cancer, prostate adenocarcinoma, skin cancer, melanoma, malignant melanoma, cutaneous melanoma, small intestine carcinomas, stomach cancer, gastric carcinoma, gastrointestinal stromal tumor (GIST), uterine cancer, uterine sarcoma

In one embodiment, the siNA molecules of the instant invention are useful in a method for treating or preventing cancer selected from: brain cancer, breast carcinoma, cervical cancer, colorectal carcinoma, renal cell carcinoma, leukemia, hepatocellular carcinoma, lung cancer, B-cell lymphomas, multiple myeloma, ovarian carcinoma, pancreatic cancer, prostate cancer, melanoma, and gastric carcinoma. In certain embodiments, the compounds of the instant invention are useful for treating breast carcinoma, colorectal carcinoma, hepatocellular carcinoma, lung cancer, and prostate cancer. In a particular embodiment, the compounds of the instant invention are useful for treating hepatocellular carcinoma.

In another embodiment, the siNA molecules of the instant invention are useful in a method for the prevention or modulation of the metastases of cancer cells and cancer. In particular, the siNA molecules of the instant invention are useful in a method to prevent or modulate the metastases of brain cancer, breast carcinoma, cervical cancer, colorectal carcinoma, renal cell carcinoma, leukemia, hepatocellular carcinoma, lung cancer, B-cell lymphomas, multiple myeloma, ovarian carcinoma, pancreatic cancer, prostate cancer, melanoma, and gastric carcinoma.

In certain embodiments, the administration of the siNA molecule is via local administration or systemic administration. In other embodiments, the invention features contacting the subject or organism with an siNA molecule of the invention via local administration to relevant tissues or cells, such as lung cells and tissues, such as via pulmonary delivery. In yet other embodiments, the invention features contacting the subject or organism with an siNA molecule of

the invention via systemic administration (such as via intravenous or subcutaneous administration of siNA) to relevant tissues or cells, such as cancerous tissues or cells in a subject or organism.

siNA molecules of the invention are also used as reagents in ex vivo applications. For example, siNA reagents are introduced into tissue or cells that are transplanted into a subject for therapeutic effect. The cells and/or tissue can be derived from an organism or subject that alter receives the explant, or can be derived from another organism or subject prior to transplantation. The siNA molecules can be used to modulate the expression of one or more genes in the cells or tissue, such that the cells or tissue obtain a desired phenotype or are able to perform a function when transplanted in vivo. In one embodiment, certain CTNNB1 target cells from a patient are extracted. These extracted cells are contacted with CTNNB1 siNAs targeting a specific nucleotide sequence within the cells under conditions suitable for uptake of the siNAs by these cells (e.g., using delivery reagents such as cationic lipids, liposomes and the like or using techniques such as electroporation to facilitate the delivery of siNAs into cells). The cells are then reintroduced back into the same patient or other patients.

For therapeutic applications, a pharmaceutically effective dose of the siNA molecules or pharmaceutical compositions of the invention is administered to the subject. A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) a disease state. One skilled in the art can readily determine a therapeutically effective dose of the siNA of the invention to be administered to a given subject, by taking into account factors, such as the size and weight of the subject, the extent of the disease progression or penetration, the age, health, and sex of the subject, the route of administration, and whether the administration is regional or systemic. Generally, an amount between 0.1 μg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. The siNA molecules of the invention can be administered in a single dose or in multiple doses.

siNA molecules of the instant invention can be administered once monthly, once weekly, once daily (QD), or divided into multiple monthly, weekly, or daily doses, such as, for example, but not limitation, twice daily (BID), three times daily (TID), once every two weeks. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues.

In addition, the administration can be continuous, i.e., every day, or intermittently. For example, intermittent administration of a compound of the instant invention may be administration one to six days per week or it may mean administration in cycles (e.g. daily administration for two to eight consecutive weeks, then a rest period with no administration for up to one week) or it may mean administration on alternate days.

G. Administration

Compositions or formulations can be administered in a variety of ways. Non-limiting examples of administration methods of the invention include oral, buccal, sublingual, parenteral (i.e., intraarticularly, intravenously, intraperitoneally, subcutaneously, or intramuscularly), local rectal administration or other local administration. In one embodiment, the composition of the invention can be administered by insufflation and inhalation. Administration can be accomplished via single or divided doses. In some embodiments, the pharmaceutical compositions are administered intravenously or intraperiotoneally by a bolus injection (see, e.g., U.S. Pat. No. 5,286,634). Lipid nucleic acid particles can be administered by direct injection at the site of disease or by injection at a site distal from the site of disease (see, e.g., Culver, HUMAN GENE THERAPY, MaryAnn Liebert, Inc., Publishers, New York. pp. 70-71 (1994)). In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered to a cell, subject, or organism as is described herein and as is generally known in the art.

1. In Vivo Administration

In any of the methods of treatment of the invention, the siNA can be administered to the subject systemically as described herein or otherwise known in the art, either alone as a monotherapy or in combination with additional therapies described herein or as are known in the art. Systemic administration can include, for example, pulmonary (inhalation, nebulization etc.) intravenous, subcutaneous, intramuscular, catheterization, nasopharangeal, transdermal, or oral/gastrointestinal administration as is generally known in the art.

In any of the methods of treatment or prevention of the invention, the siNA can be administered to the subject locally or to local tissues as described herein or otherwise known in the art, either alone as a monotheraphy or in combination with additional therapies as are known in the art. Local administration can include, for example, inhalation, nebulization, catheterization, implantation, direct injection, dermal/transdermal application, patches, stenting, car/eye drops, or portal vein administration to relevant tissues, or any other local administration technique, method or procedure, as is generally known in the art.

In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered to the liver as is generally known in the art (see for example Wen et al., 2004, *World J Gastroenterol.,* 10, 244-9; Murao et al., 2002, *Pharm Res.,* 19, 1808-14; Liu et al., 2003, *gene Ther.,* 10, 180-7; Hong et al., 2003, *J Pharm Pharmacol.,* 54, 51-8; Herrmann et al., 2004, *Arch Virol.,* 149, 1611-7; and Matsuno et al., 2003, *gene Ther.,* 10, 1559-66).

In one embodiment, the invention features the use of methods to deliver the siNA molecules of the instant invention to hematopoietic cells, including monocytes and lymphocytes. These methods are described in detail by Hartmann et al., 1998, *J. Phamacol. Exp. Ther.,* 285 (2), 920-928; Kronenwett et al., 1998, *Blood,* 91 (3), 852-862; Filion and Phillips, 1997, *Biochim. Biophys. Acta.,* 1329 (2), 345-356; Ma and Wei, 1996, *Leuk. Res.,* 20 (11/12), 925-930; and Bongartz et al., 1994, *Nucleic Acids Research,* 22 (22), 4681-8.

In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered directly or topically (e.g., locally) to the dermis or follicles as is generally known in the art (see for example Brand, 2001, *Curr. Opin. Mol. Ther.,* 3, 244-8; Regnier et al., 1998, *J. Drug Target,* 5, 275-89; Kanikkannan, 2002, *BioDrugs,* 16, 339-47; Wraight et al., 2001, *Pharmacol. Ther.,* 90, 89-104; and Preat and Dujardin, 2001, STP PharmaSciences, 11, 57-68). In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered directly or topically using a hydroalcoholic gel formulation comprising an alcohol (e.g., ethanol or isopropanol), water, and optionally including additional agents such isopropyl myristate and carbomer 980. In other embodiments the siNA are formulated to be administered

topically to the nasal cavity. Topical preparations can be administered by one or more applications per day to the affected area; over skin areas occulusive dressings can advantageously be used. Continuous or prolonged delivery can be achieved by an adhesive reservoir system.

In one embodiment, an siNA molecule of the invention is administered iontophorectically, for example to a particular organ or compartment (e.g., the eye, back of the eye, heart, liver, kidney, bladder, prostate, tumor, CNS etc.). Non-limiting examples of iontophoretic delivery are described in, for example, WO 03/043689 and WO 03/030989, which are incorporated by reference in their entireties herein.

In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered to the lung as is described herein and as is generally known in the art. In another embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered to lung tissues and cells as is described in U.S. Patent Publication Nos. 2006/0062758; 2006/0014289; and 2004/0077540.

2. Aerosols and Delivery Devices

a. Aerosol Formulations

The compositions of the present invention, either alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation (e.g., intranasally or intratracheally) (see, Brigham et al., *Am. J. Sci.,* 298:278 (1989)). Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

In one embodiment, the siNA molecules of the invention and formulations thereof are administered via pulmonary delivery, such as by inhalation of an aerosol or spray dried formulation administered by an inhalation device or nebulizer, providing rapid local uptake of the nucleic acid molecules into relevant pulmonary tissues. Solid particulate compositions containing respirable dry particles of micronized nucleic acid compositions can be prepared by grinding dried or lyophilized nucleic acid compositions, and then passing the micronized composition through, for example, a 400 mesh screen to break up or separate out large agglomerates. A solid particulate composition comprising the siNA compositions of the invention can optionally contain a dispersant which serves to facilitate the formation of an aerosol as well as other therapeutic compounds. A suitable dispersant is lactose, which can be blended with the nucleic acid compound in any suitable ratio, such as a 1 to 1 ratio by weight.

Spray compositions comprising siNA molecules or compositions of the invention can, for example, be formulated as aqueous solutions or suspensions or as aerosols delivered from pressurized packs, such as a metered dose inhaler, with the use of a suitable liquefied propellant. In one embodiment, aerosol compositions of the invention suitable for inhalation can be either a suspension or a solution and generally contain an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, OR SEQ ID NO: 5064; or formula (A), and a suitable propellant such as a fluorocarbon or hydrogen-containing chlorofluorocarbon or mixtures thereof, particularly hydrofluoroalkanes, especially 1,1,1,2-tetrafluoroethane, 1,1,1,2,3,3,3-heptafluoro-n-propane or a mixture thereof. The aerosol composition can optionally contain additional formulation excipients well known in the art such as surfactants. Non-limiting examples include oleic acid, lecithin or an oligolactic acid or derivate such as those described in WO94/21229 and WO98/34596 and co-solvents for example ethanol. In one embodiment a pharmaceutical aerosol formulation of the invention comprising a compound of the invention and a fluorocarbon or hydrogen-containing chlorofluorocarbon or mixtures thereof as propellant, optionally in combination with a surfactant and/or a co-solvent.

The aerosol formulations of the invention can be buffered by the addition of suitable buffering agents.

Aerosol formulations can include optional additivies including preservatives if the formulation is not prepared sterile. Non-limiting examples include, methyl hydroxybenzoate, anti-oxidants, flavorings, volatile oils, buffering agents and emulsifiers and other formulation surfactants. In one embodiment, fluorocarbon or perfluorocarbon carriers are used to reduce degradation and provide safer biocompatible non-liquid particulate suspension compositions of the invention (e.g., siNA and/or LNP formulations thereof). In another embodiment, a device comprising a nebulizer delivers a composition of the invention (e.g., siNA and/or LNP formulations thereof) comprising fluorochemicals that are bacteriostatic thereby decreasing the potential for microbial growth in compatible devices.

Capsules and cartridges comprising the composition of the invention for use in an inhaler or insufflator, of for example gelatine, can be formulated containing a powder mix for inhalation of a compound of the invention and a suitable powder base such as lactose or starch. In one embodiment, each capsule or cartridge contains an siNA molecule comprising at least a 15 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, or SEQ ID NO: 5046; or formula (A), and one or more excipients. In another embodiment, the compound of the invention can be presented without excipients such as lactose.

The aerosol compositions of the present invention can be administered into the respiratory system as a formulation including particles of respirable size, e.g. particles of a size sufficiently small to pass through the nose, mouth and larynx upon inhalation and through the bronchi and alveoli of the lungs. In general, respirable particles range from about 0.5 to 10 microns in size. In one embodiment, the particulate range can be from 1 to 5 microns. In another embodiment, the particulate range can be from 2 to 3 microns. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is thus minimized. For nasal administration, a particle size in the range of 10-500 um is preferred to ensure retention in the nasal cavity.

In some embodiments, an siNA composition of the invention is administered topically to the nose for example, for the treatment of rhinitis, via pressurized aerosol formulations, aqueous formulations administered to the nose by pressurized pump or by nebulization. Suitable formulations contain water as the diluent or carrier for this purpose. In certain embodiments, the aqueous formulations for administration of the composition of the invention to the lung or nose can be provided with conventional excipients such as buffering agents, tonicity modifying agents and the like.

b. Devices

The siNA molecules of the invention can be formulated and delivered as particles and/or aerosols as discussed above and dispensed from various aerosolization devices known by those of skill in the art.

Aerosols of liquid or non-liquid particles comprising an siNA molecule or formulation of the invention can be

produced by any suitable means, such as with a device comprising a nebulizer (see for example U.S. Pat. No. 4,501,729) such as ultrasonic or air jet nebulizers.

Solid particle aerosols comprising an siNA molecule or formulation of the invention and surfactant can be produced with any solid particulate aerosol generator. One type of solid particle aerosol generator used with the siNA molecules of the invention is an insufflator. A second type of illustrative aerosol generator comprises a metered dose inhaler ("MDI"). MDIs containing siNa molecules or formulations taught herein can be prepared by methods of the art (for example, see Byron, above and WO96/32099).

The siNA molecules can also be formulated as a fluid formulation for delivery from a fluid dispenser, such as those described and illustrated in WO05/044354.

In certain embodiments of the invention, nebulizer devices are used in applications for conscious, spontaneously breathing subjects, and for controlled ventilated subjects of all ages. The nebulizer devices can be used for targeted topical and systemic drug delivery to the lung. In one embodiment, a device comprising a nebulizer is used to deliver an siNA molecule or formulation of the invention locally to lung or pulmonary tissues. In another embodiment, a device comprising a nebulizer is used to deliver a an siNA molecule or formulation of the invention systemically.

H. Other Applications/Uses of siNA Molecules of the Invention

The siNA molecules of the invention can also be used for diagnostic applications, research applications, and/or manufacture of medicants.

In one aspect, the invention features a method for diagnosing a disease, trait, or condition in a subject comprising administering to the subject a composition of the invention under conditions suitable for the diagnosis of the disease, trait, or condition in the subject.

In one embodiment, siNA molecules of the invention are used to down regulate or inhibit the expression of CTNNB1 proteins arising from haplotype polymorphisms that are associated with a trait, disease or condition in a subject or organism. Analysis of CTNNB1 genes, or CTNNB1 protein or RNA levels can be used to identify subjects with such polymorphisms or those subjects who are at risk of developing traits, conditions, or diseases described herein. These subjects are amenable to treatment, for example, treatment with siNA molecules of the invention and any other composition useful in treating diseases related to target gene expression. As such, analysis of CTNNB1 protein or RNA levels can be used to determine treatment type and the course of therapy in treating a subject. Monitoring of CTNNB1 protein or RNA levels can be used to predict treatment outcome and to determine the efficacy of compounds and compositions that modulate the level and/or activity of certain CTNNB1 proteins associated with a trait, disorder, condition, or disease.

In another embodiment, the invention comprises use of a double-stranded nucleic acid according to the invention for use in the manufacture of a medicament. In an embodiment, the medicament is for use in treating a condition that is mediated by the action, or by loss of action, of CTNNB1. In one embodiment, the medicament is for use for the treatment of cancer. In an embodiment, the medicament is for use for the treatment of brain cancer, breast carcinoma, cervical cancer, colorectal carcinoma, renal cell carcinoma, leukemia, hepatocellular carcinoma, lung cancer, B-cell lymphomas, multiple myeloma, ovarian carcinoma, pancreatic cancer, prostate cancer, melanoma, and gastric carcinoma. In a particular embodiment, the compounds of the instant invention are useful for treating hepatocellular carcinoma.

In certain embodiments, siNAs wherein at least one strand at least a 15 nucleotide sequence of SEQ ID NO: 5, SEQ ID NO: 4918, SEQ ID NO: 194, SEQ ID NO: 5107, SEQ ID NO: 196, SEQ ID NO: 5109, SEQ ID NO: 151, or SEQ ID NO: 5064; or formula (A), are for use in a method for treating a cancer, such as, for example but not limitation, brain cancer, breast carcinoma, cervical cancer, colorectal carcinoma, renal cell carcinoma, leukemia, hepatocellular carcinoma, lung cancer, B-cell lymphomas, multiple myeloma, ovarian carcinoma, pancreatic cancer, prostate cancer, melanoma, and gastric carcinoma.

I. Examples

The invention will now be illustrated with the following non-limiting examples. Those of skill in the art will readily recognize a variety of non-critical parameters which can be changed or modified to yield essentially the same results.

Example 1

Design, Synthesis, and Identification of siNAs Active Against CTNNB1

CTNNB1 siNA Synthesis

A series of siNA molecules were designed, synthesized and evaluated for efficacy against CTNNB1 gene expression. Certain CTNNB1 sequences were designed and selected by methods set forth in U.S. application Ser. No. 60/182,604. Other sequences were designed and selected using a proprietary algorithm. The primary criteria for design of certain of the CTNNB1 sequences for human siNAs were (i) homology between two species (human and rhesus monkey) and (ii) high efficacy scores as determined by a proprietary algorithm. The effects of the siNAs on CTNNB1 RNA levels. The target sequences of the siNAs that were selected are set forth in Table 1a (target sequences). The sense and antisense strands of the siNA sequences corresponding to the target sequences in Table 1a are set forth in Table 1b. Various chemically modified siNAs that were synthesized are set forth in Table 1c.

TABLE 1a

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UCGAGCUCAGAGGGUACGA	535	1
GAGGCUCUUGUGCGUACUG	1601	2
GCCCAGAAUGCAGUUCGCC	1709	3
CGAGCUCAGAGGGUACGAG	536	4
CUGUUGGAUUGAUUCGAAA	1797	5
GUCUGCUAUUGUACGUACC	853	6
AAUUCUUGGCUAUUACGAC	1143	7
GGAUGUUCACAACCGAAUU	2014	8
ACAGUAUGCAAUGACUCGA	520	9
AGCUUCCAGACACGCUAUC	814	10
UGUCUGCUAUUGUACGUAC	852	11

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
ACUGUUGGAUUGAUUCGAA	1796	12
CAGGAUACCCAGCGCCGUA	1901	13
GACACGCUAUCAUGCGUUC	822	14
UACUGUUGGAUUGAUUCGA	1795	15
UUCUUGGCUAUUACGACAG	1145	16
ACACGCUAUCAUGCGUUCU	823	17
CAGACACGCUAUCAUGCGU	820	18
UGUUGGAUUGAUUCGAAAU	1798	19
CAGAUCCAAGUCAACGUCU	1380	20
AGGCUCUUGUGCGUACUGU	1602	21
GCGUACUGUCCUUCGGGCU	1612	22
ACUAAUGUCCAGCGUUUGG	626	23
CACAUCCUAGCUCGGGAUG	2000	24
GUUGCUGAGAGGGCUCGAG	2665	25
CAUCUGACCAGCCGACACC	1676	26
UGCGUACUGUCCUUCGGGC	1611	27
ACAAGAUUACAAGAAACGG	2269	28
GUUGUAAACUUGAUUAACU	674	29
UAAACUUGAUUAACUAUCA	678	30
AUAUAAUGAGGACCUAUAC	1245	31
AAACUUGAUUAACUAUCAA	679	32
GAAAUAGUUGAAGGUUGUA	1970	33
AUAAUGAGGACCUAUACUU	1247	34
UUAAAUUCUUGGCUAUUAC	1140	35
UGUAAACUUGAUUAACUAU	676	36
GUAAACUUGAUUAACUAUC	677	37
UUGUAAACUUGAUUAACUA	675	38
GCUUUAGUAAAUAUAAUGA	1235	39
UGGCCACCACCCUGGUGCU	2488	40
CUUUAGUAAAUAUAAUGAG	1236	41
UUUAGUAAAUAUAAUGAGG	1237	42
GUAAAUCGUCCUUUAGGUA	2555	43
ACCUCACUUGCAAUAAUUA	1545	44
UACCAUUCCAUUGUUUGUG	2050	45
UCCAAAGAGUAGCUGCAGG	2097	46
UAUCCAGUUGAUGGGCUGC	2410	47
CAUGCAGAAUACAAAUGAU	871	48

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
CCAAAGAGUAGCUGCAGGG	2098	49
CACCAUCCCACUGGCCUCU	1767	50
ACCAUGCAGAAUACAAAUG	869	51
AAGACAUCACUGAGCCUGC	1641	52
AAUCAGCUGGCCUGGUUUG	2582	53
AACCUCACUUGCAAUAAUU	1544	54
ACCUCAUGGAUGGGCUGCC	2550	55
ACCAUUCCAUUGUUUGUGC	2051	56
CCAUGCAGAAUACAAAUGA	870	57
CUUCGUCAUCUGACCAGCC	1670	58
CUGUGAACUUGCUCAGGAC	2122	59
AGACAUCACUGAGCCUGCC	1642	60
GAGCCAAUGGCUUGGAAUG	2324	61
ACUGAGCCUGCCAUCUGUG	1649	62
AUUGAAGCUGAGGGAGCCA	2159	63
GUUAUGGUCCAUCAGCUUU	785	64
AAUGUGGUCACCUGUGCAG	1511	65
AGCUGGCCUGGUUUGAUAC	2586	66
UGGCUGAACCAUCACAGAU	642	67
CACCCACCAUCCCACUGGC	1763	68
CAAUGGCUUGGAAUGAGAC	2328	69
UGGACCACAAGCAGAGUGC	1280	70
CCAUUCCAUUGUUUGUGCA	2052	71
CAGGACCUCAUGGAUGGGC	2546	72
GUGAACUUGCUCAGGACAA	2124	73
CCAGGACCUCAUGGAUGGG	2545	74
GGCUGAACCAUCACAGAUG	643	75
GGUGCUGACUAUCCAGUUG	2501	76
AUGGCUUGGAAUGAGACUG	2330	77
GGGAAGACAUCACUGAGCC	1638	78
UGGUGACAGGGAAGACAUC	1630	79
UGCUCAUCCCACUAAUGUC	616	80
CUAUCCAGUUGAUGGGCUG	2509	81
GGACCUCAUGGAUGGGCUG	2548	82
CCCACUGGCCUCUGAUAAA	1773	83
UCCGAAUGUCUGAGGACAA	2247	84
UGGCUUGGAAUGAGACUGC	2331	85

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UUCAGAUGAUAUAAAUGUG	1498	86
CCACAAGAUUACAAGAAAC	2267	87
CUCACUUGCAAUAAUUAUA	1547	88
CACUUGCAAUAAUUAUAAG	1549	89
GUACCAUGCAGAAUACAAA	867	90
UCAACGUCUUGUUCAGAAC	1390	91
AUCCCAUCUACACAGUUUG	593	92
UACUCAAGCUGAUUUGAUG	274	93
ACCAGGUGGUGGUUAAUAA	759	94
GCUGCAACUAAACAGGAAG	1439	95
UGGAUUGAUUCGAAAUCUU	1801	96
CAGAUGAUAUAAAUGUGGU	1500	97
AUGGUGUCUGCUAUUGUAC	848	98
CACAAGAUUACAAGAAACG	2268	99
CAAAUGAUGUAGAAACAGC	882	100
GCCACAAGAUUACAAGAAA	2266	101
UACAAAUGAUGUAGAAACA	880	102
UCGAAAUCUUGCCCUUUGU	1810	103
GAUUAACUAUCAAGAUGAU	685	104
CCAGUGGAUUCUGUGUUGU	1007	105
AAAGGCUACUGUUGGAUUG	1789	106
ACAAGUAGCUGAUAUUGAU	499	107
GAUGGAACAUGAGAUGGGU	2470	108
UCAAGAUGAUGCAGAACUU	694	109
CAAGCUGAUUUGAUGGAGU	278	110
UGGACUCUCAGGAAUCUUU	1415	111
UAAAUACCAUUCCAUUGUU	2046	112
AUUACAUCAAGAAGGAGCU	1057	113
UCAGGAAUCUUUCAGAUGC	1422	114
UGAUUAACUAUCAAGAUGA	684	115
ACUUCACUCUAGGAAUGAA	2197	116
AACAUGCAGUUGUAAACUU	666	117
AAGCUGAUUUGAUGGAGUU	279	118
UCUGGGUUCAGAUGAUAUA	1492	119
UUACUUCACUCUAGGAAUG	2195	120
AGGAAUCUUUCAGAUGCUG	1424	121
GCUGAAACAUGCAGUUGUA	661	122

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GUUGCUUGUUCGUGCACAU	1882	123
GGAAGAAAUAGUUGAAGGU	1966	124
AGGACAAGCCACAAGAUUA	2259	125
CAUGCGUUCUCCUCAGAUG	832	126
GAUGAUCCCAGCUACCGUU	2346	127
AGCCUGCCAUCUGUGCUCU	1653	128
UGGAUAUCGCCAGGAUGAU	2389	129
UCUUCGUCAUCUGACCAGC	1669	130
UGUGAACUUGCUCAGGACA	2123	131
CCUGUGCAGCUGGAAUUCU	1521	132
UGAACUUGCUCAGGACAAG	2125	133
UGCUGACUAUCCAGUUGAU	2503	134
GAUGAUAUAAAUGUGGUCA	1502	135
GUGCUGACUAUCCAGUUGA	2502	136
UGACUAUCCAGUUGAUGGG	2506	137
AACUUGCUCAGGACAAGGA	2127	138
CUGACUAUCCAGUUGAUGG	2505	139
GCUCAUCCCACUAAUGUCC	617	140
GCUGACUAUCCAGUUGAUG	2504	141
AUGAUAUAAAUGUGGUCAC	1503	142
CUCAUCCCACUAAUGUCCA	618	143
GCUUUAUUCUCCCAUUGAA	2074	144
CUGGUGCUGACUAUCCAGU	2499	145
AACUGUCUUUGGACUCUCA	1406	146
AGGGCAUGCAGAUCCCAUC	582	147
GAUAUAAAUGUGGUCACCU	1505	148
UUCAGAUGCUGCAACUAAA	1432	149
AAGAAAUAGUUGAAGGUUG	1968	150
CCAGGAUGAUCCUAGCUAU	2398	151
UGGCCAUCUUUAAGUCUGG	954	152
AGCUGAUAUUGAUGGACAG	505	153
UCGGGAUGUUCACAACCGA	2011	154
UGUAGAAGCUGGUGGAAUG	1339	155
UAAAUAUAAUGAGGACCUA	1242	156
CUGAGACAUUAGAUGAGGG	567	157
AGUAAAUAUAAUGAGGACC	1240	158
UGGAUACCUCCCAAGUCCU	438	159

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
AGGAUGCCUUGGGUAUGGA	2445	160
AUUGUACGUACCAUGCAGA	860	161
UUUGGACUCUCAGGAAUCU	1413	162
UUGGAUUGAUUCGAAAUCU	1800	163
UCAGAGGACUAAAUACCAU	2037	164
CCAGGAUGCCUUGGGUAUG	2443	165
AUGGAACAUGAGAUGGGUG	2471	166
GGCUACUGUUGGAUUGAUU	1792	167
AGGACCUCAUGGAUGGGCU	2547	168
UCUGUGCUCUUCGUCAUCU	1662	169
UGAUGGAGUUGGACAUGGC	288	170
AUGAGGGCAUGCAGAUCCC	579	171
ACUAUCCAGUUGAUGGGCU	2508	172
UGAGGGCAUGCAGAUCCCA	580	173
UUGGAUAUCGCCAGGAUGA	2388	174
GCCCAGGACCUCAUGGAUG	2543	175
AACUUGCCACACGUGCAAU	708	176
CCCAAGUCCUGUAUGAGUG	447	177
CACAGAUGCUGAAACAUGC	654	178
CUGGGACCUUGCAUAACCU	912	179
AGUGGAUUCUGUGUUGUUU	1009	180
AAUGCAAGCUUUAGGACUU	1354	181
AGAAAUAGUUGAAGGUUGU	1969	182
UCCGCAUGGAAGAAAUAGU	1659	183
GCUAUGUUCCCUGAGACAU	557	184
UCUGAGUGGUAAAGGCAAU	403	185
UGCAAGCUUUAGGACUUCA	1356	186
UGGACAGUAUGCAAUGACU	517	187
UUAGUAAAUAUAAUGAGGA	1238	188
CUCAGAUGGUGUCUGCUAU	843	189
AGAACAAGUAGCUGAUAUU	496	190
CUUGGAUAUCGCCAGGAUG	2387	191
CAUCUGUGCUCUUCGUCAU	1660	192
CCCUGGUGCUGACUAUCCA	2497	193
ACGACUAGUUCAGUUGCUU	1870	194
UCUUGGACUUGAUAUUGGU	2353	195
GGAUGAUCCUAGCUAUCGU	2401	196

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
AAUACAAAUGAUGUAGAAA	878	197
GAACCAUCACAGAUGCUGA	647	198
UUCACAUCCUAGCUCGGGA	1998	199
UGCAGAUCCCAUCUACACA	588	200
GGACUAAAUACCAUUCCAU	2042	201
CUGCUAUUGUACGUACCAU	855	202
CAGAGGACUAAAUACCAUU	2038	203
GAUAAAGGCUACUGUUGGA	1786	204
AGAUGAUAUAAAUGUGGUC	1501	205
AAAUCAUGCACCUUUGCGU	1834	206
ACGACAGACUGCCUUCAAA	1157	207
UAGUAAAUAUAAUGAGGAC	1239	208
UAAUGAGGACCUAUACUUA	1248	209
UGCUGAAACAUGCAGUUGU	660	210
AUUUGAUGGAGUUGGACAU	285	211
CUGCCAAGUGGGUGGUAUA	1582	212
UGGACUACCAGUUGUGGUU	1735	213
UUAAUAAGGCUGCAGUUAU	771	214
ACAUCAAGAAGGAGCUAAA	1060	215
GGAUAUCGCCAGGAUGAUC	2390	216
CUGACAGAGUUACUUCACU	2186	217
GUGACAGGGAAGACAUCAC	1632	218
UCAUCCCACUAAUGUCCAG	619	219
CUGCCAUCUGUGCUCUUCG	1656	220
AUAUAAAAUGUGGUCACCUG	1506	221
CCACCCUGGUGCUGACUAU	2494	222
UGCUCUUCGUCAUCUGACC	1666	223
ACAGGGAAGACAUCACUGA	1635	224
AGUUGGACAUGGCCAUGGA	294	225
UUGGCUGAACCAUCACAGA	641	226
UAGAUGAGGGCAUGCAGAU	576	227
AGAUGAGGGCAUGCAGAUC	577	228
AUCUGUGCUCUUCGUCAUC	1661	229
GAACUUGCCACACGUGCAA	707	230
CCAUCUGUGCUCUUCGUCA	1659	231
AUGGCAACCAAGAAAGCAA	1185	232
GAAACAUGCAGUUGUAAAC	664	233

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UGGUUAAGCUCUUACACCC	1749	234
AGCUUUAGUAAAUAUAAUG	1234	235
CUAUCAAGAUGAUGCAGAA	691	236
AAGUCAACGUCUUGUUCAG	1387	237
GAUCCAAGUCAACGUCUUG	1382	238
CUAUCAUGCGUUCUCCUCA	828	239
AAUAUAAUGAGGACCUAUA	1244	240
GUGCUAUCUGUCUGCUCUA	1304	241
GAAGCUUCCAGACACGCUA	812	242
UAAUUAUAAGAACAAGAUG	1558	243
AUACAAAUGAUGUAGAAAC	879	244
CUGUCUGCUCUAGUAAUAA	1311	245
UGCUAUUGUACGUACCAUG	856	246
UGCUGAAGGUGCUAUCUGU	1296	247
UCUUUAAGUCUGGAGGCAU	960	248
AUACCAUUCCAUUGUUUGU	2049	249
AGGCUACUGUUGGAUUGAU	1791	250
CAGUUAUGGUCCAUCAGCU	783	251
ACAAGAUGAUGGUCUGCCA	1569	252
GACAUAUGCAGCUGCUGUU	2224	253
CCAUCAUCGUGAGGGCUUA	934	254
GACAGAUCCAAGUCAACGU	1378	255
GAGACAUUAGAUGAGGGCA	569	256
UUCGCCUUCACUAUGGACU	1722	257
UGUUCAGCUUCUGGGUUCA	1483	258
AUCUUGGACUUGAUAUUGG	2352	259
CGUGCAAUCCCUGAACUGA	719	260
AGGUGGUGGUUAAUAAGGC	762	261
UCUACACAGUUUGAUGCUG	599	262
AGAUGGCCCAGAAUGCAGU	1704	263
CAAGAUUACAAGAAACGGC	2270	264
CUGAAACAUGCAGUUGUAA	662	265
CUCCUUCUCUGAGUGGUAA	396	266
AGCAAGCUCAUCAUACUGG	1199	267
AUUAUAAGAACAAGAUGAU	1560	268
UCUGUCUGCUCUAGUAAUA	1310	269
AAGCUUUAGUAAAUAUAAU	1233	270

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GCCGGCUAUUGUAGAAGCU	1330	271
UGUCUGCUCUAGUAAUAAG	1312	272
AAUAAUUAUAAGAACAAGA	1556	273
UAUGGCCAGGAUGCCUUGG	2438	274
UGUCCCGCAAAUCAUGCAC	1826	275
CUUGUUCAGAACUGUCUUU	1397	276
GCUGUGAUACGAUGCUUCA	3181	277
GCGCCGUACGUCCAUGGGU	1912	278
AGAUGGUGUCUGCUAUUGU	846	279
AGAACUGUCUUUGGACUCU	1404	280
CAUGCAGAUCCCAUCUACA	586	281
CUCCUUGGGACUCUUGUUC	1469	282
GGUGCCACUACCACAGCUC	380	283
AGCUGGUGGAAUGCAAGCU	1345	284
CCAUUCCACGACUAGUUCA	1863	285
CAGCGUUUGGCUGAACCAU	635	286
AUCUUUAAGUCUGGAGGCA	959	287
UGGCCAGGAUGCCUUGGGU	2440	288
GAAUACAAAUGAUGUAGAA	877	289
UGGAUGGGCUGCCUCCAGG	2556	290
CGUACGUCCAUGGGUGGGA	1916	291
GGUGUCUGCUAUUGUACGU	850	292
GGUGCUAUCUGUCUGCUCU	1303	293
CCUUCACUAUGGACUACCA	1726	294
GACUCUUGUUCAGCUUCUG	1477	295
AUCUACACAGUUUGAUGCU	598	296
GUUUGUGCAGCUGCUUUAU	2062	297
CAAGAAACGGCUUUCAGUU	2278	298
GUUCAGUUGCUUGUUCGUG	1877	299
UCAGAUGAUAUAAAUGUGG	1499	300
AAUGUUAAAUUCUUGGCUA	1136	301
UGGGUUCAGAUGAUAUAAA	1494	302
AAUAGUUGAAGGUUGUACC	1972	303
CAUGCAGUUGUAAACUUGA	668	304
AAUCUGAAUAAAGUGUAAC	2945	305
CACCACCCUGGUGCUGACU	2492	306
GAGUUGGACAUGGCCAUGG	293	307

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
AUACCCAGCGCCGUACGUC	1905	308
GAGGGCUUACUGGCCAUCU	944	309
GAGGGCAUGCAGAUCCCAU	581	310
GAAGGGAUGGAAGGUCUCC	1454	311
GUCUGAGGACAAGCCACAA	2254	312
UCAUGCACCUUUGCGUGAG	1837	313
GGAAUCUUUCAGAUGCUGC	1425	314
UCACCUGACAGAUCCAAGU	1372	315
CUGAAGGUGCUAUCUGUCU	1298	316
GUCAUCUGACCAGCCGACA	1674	317
CAUUCCACGACUAGUUCAG	1864	318
UGAUCCUAGCUAUCGUUCU	2404	319
GAGCCCUUCACAUCCUAGC	1992	320
GAUGAGGGCAUGCAGAUCC	578	321
AUGGGUAGGGUAAAUCAGU	3091	322
GUGCAAUCCCUGAACUGAC	720	323
AUUCCAUUGUUUGUGCAGC	2054	324
CAUUCUGGUGCCACUACCA	274	325
UACCAUGCAGAAUACAAAU	868	326
AUGCAGUUCGCCUUCACUA	1716	327
UUACUGGCCAUCUUUAAGU	950	328
GCUUCUGGGUUCAGAUGAU	1489	329
CAGGAAGGGAUGGAAGGUC	1451	330
GCUUAUGGCAACCAAGAAA	1181	331
UGACAGGGAAGACAUCACU	1633	332
AUCGCCAGGAUGAUCCUAG	2394	333
AGUAAUAAGCCGGCUAUUG	1322	334
AAUGAUGUAGAAACAGCUC	884	335
UCUGAGGACAAGCCACAAG	2255	336
GGUCUCCUUGGGACUCUUG	1466	337
UGUUCAGAACUGUCUUUGG	1399	338
CUGGUGCCACUACCACAGC	378	339
GUCCAUGGGUGGGACACAG	1921	340
GUGCGUUUAGCUGGUGGGC	1085	341
ACGUACCAUGCAGAAUACA	865	342
GAUGUUCACAACCGAAUUG	2015	343
AGAAAGCAAGCUCAUCAUA	1195	344

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GUUCAGCUUCUGGGUUCAG	1484	345
GCAGGGUGCCAUUCCACGA	1855	346
UAGAAGCUGGUGGAAUGCA	1341	347
CAUGGAAGAAAUAGUUGAA	1963	348
UGAUAUUGGUGCCCAGGGA	2362	349
GGCAUGCAGAUCCCAUCUA	584	350
CGUACUGUCCUUCGGGCUG	1613	351
UUACGACAGACUGCCUUCA	1155	352
UAGUCACUGGCAGCAACAG	334	353
GCCAUUACAACUCUCCACA	1031	354
GCCUUCACUAUGGACUACC	1725	355
GUUCACAACCGAAUUGUUA	2018	356
GGGACCUUGCAUAACCUUU	914	357
AAGCCACAAGAUUACAAGA	2264	358
GCAGCAACAGUCUUACCUG	343	359
UAUUACAUCAAGAAGGAGC	1056	360
UAAUAAGGCUGCAGUUAUG	772	361
GGUGGUGGUUAAUAAGGCU	763	362
UAAUGUCCAGCGUUUGGCU	628	363
CUUCUCUGAGUGGUAAAGG	399	364
ACCAGCCGACACCAAGAAG	1682	365
AUACCUCCCAAGUCCUGUA	441	366
UCACUAUGGACUACCAGUU	1729	367
AGGAUACCCAGCGCCGUAC	1902	368
AGGGAAGACAUCACUGAGC	1637	369
GAUAUCGCCAGGAUGAUCC	2391	370
AAGUAGCUGAUAUUGAUGG	501	371
CAAGCUUUAGGACUUCACC	1358	372
CCCUUUGUCCCGCAAAUCA	1821	373
UUAGAUGAGGGCAUGCAGA	575	374
CAAUGACUCGAGCUCAGAG	528	375
GUGGAUAUGGCCAGGAUGC	2433	376
GUUCAGAUGAUAUAAAUGU	1497	377
UCAGGACAAGGAAGCUGCA	2134	378
UUGAAGCUGAGGGAGCCAC	2160	379
UGGAGUUGGACAUGGCCAU	291	380
AGAUGCUGAAACAUGCAGU	657	381

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UGAUGGUCUGCCAAGUGGG	1575	382
ACAUGCAGUUGUAAACUUG	667	383
CAGAGUUACUUCACUCUAG	2190	384
GACUCGAGCUCAGAGGGUA	532	385
CUGGCCAUCUUUAAGUCUG	953	386
UACGAUGCUUCAAGAGAAA	3188	387
UGACCAGCUCUCUCUUCAG	2301	388
CUCUCUUCAGAACAGAGCC	2310	389
GCUUUCAGUUGAGCUGACC	2287	390
GGGUGGGACACAGCAGCAA	1927	391
UGCCACACGUGCAAUCCCU	712	392
UCUGUGAACUUGCUCAGGA	2121	393
UGAGUAAUGGUGUAGAACA	2898	394
GUUGGAUUGAUUCGAAAUC	1799	395
UACAACUCUCCACAACCUU	1036	396
CAAGUCCUGUAUGAGUGGG	449	397
AGGAAGGGAUGGAAGGUCU	1452	398
AGCUCAUCAUACUGGCUAG	1203	399
GCAAGCUUUAGGACUUCAC	1357	400
AUGUGGUCACCUGUGCAGC	1512	401
ACUCAAGCUGAUUUGAUGG	275	402
GACAUGGCCAUGGAACCAG	299	403
GUAAAUAUAAUGAGGACCU	1241	404
CGCAUGGAAGAAAUAGUUG	1961	405
GAUGCUGCAACUAAACAGG	1436	406
UGAUGGAACAUGAGAUGGG	2469	407
CCAGGUGGUGGUUAAUAAG	760	408
UGAGGACAAGCCACAAGAU	2257	409
ACUGGCCAUCUUUAAGUCU	952	410
AACGGCUUUCAGUUGAGCU	2283	411
CUACUGUUGGAUUGAUUCG	1794	412
GUUGUGGUUAAGCUCUUAC	1745	413
AUACUGGCUAGUGGUGGAC	1211	414
GACCUCAUGGAUGGGCUGC	2549	415
UAGCUCGGGAUGUUCACAA	2007	416
GAACAUGAGAUGGGUGGCC	2474	417
CAGAAUGCAGUUCGCCUUC	1712	418

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
ACGUCCAUGGGUGGGACAC	1919	419
UGGUUCACCAGUGGAUUCU	1000	420
AUAUCGCCAGGAUGAUCCU	2392	421
AACAGGAAGGGAUGGAAGG	1449	422
GUUGAGCUGACCAGCUCUC	2294	423
AAAUGUUAAAUUCUUGGCU	1135	424
GGCUAUUGUAGAAGCUGGU	1333	425
CAGUUGUGGUUAAGCUCUU	1743	426
CUACACAGUUUGAUGCUGC	600	427
UGGAGGCAUUCCUGCCCUG	970	428
GGACAGUUUACCAGUUGCC	3137	429
UCCAUUCUGGUGCCACUAC	372	430
UACACCCACCAUCCCACUG	1761	431
CUGAGCCUGCCAUCUGUGC	1650	432
GAGGCAUUCCUGCCCUGGU	972	433
CUUGGCUAUUACGACAGAC	1147	434
CCCUGAGACAUUAGAUGAG	565	435
AUGCAAUGACUCGAGCUCA	525	436
UAGAGGCUCUUGUGCGUAC	1599	437
UUCACUCUAGGAAUGAAGG	2199	438
GACAAGCCACAAGAUUACA	2261	439
CAGAACUUGCCACACGUGC	705	440
GACCUUGCAUAACCUUUCC	916	441
CACUACCACAGCUCCUUCU	385	442
CUAUUUGGGAUAUGUAUGG	3076	443
UCUUGUUCAGAACUGUCUU	1396	444
GAUGCCUUGGGUAUGGACC	2447	445
UUGUAGAAGCUGGUGGAAU	1338	446
AGGUGUGGCGACAUAUGCA	2215	447
GCAAUCCCUGAACUGACAA	722	448
UGCUCUAGUAAUAAGCCGG	1316	449
CCGACACCAAGAAGCAGAG	1687	450
AGAUGAUGCAGAACUUGCC	697	451
UUGAUGGGCUGCCAGAUCU	2517	452
AGCCGACACCAAGAAGCAG	1685	453
UAUGGGUAGGGUAAAUCAG	3090	454
CUCAUCAUACUGGCUAGUG	1205	455

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UAUUACGACAGACUGCCUU	1153	456
CAAUCCCUGAACUGACAAA	723	457
UCUCCUUGGGACUCUUGUU	1468	458
GAGAUGGGUGGCCACCACC	2480	459
CAGGGUGCCAUUCCACGAC	1856	460
AGUUACUUCACUCUAGGAA	2193	461
UUGGACUUGAUAUUGGUGC	2355	462
CCCUUCACAUCCUAGCUCG	1995	463
AGACACGCUAUCAUGCGUU	821	464
AAUGCAGUUCGCCUUCACU	1715	465
CUUAUGGCAACCAAGAAAG	1182	466
CUCCCAAGUCCUGUAUGAG	445	467
CUUACACCCACCAUCCCAC	1759	468
UGGAAGGUCUCCUUGGGAC	1461	469
AGCCCUUCACAUCCUAGCU	1993	470
GAUGGGCUGCCUCCAGGUG	2558	471
AGCUUCUGGGUUCAGAUGA	1488	472
GAGCCUGCCAUCUGUGCUC	1652	473
UUAAGUCUGGAGGCAUUCC	963	474
ACCUGUGCAGCUGGAAUUC	1520	475
UCCCGCAAAUCAUGCACCU	1828	476
AAGGUGUGGCGACAUAUGC	2214	477
AGCUAUUGAAGCUGAGGGA	2155	478
GUUAGUCACUGGCAGCAAC	332	479
UUCAGUUGCUUGUUCGUGC	1878	480
GAUGAUGGUCUGCCAAGUG	1573	481
CUAAACAGGAAGGGAUGGA	1446	482
CCACGACUAGUUCAGUUGC	1868	483
ACUAGUUCAGUUGCUUGUU	1873	484
GUUCACCAGUGGAUUCUGU	1002	485
GUGGUAAAGGCAAUCCUGA	408	486
UUGAUGGAGUUGGACAUGG	287	487
ACUUGCUCAGGACAAGGAA	2128	488
CCAGUUGAUGGGCUGCCAG	2513	489
GAAAGCAAGCUCAUCAUAC	1196	490
ACAUUAGAUGAGGGCAUGC	572	491
UCCCACUAAUGUCCAGCGU	622	492

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GGCAACCAAGAAAGCAAGC	1187	493
AAAUAGUUGAAGGUUGUAC	1971	494
GGAUAUGUAUGGGUAGGGU	3083	495
UAAUCUGAAUAAAGUGUAA	2944	496
UGCACAUCAGGAUACCCAG	1894	497
GUAAUAAGCCGGCUAUUGU	1323	498
AAGCUCAUCAUACUGGCUA	1202	499
ACGUGCAAUCCCUGAACUG	718	500
AGUUGUGGUUAAGCUCUUA	1744	501
AGGACCAGGUGGUGGUUAA	756	502
GCUCUAGUAAUAAGCCGGC	1317	503
GAUUUGAUGGAGUUGGACA	284	504
UGAUGUAGAAACAGCUCGU	886	505
CUGGUGGAUAUGGCCAGGA	2430	506
CAUCAUACUGGCUAGUGGU	1207	507
GAUCCCAUCUACACAGUUU	592	508
CACGCUAUCAUGCGUUCUC	824	509
GACAGUAUGCAAUGACUCG	519	510
AAGUUGUUGUAACCUGCUG	3166	511
GCUAUUACGACAGACUGCC	1151	512
GCCUCCAGGUGACAGCAAU	2566	513
UCCUGUAUGAGUGGGAACA	453	514
AUGCAGAUCCCAUCUACAC	587	515
UUUCCCAUCAUCGUGAGGG	930	516
CCAAGUGGGUGGUAUAGAG	1585	517
GGACCUUGCAUAACCUUUC	915	518
UCCCAAGUCCUGUAUGAGU	446	519
CACGACUAGUUCAGUUGCU	1869	520
CCGCAUGGAAGAAAUAGUU	1960	521
GGCCCAGAAUGCAGUUCGC	1708	522
CCAUGGAACCAGACAGAAA	306	523
GAAACGGCUUUCAGUUGAG	2281	524
GGGAUAUGUAUGGGUAGGG	3082	525
UUGGGACUCUUGUUCAGCU	1473	526
UAUGUUCCCUGAGACAUUA	559	527
GGACUCUCAGGAAUCUUUC	1416	528
AAGCUGCAGAAGCUAUUGA	2145	529

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GCCCUUCACAUCCUAGCUC	1994	530
AGAGAUGGCCCAGAAUGCA	1702	531
GCAAUCCUGAGGAAGAGGA	417	532
CAGGAUGCCUUGGGUAUGG	2444	533
CUGCUAUGUUCCCUGAGAC	555	534
UUCACAACCGAAUUGUUAU	2019	535
AAAGCAAGCUCAUCAUACU	1197	536
AGGCAAUCCUGAGGAAGAG	415	537
UGUUUGUGCAGCUGCUUUA	2061	538
GGAAUGCAAGCUUUAGGAC	1352	539
CCGGCUAUUGUAGAAGCUG	1331	540
AAUAAGCCGGCUAUUGUAG	1325	541
UCAGCUUCUGGGUUCAGAU	1486	542
CCUGUAUGAGUGGGAACAG	454	543
CACUCAAGAACAAGUAGCU	490	544
CCUUCACAUCCUAGCUCGG	1996	545
AUGCACCUUUGCGUGAGCA	1839	546
UGUUCGUGCACAUCAGGAU	1888	547
UCAGUUGCUUGUUCGUGCA	1879	548
CCCGCAAAUCAUGCACCUU	1829	549
GCUGAUUUGAUGGAGUUGG	281	550
AUAGAGGCUCUUGUGCGUA	1598	551
CAGGACAAGGAAGCUGCAG	2135	552
AGCUCUUACACCCACCAUC	1755	553
CAUCACAGAUGCUGAAACA	651	554
CUAUUGUAGAAGCUGGUGG	1335	555
AUGCCCAGGACCUCAUGGA	2541	556
UGACUCGAGCUCAGAGGGU	531	557
AGUUUGAUGCUGCUCAUCC	606	558
UCCUUCGGGCUGGUGACAG	1620	559
AUGAAGGUGUGGCGACAUA	2211	560
AGUUGAGCUGACCAGCUCU	2293	561
CUGUAUGAGUGGGAACAGG	455	562
CUCAGAGGGUACGAGCUGC	540	563
GGCAAUCCUGAGGAAGAGG	416	564
CAUACUGGCUAGUGGUGGA	1210	565
ACAAGCCACAAGAUUACAA	2262	566

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GCUCUUGUGCGUACUGUCC	1604	567
AUGUGGAUACCUCCCAAGU	435	568
UUGUUUGUGCAGCUGCUUU	2060	569
ACAUAUGCAGCUGCUGUUU	2225	570
UCAGUCCUUCACUCAAGAA	481	571
ACCUUGCAUAACCUUUCCC	917	572
GGCGACAUAUGCAGCUGCU	2221	573
UGGUGUCUGCUAUUGUACG	849	574
GUUCCCUGAGACAUUAGAU	562	575
AUAAAGGCUACUGUUGGAU	1787	576
GUGCCAUUCCACGACUAGU	1860	577
UGGGUGGUAUAGAGGCUCU	1590	578
GGCCAUCUUUAAGUCUGGA	955	579
UAUUGGUGCCCAGGGAGAA	2365	580
CUCGAGCUCAGAGGGUACG	534	581
AGAACUUGCCACACGUGCA	706	582
UACCAGUUGUGGUUAAGCU	1740	583
CGUUUGGCUGAACCAUCAC	638	584
GCUAUUGUAGAAGCUGGUG	1334	585
GGAGGCAUUCCUGCCCUGG	971	586
ACCACCCUGGUGCUGACUA	2493	587
AAUCUUGCCCUUUGUCCCG	1814	588
CGUUUAGCUGGUGGGCUGC	1088	589
CAGUUGAGCUGACCAGCUC	2292	590
UGAUAUAAAUGUGGUCACC	1504	591
CUGAGUGGUAAAGGCAAUC	404	592
AAGGUGCUAUCUGUCUGCU	1301	593
UCCUAGCUCGGGAUGUUCA	2004	594
UCAAGCUGAUUUGAUGGAG	277	595
CCAGCUCUCUCUUCAGAAC	2304	596
ACAUGGCCAUGGAACCAGA	300	597
UACCCAGCGCCGUACGUCC	1906	598
AUAGUUGAAGGUUGUACCG	1973	599
AGCUUUAGGACUUCACCUG	1360	600
ACAUCCAAAGAGUAGCUGC	2094	601
UUGCAUAACCUUUCCCAUC	920	602
UGGCCCAGAAUGCAGUUCG	1707	603

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
AUUCGAAAUCUUGCCCUUU	1808	604
AUAAGCCGGCUAUUGUAGA	1326	605
CGACAGACUGCCUUCAAAU	1158	606
UGCAGUUAUGGUCCAUCAG	781	607
GUUUGAUGCUGCUCAUCCC	607	608
CUAAUGUCCAGCGUUUGGC	627	609
CAAGUAGCUGAUAUUGAUG	500	610
UCUGACAGAGUUACUUCAC	2185	611
GGUGGUAUAGAGGCUCUUG	1592	612
GACCAGGUGGUGGUUAAUA	758	613
CCUCAUGGAUGGGCUGCCU	2551	614
UGUCUUUGGACUCUCAGGA	1409	615
GAACAAGUAGCUGAUAUUG	497	616
GUGCCACUACCACAGCUCC	381	617
GCACCUUUGCGUGAGCAGG	1841	618
GACUUCACCUGACAGAUCC	1368	619
AAAUACCAUUCCAUUGUUU	2047	620
CUCAAGAACAAGUAGCUGA	492	621
UCCUCUGUGAACUUGCUCA	2118	622
UCUGGAGGCAUUCCUGCCC	968	623
AAGUCUGGAGGCAUUCCUG	965	624
UUGAAGGUUGUACCGGAGC	1977	625
ACAUCCUAGCUCGGGAUGU	2001	626
ACCAAGAAAGCAAGCUCAU	1191	627
UUUGGCUGAACCAUCACAG	640	628
CACACGUGCAAUCCCUGAA	715	629
GCUCAUCAUACUGGCUAGU	1204	630
GGGUAGGGUAAAUCAGUAA	3093	631
UUCACCUGACAGAUCCAAG	1371	632
UGGUAAAGGCAAUCCUGAG	409	633
GAUCCUAGCUAUCGUUCUU	2405	634
UUCGUCAUCUGACCAGCCG	1671	635
AAUCUUUCAGAUGCUGCAA	1427	636
UGCAGUUCGCCUUCACUAU	1717	637
AGGAUGAUCCUAGCUAUCG	2400	638
CAGCUCUCUCUUCAGAACA	2305	639
GGUGGGACACAGCAGCAAU	1928	640

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
CAGGAUGAUCCUAGCUAUC	2399	641
AGGAAGAGGAUGUGGAUAC	426	642
AUCUGUCUGCUCUAGUAAU	1309	643
UAACCUUUCCCAUCAUCGU	925	644
CUGCUUUAUUCUCCCAUUG	2072	645
AAUUGUAAUCUGAAUAAAG	2939	646
UCUUGUUCAGCUUCUGGGU	1489	647
GUUCGUGCACAUCAGGAUA	1889	648
AUGAUGCAGAACUUGCCAC	699	649
GCUGAUAUUGAUGGACAGU	506	650
GGUUAAGCUCUUACACCCA	1750	651
GCCCUUUGUCCCGCAAAUC	1820	652
UCAGAGGGUACGAGCUGCU	541	653
AAACAUGCAGUUGUAAACU	665	654
CUUGCCCUUUGUCCCGCAA	1817	655
UUACAAGAAACGGCUUUCA	2275	656
CACUCUGGUGGAUAUGGCC	2426	657
CAUCUUUAAGUCUGGAGGC	958	658
UGCCAUCUGUGCUCUUCGU	1657	659
UCUUGGCUAUUACGACAGA	1146	660
AUUUGGGAUAUGUAUGGGU	3078	661
CAGUGGAUUCUGUGUUGUU	1008	662
CCUUCGGGCUGGUGACAGG	1621	663
GGACACAGCAGCAAUUUGU	1932	664
CCAGCGCCGUACGUCCAUG	1909	665
AAGAAACGGCUUUCAGUUG	2279	666
AUUAGAUGAGGGCAUGCAG	574	667
ACCAGCUCUCUCUUCAGAA	2303	668
AGUUAUGGUCCAUCAGCUU	784	669
GACUAUCCAGUUGAUGGGC	2507	670
AUGCUUGGUUCACCAGUGG	993	671
CUAGCUCGGGAUGUUCACA	2006	672
CUCUUACACCCACCAUCCC	1757	673
CUUGCUCAGGACAAGGAAG	2129	674
AGAUUACAAGAAACGGCUU	2272	675
ACCACAGCUCCUUCUCUGA	389	676
AGAUGCUGCAACUAAACAG	1435	677

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UUAAGCUCUUACACCCACC	1752	678
AAUAAGGCUGCAGUUAUGG	773	679
UUGGGAUAUGUAUGGGUAG	3080	680
GUAACCUGCUGUGAUACGA	3174	681
UGGUCUGCCAAGUGGGUGG	1578	682
CCUUCUCUGAGUGGUAAAG	398	683
GAAGCUAUUGAAGCUGAGG	2153	684
AUGCAGAACUUGCCACACG	702	685
GUAGCUGAUAUUGAUGGAC	503	686
CUCAAGCUGAUUUGAUGGA	275	687
GCAUGGAAGAAAUAGUUGA	1962	688
CUGGUGGAAUGCAAGCUUU	1348	689
CCCAGGACCUCAUGGAUGG	2544	690
UUUGGGAUAUGUAUGGGUA	3079	691
CAAAGUUGUUGUAACCUGC	3164	692
CCGAAUUGUUAUCAGAGGA	2026	693
UAAUUGUAAUCUGAAUAAA	2938	694
AUUGUAAUCUGAAUAAAGU	2940	695
CGAAUUGUUAUCAGAGGAC	2027	696
CCAAGUGGUGUAUGAGUGG	448	697
AAGCCGGCUAUUGUAGAAG	1328	698
AUCCUAGCUAUCGUUCUUU	2406	699
AUAACCUUUCCCAUCAUCG	924	700
GCCAAGUGGGUGGUAUAGA	1584	701
CGACUAGUUCAGUUGCUUG	1871	702
UUGGUUCACCAGUGGAUUC	999	703
GUUCAGAACUGUCUUUGGA	1400	704
UGCUGUGAUACGAUGCUUC	3180	705
UCCAGGUGACAGCAAUCAG	2569	706
UAUGGUCCAUCAGCUUUCU	787	707
UGCCAUUCCACGACUAGUU	1861	708
AACCAAGAAAGCAAGCUCA	1190	709
AUAAUUAUAAGAACAAGAU	1557	710
GUUAAGCUCUUACACCCAC	1751	711
UUGAGUAAUGGUGUAGAAC	2897	712
GUGUGGCGACAUAUGCAGC	2217	713
GACCAGCUCUCUCUUCAGA	2302	714

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UUGUACCGGAGCCCUUCAC	1984	715
AUGGCCAUGGAACCAGACA	302	716
UGGUGGAUAUGGCCAGGAU	2431	717
CCUCUGACAGAGUUACUUC	2183	718
AUGAUCCUAGCUAUCGUUC	2403	719
AUGGUCCAUCAGCUUUCUA	788	720
GGACUCUUGUUCAGCUUCU	1476	721
GCUAUCAUGCGUUCUCCUC	827	722
GCUGACCAGCUCUCUCUUC	2299	723
UCGUGCACAUCAGGAUACC	1891	724
UACUUCACUCUAGGAAUGA	2196	725
UGAAACAUGCAGUUGUAAA	663	726
UAUGCCAUUACAACUCUCC	1028	727
UGUUAUCAGAGGACUAAAU	2032	728
GAUGGAAGGUCUCCUUGGG	1459	729
CAUCCAAAGAGUAGCUGCA	2095	730
GCCGACACCAAGAAGCAGA	1686	731
CUUUGGACUCUCAGGAAUC	1412	732
GGAACAUGAGAUGGGUGGC	2473	733
UGGCAGUGCGUUUAGCUGG	1080	734
GGAAGCUGCAGAAGCUAUU	2143	735
CUCUAGGAAUGAAGGUGUG	2203	736
GUACGAGCUGCUAUGUUCC	548	737
UCCACGACUAGUUCAGUUG	1867	738
CCUCAGAUGGUGUCUGCUA	842	739
CUCUGUGAACUUGCUCAGG	2120	740
GCAGUUAUGGUCCAUCAGC	782	741
UCUUACACCCACCAUCCCA	1758	742
CGCCAGGAUGAUCCUAGCU	2396	743
CACCUGACAGAUCCAAGUC	1373	744
UCACCUGUGCAGCUGGAAU	1518	745
GGAUGGGCUGCCUCCAGGU	2557	746
UACCGGAGCCCUUCACAUC	1987	747
UGAGACAUUAGAUGAGGGC	568	748
CACUCUAGGAAUGAAGGUG	2201	749
UUGAUGCUGCUCAUCCCAC	609	750
UUCUCUGAGUGGUAAAGGC	400	751

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UGUUAGUCACUGGCAGCAA	331	752
GAAGAAAUAGUUGAAGGUU	1967	753
CUUCACUCUAGGAAUGAAG	2198	754
CUGGGUUCAGAUGAUAUAA	1493	755
GGACAAGCCACAAGAUUAC	2260	756
ACCCUGGUGCUGACUAUCC	2496	757
UUGAUAUUGGUGCCCAGGG	2361	758
ACCUCCCAAGUCCUGUAUG	443	759
GUAUGCAAUGACUCGAGCU	523	760
CCAGUUGUGGUUAAGCUCU	1742	761
AUGACUCGAGCUCAGAGGG	530	762
UUGUUGUAACCUGCUGUGA	3169	763
CCAAGUCAACGUCUUGUUC	1385	764
AUCAGAGGACUAAAUACCA	2036	765
UGUAUGGGUAGGGUAAAUC	3088	766
CGUGAGCAGGGUGCCAUUC	1850	767
UGAUGGGCUGCCAGAUCUG	2518	768
CUUGUUCGUGCACAUCAGG	1886	769
CCAUCACAGAUGCUGAAAC	650	770
ACAGUUUACCAGUUGCCUU	3139	771
ACCGAAUUGUUAUCAGAGG	2025	772
GCAGUGCGUUUAGCUGGUG	1082	773
AACAUGAGAUGGGUGGCCA	2475	774
CCUGACAGAUCCAAGUCAA	1375	775
GGGAUGUUCACAACCGAAU	2013	776
GGAUUGAUUCGAAAUCUUG	1802	777
GAAGCUGCAGAAGCUAUUG	2144	778
AAUGACUCGAGCUCAGAGG	529	779
UUGUUCAGCUUCUGGGUUC	1482	780
CCUCACUUGCAAUAAUUAU	1546	781
CAGAUGGUGUCUGCUAUUG	845	782
CUUCACUCAAGAACAAGUA	487	783
AUCACAGAUGCUGAAACAU	652	784
AGUUCGCCUUCACUAUGGA	1720	785
UACUGGCCAUCUUUAAGUC	951	786
CAAGCUUUAGUAAAUAUAA	1232	787
AGCCACAAGAUUACAAGAA	2265	788

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
AAGCAGAGAUGGCCCAGAA	1698	789
GAUGCAGAACUUGCCACAC	701	790
AUCUUUCAGAUGCUGCAAC	1428	791
UGGGACACAGCAGCAAUUU	1930	792
ACAGAUCCAAGUCAACGUC	1379	793
ACAGCAGCAAUUUGUGGAG	1936	794
UGCAACUAAACAGGAAGGG	1441	795
GCUCAGGACAAGGAAGCUG	2132	796
GACUAAAAUACCAUUCCAUU	2043	797
UUUGAUGCUGCUCAUCCCA	608	798
UGGCAGCAACAGUCUUACC	341	799
AAGAAAGCAAGCUCAUCAU	1194	800
UGAUCUUGGACUUGAUAUU	2350	801
CUGAAUAAAGUGUAACAAU	2948	802
ACUAAAAUACCAUUCCAUUG	2044	803
AUCCCACUAAUGUCCAGCG	621	804
CCACUACCACAGCUCCUUC	384	805
CAUCAGGAUACCCAGCGCC	1898	806
UCACAGAUGCUGAAACAUG	653	807
UUUGCGUGAGCAGGGUGCC	1846	808
GCUGAUCUUGGACUUGAUA	2348	809
GGCUAUUACGACAGACUGC	1150	810
GGACAUGGCCAUGGAACCA	298	811
AACAAGAUGAUGGUCUGCC	1568	812
UUACAUCAAGAAGGAGCUA	1058	813
AAUCAUGCACCUUUGCGUG	1835	814
GCAAAUCAUGCACCUUUGC	1832	815
GAGUGGUAAAGGCAAUCCU	406	816
UCGCCUUCACUAUGGACUA	1723	817
AUCCAUUCUGGUGCCACUA	371	818
AUCAGGAUACCCAGCGCCG	1899	819
AGUAUGCAAUGACUCGAGC	522	820
CGGCUUUCAGUUGAGCUGA	2285	821
GCUGCAGUUAUGGUCCAUC	779	822
AUUGAGUAAUGGUGUAGAA	2896	823
GUAAUCUGAAUAAAGUGUA	2943	824
UUGAUGGACAGUAUGCAAU	513	825

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GAUAUGUAUGGGUAGGGUA	3084	826
GAACAAGAUGAUGGUCUGC	1567	827
UUAUCAGAGGACUAAAUAC	2034	828
UUCACCAGUGGAUUCUGUG	1003	829
AAGGUUGUACCGGAGCCCU	1980	830
GUAGAAGCUGGUGGAAUGC	1340	831
AUGCUGCAACUAAACAGGA	1437	832
UCACUCUGGUGGAUAUGGC	2425	833
CUGAUUUGAUGGAGUUGGA	282	834
UCAUCAUACUGGCUAGUGG	1206	835
GCUUGUUCGUGCACAUCAG	1885	836
UCUGCUCUAGUAAUAAGCC	1314	837
UAUCUGUCUGCUCUAGUAA	1308	838
GCAAGCUCAUCAUACUGGC	1200	839
AGAGGGUACGAGCUGCUAU	543	840
UGUGCGUACUGUCCUUCGG	1609	841
GGAAGGGAUGGAAGGUCUC	1453	842
AUGCGUUCUCCUCAGAUGG	833	843
GACAGAGUUACUUCACUCU	2188	844
UUGGCUAUUACGACAGACU	1148	845
GGACUACCAGUUGUGGUUA	1736	846
UUCAGAACUGUCUUUGGAC	1401	847
AUCUGACCAGCCGACACCA	1677	848
ACACAGCAGCAAUUUGUGG	1934	849
UACCACAGCUCCUUCUCUG	388	850
CGUCCAUGGGUGGGACACA	1920	851
UGUGGUUAAGCUCUUACAC	1747	852
UUGUACGUACCAUGCAGAA	861	853
GAUACCCAGCGCCGUACGU	1904	854
UCAUGCGUUCUCCUCAGAU	861	855
GCACAUCAGGAUACCCAGC	1895	856
GAUUACAAGAAACGGCUUU	2273	857
ACUACCAGUUGUGGUUAAG	1738	858
GUCUUGUUCAGAACUGUCU	1395	859
UCAUCUGACCAGCCGACAC	1675	860
CUUUGCGUGAGCAGGGUGC	1845	861
CUGUCUUUGGACUCUCAGG	1408	862

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UACAUCAAGAAGGAGCUAA	1059	863
AGAUCCAAGUCAACGUCUU	1381	864
CAAGUCAACGUCUUGUUCA	1386	865
UCCUUGGGACUCUUGUUCA	1470	866
GGUGGAAUGCAAGCUUUAG	1349	867
CUGCAACUAAACAGGAAGG	1440	868
UUAGGACUUCACCUGACAG	1364	869
AGUAGCUGAUAUUGAUGGA	502	870
UAUAAUGAGGACCUAUACU	1246	871
CCUGCUGUGAUACGAUGCU	3178	872
AUGGGUGGCCACCACCCUG	23483	873
GACUCUCAGGAAUCUUUCA	1417	874
GUGCACAUCAGGAUACCCA	1893	875
UUCCAGACACGCUAUCAUG	817	876
UUGCCACACGUGCAAUCCC	711	877
UCAGAUGCUGCAACUAAAC	1433	878
CUUUAGGACUUCACCUGAC	1362	879
CAUGCACCUUUGCGUGAGC	1838	880
ACAACUCUCCACAACCUUU	1038	881
UGGGACUCUUGUUCAGCUU	1474	882
GCUUGGUUCACCAGUGGAU	997	883
UUCCCAUCAUCGUGAGGGC	931	884
GUCUGCUCUAGUAAUAAGC	1313	885
CAGCUUCUGGGUUCAGAUG	1487	886
CGUCAUCUGACCAGCCGAC	1673	887
UGUUCCCUGAGACAUUAGA	561	888
GCAACCAAGAAAGCAAGCU	1188	889
GGAGUUGGACAUGGCCAUG	292	890
GUCCGCAUGGAAGAAAUAG	1958	891
CUGAUCUUGGACUUGAUAU	2349	892
AUGGAAGGUCUCCUUGGGA	1460	893
GAUGGUCUGCCAAGUGGGU	1576	894
ACUAUCAAGAUGAUGCAGA	690	895
ACAGAUGCUGAAACAUGCA	655	896
UUCAGUUGAGCUGACCAGC	2290	897
AGAGGCUCUUGUGCGUACU	1600	898
GGUGGAUAUGGCCAGGAUG	2432	899

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
CUUGCCACACGUGCAAUCC	710	900
GAAUGCAGUUCGCCUUCAC	1714	901
CCUAGCUCGGGAUGUUCAC	2005	902
UUCACUAUGGACUACCAGU	1728	903
GAUGGGUGGCCACCACCCU	2482	904
UGGUUAAUAAGGCUGCAGU	768	905
AUCAAGAUGAUGCAGAACU	693	906
CUGCUGUGAUACGAUGCUU	3179	907
AUGCCUUGGGUAUGGACCC	2448	908
UGUGAUACGAUGCUUCAAG	3183	909
GAGUGCUGAAGGUGCUAUC	1293	910
GAGGGUACGAGCUGCUAUG	544	911
UUAAUUGUAAUCUGAAUAA	2937	912
CACCAAGAAGCAGAGAUGG	1691	913
GAAUGCAAGCUUUAGGACU	1353	914
ACCUUUGCGUGAGCAGGGU	1843	915
AGGUGCUAUCUGUCUGCUC	1302	916
UUGCUCAGGACAAGGAAGC	2130	917
GCUGAGGGAGCCACAGCUC	2165	918
CUACCACAGCUCCUUCUCU	387	919
UGGAACAUGAGAUGGGUGG	2472	920
GCUAUUGUACGUACCAUGC	857	921
UCUUGCCCUUUGUCCCGCA	1816	922
UUAUAAGAACAAGAUGAUG	1561	923
GGAAGCUUCCAGACACGCU	811	924
UAAGCCGGCUAUUGUAGAA	1327	925
GGACCAGGUGGUGGUUAAU	757	926
CUGAUAUUGAUGGACAGUA	507	927
UGGGUAGGGUAAAUCAGUA	3092	928
ACUUGAUAUUGGUGCCCAG	2359	929
UAAGCUCUUACACCCACCA	1753	930
CUACUCAAGCUGAUUUGAU	273	931
GGUGCCAUUCCACGACUAG	1859	932
UUGGACAUGGCCAUGGAAC	296	933
CUGCUCAUCCCACUAAUGU	615	934
CAUGGCCAUGGAACCAGAC	301	935
AUAGGCAACCAAGAAAGCA	1184	936

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
ACCAGUGGAUUCUGUGUUG	1006	937
ACAGAGUUACUUCACUCUA	2189	938
UAGGACUUCACCUGACAGA	1365	939
GCCAGGAUGCCUUGGGUAU	2442	940
AAUGAGGACCUAUACUUAC	1249	941
AUUCUUGGCUAUUACGACA	1144	942
CUUUAUUCUCCCAUUGAAA	2075	943
UAGCUGAUAUUGAUGGACA	504	944
GAACUGUCUUUGGACUCUC	1405	945
UUAGUCACUGGCAGCAACA	333	946
CCAUUACAACUCUCCACAA	1032	947
GUGGUUAAGCUCUUACACC	1748	948
UGAUUUGAUGGAGUUGGAC	283	949
GCAGAGAUGGCCCAGAAUG	1700	950
ACUAAACAGGAAGGGAUGG	1445	951
ACAAAUGUUAAAUUCUUGG	1133	952
GCAAUGACUCGAGCUCAGA	527	953
CUCGGGAUGUUCACAACCG	2010	954
GUGUCUGCUAUUGUACGUA	851	955
UGUGGAUACCUCCCAAGUC	436	956
GGAUGCCUUGGGUAUGGAC	2446	957
AAAUUCUUGGCUAUUACGA	1142	958
UACGAGCUGCUAUGUUCCC	549	959
CAGUGCGUUUAGCUGGUGG	1083	960
CAAGAUGAUGCAGAACUUG	695	961
AUGAUGUAGAAACAGCUCG	885	962
UGCAGCUGCUUUAUUCUCC	2067	963
CCACAGCUCCUUCUCUGAG	390	964
CAGUUCGCCUUCACUAUGG	1719	965
AAGCUUCCAGACACGCUAU	813	966
UUUCAGUUGAGCUGACCAG	2289	967
UCUGGUGCCACUACCACAG	377	968
CGCUAUCAUGCGUUCUCCU	826	969
GACAGGGAAGACAUCACUG	1634	970
AUCAUACUGGCUAGUGGUG	1208	971
GCUGGUGACAGGGAAGACA	1628	972
AUCCUAGCUCGGGAUGUUC	2003	973

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GUCCUGUAUGAGUGGGAAC	452	974
UGGGAUAUGUAUGGGUAGG	3081	975
CUUGGACUUGAUAUUGGUG	2354	976
CCUUUGUCCCGCAAAUCAU	1822	977
UGAAGGUGCUAUCUGUCUG	1299	978
CCUUCACUCAAGAACAAGU	486	979
GAAGGUCUCCUUGGGACUC	1463	980
AGAAACGGCUUUCAGUUGA	2280	981
ACCCAGCGCCGUACGUCCA	1907	982
CAUAACCUUUCCCAUCAUC	925	983
GAAGGUUGUACCGGAGCCC	1979	984
GUCCCGCAAAUCAUGCACC	1827	985
CAAGCUCAUCAUACUGGCU	1201	986
CGCCGUACGUCCAUGGGUG	1913	987
AGAGUUACUUCACUCUAGG	2191	988
GUUGGACAUGGCCAUGGAA	295	989
UGGCUAUUACGACAGACUG	1149	990
ACUCGAGCUCAGAGGGUAC	533	991
ACAGUUUGAUGCUGCUCAU	604	992
GGUGGUUAAUAAGGCUGCA	766	993
CUUUGUCCCGCAAAUCAUG	1823	994
AAUACCAUUCCAUUGUUUG	2048	995
CCACACGUGCAAUCCCUGA	714	996
AUGGCCAGGAUGCCUUGGG	2439	997
GGAUACCCAGCGCCGUACG	1903	998
UCGCCAGGAUGAUCCUAGC	2395	999
UGGUCCAUCAGCUUUCUAA	789	1000
AUAUGUAUGGGUAGGGUAA	3085	1001
CCCAGAAUGCAGUUCGCCU	1710	1002
UAUUGUAGAAGCUGGUGGA	1336	1003
GUAUGGGUAGGGUAAAUCA	3089	1004
GAUCUUGGACUUGAUAUUG	2351	1005
ACACGUGCAAUCCCUGAAC	716	1006
AGCGCCGUACGUCCAUGGG	1911	1007
UGUACCGGAGCCCUUCACA	1985	1008
GUUGAUGGGCUGCCAGAUC	2516	1009
ACACCCACCAUCCCACUGG	1762	1010

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UACGACAGACUGCCUUCAA	1156	1011
UUGUUCGUGCACAUCAGGA	1887	1012
CAAAUCAUGCACCUUUGCG	1833	1013
GUCUGGAGGCAUUCCUGCC	967	1014
CACUAUGGACUACCAGUUG	1730	1015
UAUCAUGCGUUCUCCUCAG	829	1016
GUAGAAACAGCUCGUUGUA	890	1017
CUCCUCUGACAGAGUUACU	2181	1018
UGCUCAGGACAAGGAAGCU	2131	1019
CAAGUGGGUGGUAUAGAGG	1586	1020
UGGUGGUUAAUAAGGCUGC	765	1021
ACUUCACCUGACAGAUCCA	1369	1022
GGCCUUCACUAUGGACUAC	1724	1023
UGCGUUCUCCUCAGAUGGU	834	1024
GUUGUACCGGAGCCCUUCA	1983	1025
CGACACCAAGAAGCAGAGA	1688	1026
UCACCAGUGGAUUCUGUGU	1004	1027
GGUGACAGGGAAGACAUCA	1631	1028
UCUAGUAAUAAGCCGGCUA	1319	1029
GUGGUUAAUAAGGCUGCAG	767	1030
UCCUCAGAUGGUGUCUGCU	841	1031
AUGGACAGUAUGCAAUGAC	516	1032
UGCGUGAGCAGGGUGCCAU	1848	1033
ACUCUAGGAAUGAAGGUGU	2202	1034
GACAUUAGAUGAGGGCAUG	571	1035
CUGGUGACAGGGAAGACAU	1629	1036
UGAUUCGAAAUCUUGCCCU	1806	1037
GCUCUUACACCCACCAUCC	1756	1038
GUCCUUCGGGCUGGUGACA	1619	1039
GUGCGUACUGUCCUUCGGG	1610	1040
UGGUGCUGACUAUCCAGUU	2500	1041
GCUAUUGAAGCUGAGGGAG	2156	1042
CAACCAAGAAAGCAAGCUC	1189	1043
GUGCAGCUGCUUUAUUCUC	2066	1044
CUAUCUGUCUGCUCUAGUA	1307	1045
AAACAGGAAGGGAUGGAAG	1448	1046
ACUGGCUAGUGGUGGACCC	1213	1047

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
CCUCUGUGAACUUGCUCAG	2119	1048
UGUAGAAACAGCUCGUUGU	889	1049
CUGACAGAUCCAAGUCAAC	1376	1050
GGAAGAGGAUGUGGAUACC	427	1051
ACCAUCACAGAUGCUGAAA	649	1052
CCGUACGUCCAUGGGUGGG	1915	1053
CAUUCCAUUGUUUGUGCAG	2053	1054
CUCCAGGUGACAGCAAUCA	2568	1055
CUACCAGUUGUGGUUAAGC	1739	1056
UUGUGGUUAAGCUCUUACA	1746	1057
UAGUAAUAAGCCGGCUAUU	1321	1058
CAGUCCUUCACUCAAGAAC	482	1059
AGCUGAUUUGAUGGAGUUG	280	1060
AGGUCUCCUUGGGACUCUU	1465	1061
ACUAUGGACUACCAGUUGU	1731	1062
CAGCAGCAAUUUGUGGAGG	1937	1063
CGUGCACAUCAGGAUACCC	1892	1064
CGUUCUCCUCAGAUGGUGU	936	1065
CAGUAUGCAAUGACUCGAG	521	1066
GGUAUAGAGGCUCUUGUGC	1595	1067
AUCCAGUUGAUGGGCUGCC	2511	1068
UGCCAAGUGGGUGGUAUAG	1583	1069
ACAUCAGGAUACCCAGCGC	1897	1070
GCCAUCUUUAAGUCUGGAG	956	1071
AACCUUUCCCAUCAUCGUG	926	1072
CUAGUUCAGUUGCUUGUUC	1874	1073
UUCACUCAAGAACAAGUAG	488	1074
AAGAAGCAGAGAUGGCCCA	1695	1075
UCCUCUGACAGAGUUACUU	2182	1076
AAUUGUUAUCAGAGGACUA	2029	1077
UCUCAGUCCUUCACUCAAG	479	1078
UCCAGACACGCUAUCAUGC	818	1079
CACUAAUGUCCAGCGUUUG	625	1080
UUGUAACCUGCUGUGAUAC	3172	1081
CUUCUGGGUUCAGAUGAUA	1490	1082
GCCGUACGUCCAUGGGUGG	1914	1083
UAGUUGAAGGUUGUACCGG	1974	1084

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GAGGACAAGCCACAAGAUU	2258	1085
GGGAGCCACAGCUCCUCUG	2170	1086
CUUCACCUGACAGAUCCAA	1370	1087
UCUUUCAGAUGCUGCAACU	1429	1088
UGUAACCUGCUGUGAUACG	3173	1089
CCUCCCAAGUCCUGUAUGA	444	1090
GGCAGUGCGUUUAGCUGGU	1081	1091
CUCUAGUAAUAAGCCGGCU	1318	1092
GCUGUUAGUCACUGGCAGC	329	1093
GUCAACGUCUUGUUCAGAA	1389	1094
GAAGAGGAUGUGGAUACCU	428	1095
UAACCUGCUGUGAUACGAU	3175	1096
GUUAUUUGGAACCUUGUUU	3117	1097
UCACAACCGAAUUGUUAUC	2020	1098
CGGGCUGGUGACAGGGAAG	1625	1099
ACAACCGAAUUGUUAUCAG	2022	1100
CCACUAAUGUCCAGCGUUU	624	1101
CACUGAGCCUGCCAUCUGU	1648	1102
GGUCCAUCAGCUUUCUAAA	790	1103
AUCCCAAAGUUGUUGUAAC	3160	1104
UGAGGACCUAUACUUACGA	1251	1105
UGUCUGAGGACAAGCCACA	2253	1106
AGUUGAUGGGCUGCCAGAU	2515	1107
UGACCAGCCGACACCAAGA	1680	1108
AGGGAGCCACAGCUCCUCU	2169	1109
AAAGUUGUUGUAACCUGCU	3165	1110
CUGCAGUUAUGGUCCAUCA	780	1111
UGAAGGUUGUACCGGAGCC	1978	1112
UUCCCUGAGACAUUAGAUG	563	1113
CUUCGGGCUGGUGACAGGG	1622	1114
UUGAGCUGACCAGCUCUCU	2295	1115
GAACUUGCUCAGGACAAGG	2126	1116
CCAGCCGACACCAAGAAGC	1683	1117
AGGGUGCCAUUCCACGACU	1857	1118
UUGUGCAGCUGCUUUAUUC	2064	1119
UCACUCAAGAACAAGUAGC	489	1120
GCUGGUGGAAUGCAAGCUU	1346	1121

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GCAACUAAACAGGAAGGGA	1442	1122
AGGUUGUACCGGAGCCCUU	1981	1123
AGGCUGCAGUUAUGGUCCA	777	1124
GCAGAUCCCAUCUACACAG	589	1125
CUAGGAAUGAAGGUGUGGC	2205	1126
AGCUCCUUCUCUGAGUGGU	394	1127
UUACAACUCUCCACAACCU	1035	1128
GGUAAAGGCAAUCCUGAGG	410	1129
GUUCGCCUUCACUAUGGAC	1721	1130
CAAAUGUUAAAUUCUUGGC	1134	1131
CUGUGAUACGAUGCUUCAA	3182	1132
ACAAAUGAUGUAGAAACAG	881	1133
GGUACGAGCUGCUAUGUUC	547	1134
GAAUUGUUAUCAGAGGACU	2028	1135
CAACCGAAUUGUUAUCAGA	2023	1136
GUGAUACGAUGCUUCAAGA	3184	1137
AAAGGCAAUCCUGAGGAAG	413	1138
CAGCUCCUCUGACAGAGUU	2178	1139
AUGGUCUGCCAAGUGGGUG	1577	1140
GCUACUGUUGGAUUGAUUC	1793	1141
UGCAAUGACUCGAGCUCAG	526	1142
GACUUGAUAUUGGUGCCCA	2358	1143
CAGAACUGUCUUUGGACUC	1403	1144
UAGUUCAGUUGCUUGCCGC	1875	1145
ACAGACUGCCUUCAAAUUU	1160	1146
GGGUGGUAUAGAGGCUCUU	1591	1147
AUGGACUACCAGUUGUGGU	1734	1148
AUUGUUAUCAGAGGACUAA	2030	1149
UAAGGCUGCAGUUAUGGUC	775	1150
AAAUCUUGCCCUUUGUCCC	1813	1151
AGCAGCAAUUUGUGGAGGG	1938	1152
AGAGGACUAAAUACCAUUC	2039	1153
GCUGAAGGUGCUAUCUGUC	1297	1154
UGUAUGAGUGGGAACAGGG	456	1155
CAGAUCCCAUCUACACAGU	590	1156
GACACAGCAGCAAUUUGUG	1933	1157
GGGCAUGCAGAUCCCAUCU	583	1158

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
CAUGCCCAGGACCUCAUGG	2540	1159
GAAGCUGAGGGAGCCACAG	2162	1160
CUGUUAGUCACUGGCAGCA	330	1161
CUUGUUCAGCUUCUGGGUU	1481	1162
AAGCUGGUGGAAUGCAAGC	1344	1163
GAGGAUGUGGAUACCUCCC	431	1164
AUAAAUGUGGUCACCUGUG	1508	1165
UACGUCCAUGGGUGGGACA	1918	1166
GAUGGAGUUGGACAUGGCC	289	1167
UGUCCAGCGUUUGGCUGAA	631	1168
GAGCAGGGUGCCAUUCCAC	1853	1169
AAAUAUAAUGAGGACCUAU	1243	1170
UACUGGCUAGUGGUGGACC	1212	1171
UGCUUGGUUCACCAGUGGA	996	1172
CUGAGGACAAGCCACAAGA	2256	1173
CUUGUGCGUACUGUCCUUC	1607	1174
UGUUAUUUGGAACCUUGUU	3116	1175
UAGCUUAUGGCAACCAAGA	1179	1176
UGAUACGAUGCUUCAAGAG	3185	1177
UGGUAUAGAGGCUCUUGUG	1594	1178
GAUGUAGAAACAGCUCGUU	887	1179
CCUUUCCCAUCAUCGUGAG	928	1180
GCGUUCUCCUCAGAUGGUG	835	1181
UCAGGAUACCCAGCGCCGU	1900	1182
ACGGCUUUCAGUUGAGCUG	2284	1183
GUUGAAGGUUGUACCGGAG	1976	1184
UAUCGCCAGGAUGAUCCUA	2393	1185
GUGCUGAAGGUGCUAUCUG	1295	1186
GUCUUUGGACUCUCAGGAA	1410	1187
GGGAUGGAAGGUCUCCUUG	1457	1188
UGAGCUGACCAGCUCUCUC	2296	1189
CUUUCCCAUCAUCGUGAGG	929	1190
AAGCUUUAGGACUUCACCU	1359	1191
UGGAAUGCAAGCUUUAGGA	1351	1192
CUGGAGGCAUUCCUGCCCU	969	1193
AGUUCAGUUGCUUGUUCGU	1876	1194
GAGCUGCUAUGUUCCCUGA	552	1195

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GGCCAGGAUGCCUUGGGUA	2441	1196
GAUGAUCCUAGCUAUCGUU	2402	1197
GAUUGAUUCGAAAUCUUGC	1803	1198
CAGAGAUGGCCCAGAAUGC	1701	1199
CAGCGCCGUACGUCCAUGG	1910	1200
AUGUAGAAACAGCUCGUUG	888	1201
AGUGCUGAAGGUGCUAUCU	1294	1202
GACUACCAGUUGUGGUUAA	1737	1203
ACAGGAAGGGAUGGAAGGU	1430	1204
CAGGUGGUGGUUAAUAAGG	761	1205
AAGGCUGCAGUUAUGGUCC	776	1206
UAAAUGUGGUCACCUGUGC	1509	1207
UAAAGGCUACUGUUGGAUU	1788	1208
GAUGGACAGUAUGCAAUGA	515	1209
UUCUGGGUUCAGAUGAUAU	1491	1210
GUACUGUCCUUCGGGCUGG	1614	1211
CUUGGUUCACCAGUGGAUU	998	1212
UAUUGAAGCUGAGGGAGCC	2158	1213
GUUGUUGUAACCUGCUGUG	3168	1214
AGCAGGGUGCCAUUCCACG	1854	1215
GUCCUCUGUGAACUUGCUC	2117	1216
UCUGACCAGCCGACACCAA	1678	1217
GCCAUGGAACCAGACAGAA	305	1218
AAGCUAUUGAAGCUGAGGG	2154	1219
GAUUCGAAAUCUUGCCCUU	1807	1220
AGUUGCUUGUUCGUGCACA	1881	1221
AAGAACAAGAUGAUGGUCU	1565	1222
AGUGGUAAAGGCAAUCCUG	407	1223
CAGAUGCUGCAACUAAACA	1434	1224
CCUGAGACAUUAGAUGAGG	566	1225
UCCCAAAGUUGUUGUAACC	3161	1226
CUGACCAGCCGACACCAAG	1679	1227
AUCCAAAGAGUAGCUGCAG	2096	1228
AUGUCCAGCGUUUGGCUGA	630	1229
UCUUGUGCGUACUGUCCUU	1606	1230
AGGAUGUGGAUACCUCCCA	432	1231
GGCUGCAGUUAUGGUCCAU	778	1232

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UCACAUCCUAGCUCGGGAU	1999	1233
ACCAAGAAGCAGAGAUGGC	1692	1234
GCCACCACCCUGGUGCUGA	2490	1235
CCCACUAAUGUCCAGCGUU	623	1236
ACUGGCAGCAACAGUCUUA	339	1237
AUCUGAAUAAAGUGUAACA	2946	1238
GCCUGCCAUCUGUGCUCUU	1654	1239
CAUUACAACUCUCCACAAC	1033	1240
CUCCUCAGAUGGUGUCUGC	840	1241
CAGUUGCUUGUUCGUGCAC	1880	1242
AUCCUGAGGAAGAGGAUGU	420	1243
CACCAGUGGAUUCUGUGUU	1005	1244
CAAGAAAGCAAGCUCAUCA	1193	1245
CUUGCAUAACCUUUCCCAU	919	1246
CUUCACUAUGGACUACCAG	1727	1247
UUGCUUGUUCGUGCACAUC	1883	1248
UAUUGUACGUACCAUGCAG	859	1249
GAAAUCUUGCCCUUUGUCC	1812	1250
CUCUUGUGCGUACUGUCCU	1605	1251
CACAACCGAAUUGUUAUCA	2021	1252
GCUCCUCUGACAGAGUUAC	2180	1253
AGCGUUUGGCUGAACCAUC	636	1254
AAACGGCUUUCAGUUGAGC	2282	1255
UUUGUCCCGCAAAUCAUGC	1824	1256
UCUAGGAAUGAAGGUGUGG	2204	1257
AAGUCCUGUAUGAGUGGGA	450	1258
GGUUCACCAGUGGAUUCUG	1001	1259
GGUCUGCCAAGUGGGUGGU	1579	1260
AGCUCCUCUGACAGAGUUA	2179	1261
UUCUGGUGCCACUACCACA	376	1262
UGCUAUGUUCCCUGAGACA	556	1263
AUUGAUUCGAAAUCUUGCC	1804	1264
CUCAUGGAUGGGCUGCCUC	2552	1265
GCUGCUUUAUUCUCCCAUU	2071	1266
AUCAUGCACCUUUGCGUGA	1836	1267
GUCACUGGCAGCAACAGUC	336	1268
UGAGUGGGAACAGGGAUUU	460	1269

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
AAUUAUAAGAACAAGAUGA	1559	1270
UGGACAGUUUACCAGUUGC	3136	1271
AUGAGGACCUAUACUUACG	1250	1272
GGAAGGUCUCCUUGGGACU	1462	1273
UGGAAGAAAUAGUUGAAGG	1965	1274
GGUGUUAUUUGGAACCUUG	3114	1275
GUGCUCUUCGUCAUCUGAC	1665	1276
GGCCAUGGAACCAGACAGA	304	1277
CGGCUGUUAGUCACUGGCA	327	1278
UUCCACGACUAGUUCAGUU	1866	1279
AGCAGAGAUGGCCCAGAAU	1699	1280
GCCAGGAUGAUCCUAGCUA	2397	1281
GCCAUCUGUGCUCUUCGUC	1658	1282
UAGAAACAGCUCGUUGUAC	891	1283
AGAUGAUGGUCUGCCAAGU	1572	1284
ACCUUUCCCAUCAUCGUGA	927	1285
AUGGAGUUGGACAUGGCCA	290	1286
CUGUGCUCUUCGUCAUCUG	1663	1287
UAUAAGAACAAGAUGAUGG	1562	1288
UCUGAAUAAAGUGUAACAA	2947	1289
CCAGAAUGCAGUUCGCCUU	1711	1290
AGAACAAGAUGAUGGUCUG	1566	1291
AUCUUGCCCUUUGUCCCGC	1815	1292
GCGUUUAGCUGGUGGGCUG	1087	1293
GGGUUCAGAUGAUAUAAAU	1495	1294
UUUAGGACUUCACCUGACA	1363	1295
CACAGCUCCUUCUCUGAGU	391	1296
AACGUCUUGUUCAGAACUG	1392	1297
CACAGCAGCAAUUUGUGGA	1935	1298
GACUAGUUCAGUUGCUUGU	1872	1299
GACAGACUGCCUUCAAAUU	1159	1300
CUCUCUCUUCAGAACAGAG	2308	1301
GUCCAGCGUUUGGCUGAAC	632	1302
UAAGAACAAGAUGAUGGUC	1564	1303
UCCAAGUCAACGUCUUGUU	1384	1304
ACACCAAGAAGCAGAGAUG	1690	1305
CUCAGGAAUCUUUCAGAUG	1421	1306

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
UAAAUUCUUGGCUAUUACG	1141	1307
CUAUGGACUACCAGUUGUG	1732	1308
CCAGCGUUUGGCUGAACCA	634	1309
UCCCAUCAUCGUGAGGGCU	932	1310
AGGACUUCACCUGACAGAU	1366	1311
UUGUGCGUACUGUCCUUCG	1608	1312
CCAUGGGUGGGACACAGCA	1923	1313
GGAUGGAAGGUCUCCUUGG	1458	1314
CCCAGCGCCGUACGUCCAU	1908	1315
GCUCAGAGGGUACGAGCUG	539	1316
AUGUUCACAACCGAAUUGU	2016	1317
UGCUUGUUCGUGCACAUCA	1884	1318
AUGUUCCCUGAGACAUUAG	560	1319
GUAAAGGCAAUCCUGAGGA	411	1320
CACUGGCAGCAACAGUCUU	338	1321
AUCAUGCGUUCUCCUCAGA	830	1322
UAUGUAUGGGUAGGGUAAA	3086	1323
GUGUUAUUUGGAACCUUGU	3115	1324
ACAGCUCCUCUGACAGAGU	2177	1325
UAUGGACUACCAGUUGUGG	1733	1326
AUUCUGGUGCCACUACCAC	375	1327
UGCCUCCAGGUGACAGCAA	2565	1328
UACCUCCCAAGUCCUGUAU	442	1329
CCAGACACGCUAUCAUGCG	819	1330
UGAUGCAGAACUUGCCACA	700	1331
GUUUAGCUGGUGGGCUGCA	1089	1332
GUCUGCCAAGUGGGUGGUA	1580	1333
GGUUGUACCGGAGCCCUUC	1982	1334
GUACCGGAGCCCUUCACAU	1986	1335
CAAUCCUGAGGAAGAGGAU	418	1336
GCUAUCUGUCUGCUCUAGU	1306	1337
UGACAGAUCCAAGUCAACG	1377	1338
CAUGAUGGAACAUGAGAUG	2467	1339
UUGGACUCUCAGGAAUCUU	1414	1340
CUCUUCGUCAUCUGACCAG	1668	1341
UUGCCCUUUGUCCCGCAAA	1818	1342
GAAGCAGAGAUGGCCCAGA	1697	1343

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
CCUUGCAUAACCUUUCCCA	918	1344
CAGUUUGAUGCUGCUCAUC	605	1345
ACCUGACAGAUCCAAGUCA	1374	1346
CUUUCAGAUGCUGCAACUA	1430	1347
GAUACGAUGCUUCAAGAGA	3186	1348
AUGCAAGCUUUAGGACUUC	1355	1349
GGAUGUGGAUACCUCCCAA	433	1350
AGAAUGCAGUUCGCCUUCA	1713	1351
CGAAAUCUUGCCCUUUGUC	1811	1352
ACUCAAGAACAAGUAGCUG	491	1353
GAAUGAAGGUGUGGCGACA	2209	1354
UGCACCUUUGCGUGAGCAG	1840	1355
ACGAGCUGCUAUGUUCCCU	550	1356
AAGAGGAUGUGGAUACCUC	429	1357
GAUAUGGCCAGGAUGCCUU	2436	1358
UAUAGAGGCUCUUGUGCGU	1597	1359
GGUUCAGAUGAUAUAAAUG	1496	1360
AGGGAUGGAAGGUCUCCUU	1456	1361
UAUCCCAAAGUUGUUGUAA	3159	1362
UCUCUCUUCAGAACAGAGC	2309	1363
CUGACCAGCUCUCUCUUCA	2300	1364
ACCUGCUGUGAUACGAUGC	3177	1365
AUGGCAGUGCGUUUAGCUG	1079	1366
AUCCAAGUCAACGUCUUGU	1383	1367
GCUGCCUCCAGGUGACAGC	2563	1368
AGUGCGUUUAGCUGGUGGG	1084	1369
AGCCGGCUAUUGUAGAAGC	1329	1370
CAUUAGAUGAGGGCAUGCA	573	1371
GAAGGUGUGGCGACAUAUG	2213	1372
AAGUGGGUGGUAUAGAGGC	1587	1373
CUGAGGGAGCCACAGCUCC	2166	1374
GCGUUUGGCUGAACCAUCA	637	1375
UCCUUCUCUGAGUGGUAAA	397	1376
GCAGUUCGCCUUCACUAUG	1718	1377
GGACUUGAUAUUGGUGCCC	2357	1378
GUUUGGCUGAACCAUCACA	639	1379
GCAUGCAGAUCCCAUCUAC	585	1380

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GAUGGGCUGCCAGAUCUGG	2519	1381
GGACUUCACCUGACAGAUC	1367	1382
CAACGUCUUGUUCAGAACU	1391	1383
GAUAUUGAUGGACAGUAUG	509	1384
UGGCCAUGGAACCAGACAG	303	1385
CAAGAACAAGUAGCUGAUA	494	1386
GGCUGUUAGUCACUGGCAG	328	1387
CAUUGUUUGUGCAGCUGCU	2058	1388
UAAACAGGAAGGGAUGGAA	1447	1389
AUAAGAACAAGAUGAUGGU	1563	1390
GUGGAAUGCAAGCUUUAGG	1350	1391
GGAAUGAAGGUGUGGCGAC	2208	1392
GACACCAAGAAGCAGAGAU	1689	1393
ACUGUCUUUGGACUCUCAG	1407	1394
GGACAAGGAAGCUGCAGAA	2137	1395
UCUGCUAUUGUACGUACCA	854	1396
AGCUGCUUUAUUCUCCCAU	2070	1397
AGGGUACGAGCUGCUAUGU	545	1398
GAAGACAUCACUGAGCCUG	1640	1399
CGGGAUGUUCACAACCGAA	2012	1400
CAGCCGACACCAAGAAGCA	1684	1401
UGUUCACAACCGAAUUGUU	2017	1402
GCUCUCUCUUCAGAACAGA	2307	1403
UCAGAUGGUGUCUGCUAUU	844	1404
UGAGUGGUAAAGGCAAUCC	405	1405
UGGUGCCACUACCACAGCU	379	1406
UUGUCCCGCAAAUCAUGCA	1825	1407
CACCCUGGUGCUGACUAUC	2495	1408
AAUGUCCAGCGUUUGGCUG	629	1409
GGGCUGCCUCCAGGUGACA	2561	1410
GAGUUACUUCACUCUAGGA	2192	1411
UUCGAAAUCUUGCCCUUUG	1809	1412
GUAUAGAGGCUCUUGUGCG	1596	1413
AGCUGACCAGCUCUCUCUU	2298	1414
CUAUUGUACGUACCAUGCA	858	1415
UAUGCAAUGACUCGAGCUC	524	1416
UGCCCAGGACCUCAUGGAU	2542	1417

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
AACAAGUAGCUGAUAUUGA	498	1418
AAGGCAAUCCUGAGGAAGA	414	1419
CAAGAUGAUGGUCUGCCAA	1570	1420
UGCCAUUACAACUCUCCAC	1030	1421
AUGUAUGGGUAGGGUAAAU	3087	1422
UGUGCUCUUCGUCAUCUGA	1664	1423
AAGGCUACUGUUGGAUUGA	1790	1424
UACUGUCCUUCGGGCUGGU	1615	1425
AUAAGGCUGCAGUUAUGGU	774	1426
UCGUCAUCUGACCAGCCGA	1672	1427
GUUGUAACCUGCUGUGAUA	3171	1428
AAGAUUACAAGAAACGGCU	2271	1429
UUAUGGCAACCAAGAAAGC	1183	1430
UCCAGUUGAUGGGCUGCCA	2512	1431
GGGACACAGCAGCAAUUUG	1931	1432
AUGAUGGAACAUGAGAUGG	2468	1433
UAUUUGGGAUAUGUAUGGG	3077	1434
CAGCUGCUUUAUUCUCCCA	2069	1435

TABLE 1a-continued

CTNNB1 Target Sequences, noting human target sites.

Target Sequence	Target Site (human)	SEQ ID NO: 1
GCUACUCAAGCUGAUUUGA	272	1436
UCCCUGAGACAUUAGAUGA	564	1437
GUGGAUACCUCCCAAGUCC	437	1438
UAGGAAUGAAGGUGUGGCG	2206	1439
UGACAGAGUUACUUCACUC	2187	1440
AGCGGCUGUUAGUCACUGG	325	1441
AUGGUUCAGAAUUAAACUU	3222	1442
AACCGAAUUGUUAUCAGAG	2024	1443
GGGUGCCAUUCCACGACUA	1858	1444
AUGAUGGUCUGCCAAGUGG	1574	1445
CACAUCAGGAUACCCAGCG	1896	1446
AGGAAUGAAGGUGUGGCGA	2207	1447
GAAGGUGCUAUCUGUCUGC	1306	1448
CCAAGAAAGCAAGCUCAUC	1192	1449
CGAGCUGCUAUGUUCCCUG	551	1450
CCUGGUGCUGACUAUCCAG	2498	1451
UGCUAUCUGUCUGCUCUAG	1305	1452
AUUGUAGAAGCUGGUGGAA	1337	1453

TABLE 1b

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
535	1	UCGAGCUCAGAGGGUACGA	UCGUACCCUCUGAGCUCGA	4914
1601	2	GAGGCUCUUGUGCGUACUG	CAGUACGCACAAGAGCCUC	4915
1709	3	GCCCAGAAUGCAGUUCGCC	GGCGAACUGCAUUCUGGGC	4916
536	4	CGAGCUCAGAGGGUACGAG	CUCGUACCCUCUGAGCUCG	4917
1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAG	4918
853	6	GUCUGCUAUUGUACGUACC	GGUACGUACAAUAGCAGAC	4919
1143	7	AAUUCUUGGCUAUUACGAC	GUCGUAAUAGCCAAGAAUU	4920
2014	8	GGAUGUUCACAACCGAAUU	AAUUCGGUUGUGAACAUCC	4921
520	9	ACAGUAUGCAAUGACUCGA	UCGAGUCAUUGCAUACUGU	4922
814	10	AGCUUCCAGACACGCUAUC	GAUAGCGUGUCUGGAAGCU	4923
852	11	UGUCUGCUAUUGUACGUAC	GUACGUACAAUAGCAGACA	4924
1796	12	ACUGUUGGAUUGAUUCGAA	UUCGAAUCAAUCCAACAGU	4925
1901	13	CAGGAUACCCAGCGCCGUA	UACGGCGCUGGGUAUCCUG	4926

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
822	14	GACACGCUAUCAUGCGUUC	GAACGCAUGAUAGCGUGUC	4927
1795	15	UACUGUUGGAUUGAUUCGA	UCGAAUCAAUCCACCAGUA	4928
1145	16	UUCUUGGCUAUUACGACAG	CUGUCGUAAUAGCCAAGAA	4929
823	17	ACACGCUAUCAUGCGUUCU	AGAACGCAUGAUAGCGUGU	4930
820	18	CAGACACGCUAUCAUGCGU	ACGCAUGAUAGCGUGUCUG	4931
1798	19	UGUUGGAUUGAUUCGAAAU	AUUUCGAAUCAAUCCAACA	4932
1380	20	CAGAUCCAAGUCAACGUCU	AGACGUUGACUUGGAUCUG	4933
1602	21	AGGCUCUUGUGCGUACUGU	ACAGUACGCACAAGAGCCU	4934
1612	22	GCGUACUGUCCUUCGGGCU	AGCCCGAAGGACAGUACGC	4935
626	23	ACUAAUGUCCAGCGUUUGG	CCAAACGCUGGACAUUAGU	4936
2000	24	CACAUCCUAGCUCGGGAUG	CAUCCCGAGCUAGGAUGUG	4937
2665	25	GUUGCUGAGAGGGCUCGAG	CUCGAGCCCUCUCAGCAAC	4938
1676	26	CAUCUGACCAGCCGACACC	GGUGUCGGCUGGUCAGAUG	4939
1611	27	UGCGUACUGUCCUUCGGGC	GCCCGAAGGACAGUACGCA	4940
2269	28	ACAAGAUUACAAGAAACGG	CCGUUUCUUGUAAUCUUGU	4941
674	29	GUUGUAAACUUGAUUAACU	AGUUAAUCAAGUUUACAAC	4942
678	30	UAAACUUGAUUAACUAUCA	UGAUAGUUAAUCAAGUUUA	4943
1245	31	AUAUAAUGAGGACCUAUAC	GUAUAGGUCCUCAUUAUAU	4944
679	32	AAACUUGAUUAACUAUCAA	UUGAUAGUUAAUCAAGUUU	4945
1970	33	GAAAUAGUUGAAGGUUGUA	UACAACCUUCAACUAUUUC	4946
1247	34	AUAAUGAGGACCUAUACUU	AAGUAUAGGUCCUCAUUAU	4947
1140	35	UUAAAUUCUUGGCUAUUAC	GUAAUAGCCAAGAAUUUAA	4948
676	36	UGUAAACUUGAUUAACUAU	AUAGUUAAUCAAGUUUACA	4949
677	37	GUAAACUUGAUUAACUAUC	GAUAGUUAAUCAAGUUUAC	4950
675	38	UUGUAAACUUGAUUAACUA	UAGUUAAUCAAGUUUACAA	4951
1235	39	GCUUUAGUAAAUAUAAUGA	UCAUUAUAUUUACUAAAGC	4952
2488	40	UGGCCACCACCCUGGUGCU	AGCACCAGGGUGGUGGCCA	4953
1236	41	CUUUAGUAAAUAUAAUGAG	CUCAUUAUAUUUACUAAAG	4954
1237	42	UUUAGUAAAUAUAAUGAGG	CCUCAUUAUAUUUACUAAA	4955
2555	43	GUAAAUCGUCCUUUAGGUA	UACCUAAAGGACGAUUUAC	4956
1545	44	ACCUCACUUGCAAUAAUUA	UAAUUAUUGCAAGUGAGGU	4957
2050	45	UACCAUUCCAUUGUUUGUG	CACAAACAAUGGAAUGGUA	4958
2097	46	UCCAAAGAGUAGCUGCAGG	CCUGCAGCUACUCUUUGGA	4959
2510	47	UAUCCAGUUGAUGGGCUGC	GCAGCCCAUCAACUGGAUA	4960
871	48	CAUGCAGAAUACAAAUGAU	AUCAUUUGUAUUCUGCAUG	4961
2098	49	CCAAAGAGUAGCUGCAGGG	CCCUGCAGCUACUCUUUGG	4962

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1767	50	CACCAUCCCACUGGCCUCU	AGAGGCCAGUGGGAUGGUG	4963
869	51	ACCAUGCAGAAUACAAAUG	CAUUUGUAUUCUGCAUGGU	4964
1641	52	AAGACAUCACUGAGCCUGC	GCAGGCUCAGUGAUGUCUU	4965
2582	53	AAUCAGCUGGCCUGGUUUG	CAAACCAGGCCAGCUGAUU	4966
1544	54	AACCUCACUUGCAAUAAUU	AAUUAUUGCAAGUGAGGUU	4967
2550	55	ACCUCAUGGAUGGGCUGCC	GGCAGCCCAUCCAUGAGGU	4968
2051	56	ACCAUUCCAUUGUUUGUGC	GCACAAACAAUGGAAUGGU	4969
870	57	CCAUGCAGAAUACAAAUGA	UCAUUUGUAUUCUGCAUGG	4970
1670	58	CUUCGUCAUCUGACCAGCC	GGCUGGUCAGAUGACGAAG	4971
2122	59	CUGUGAACUUGCUCAGGAC	GUCCUGAGCAAGUUCACAG	4972
1642	60	AGACAUCACUGAGCCUGCC	GGCAGGCUCAGUGAUGUCU	4973
2324	61	GAGCCAAUGGCUUGGAAUG	CAUUCCAAGCCAUUGGCUC	4974
1649	62	ACUGAGCCUGCCAUCUGUG	CACAGAUGGCAGGCUCAGU	4975
2159	63	AUUGAAGCUGAGGGAGCCA	UGGCUCCCUCAGCUUCAAU	4976
785	64	GUUAUGGUCCAUCAGCUUU	AAAGCUGAUGGACCAUAAC	4977
1511	65	AAUGUGGUCACCUGUGCAG	CUGCACAGGUGACCACAUU	4978
2586	66	AGCUGGCCUGGUUUGAUAC	GUAUCAAACCAGGCCAGCU	4979
642	67	UGGCUGAACCAUCACAGAU	AUCUGUGAUGGUUCAGCCA	4980
1763	68	CACCCACCAUCCCACUGGC	GCCAGUGGGAUGGUGGGUG	4981
2328	69	CAAUGGCUUGGAAUGAGAC	GUCUCAUUCCAAGCCAUUG	4982
1280	70	UGGACCACAAGCAGAGUGC	GCACUCUGCUUGUGGUCCA	4983
2052	71	CCAUUCCAUUGUUUGUGCA	UGCACAAACAAUGGAAUGG	4984
2546	72	CAGGACCUCAUGGAUGGGC	GCCCAUCCAUGAGGUCCUG	4985
2124'	73	GUGAACUUGCUCAGGACAA	UUGUCCUGAGCAAGUUCAC	4986
2545	74	CCAGGACCUCAUGGAUGGG	CCCAUCCAUGAGGUCCUGG	4987
643	75	GGCUGAACCAUCACAGAUG	CAUCUGUGAUGGUUCAGCC	4988
2501	76	GGUGCUGACUAUCCAGUUG	CAACUGGAUAGUCAGCACC	4989
2330	77	AUGGCUUGGAAUGAGACUG	CAGUCUCAUUCCAAGCCAU	4990
1638	78	GGGAAGACAUCACUGAGCC	GGCUCAGUGAUGUCUUCCC	4991
1630	79	UGGUGACAGGGAAGACAUC	GAUGUCUUCCCUGUCACCA	4992
616	80	UGCUCAUCCCACUAAUGUC	GACAUUAGUGGGAUGAGCA	4993
2509	81	CUAUCCAGUUGAUGGGCUG	CAGCCCAUCAACUGGAUAG	4994
2548	82	GGACCUCAUGGAUGGGCUG	CAGCCCAUCCAUGAGGUCC	4995
1773	83	CCCACUGGCCUCUGAUAAA	UUUAUCAGAGGCCAGUGGG	4996
2247	84	UCCGAAUGUCUGAGGACAA	UUGUCCUCAGACAUUCGGA	4997
2331	85	UGGCUUGGAAUGAGACUGC	GCAGUCUCAUUCCAAGCCA	4998
1498	86	UUCAGAUGAUAUAAAUGUG	CACAUUUAUAUCAUCUGAA	4999

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2267	87	CCACAAGAUUACAAGAAAC	GUUUCUUGUAAUCUUGUGG	5000
1547	88	CUCACUUGCAAUAAUUAUA	UAUAAUUAUUGCAAGUGAG	5001
1549	89	CACUUGCAAUAAUUAUAAG	CUUAUAAUUAUUGCAAGUG	5002
867	90	GUACCAUGCAGAAUACAAA	UUUGUAUUCUGCAUGGUAC	5003
1390	91	UCAACGUCUUGUUCAGAAC	GUUCUGAACAAGACGUUGA	5004
593	92	AUCCCAUCUACACAGUUUG	CAAACUGUGUAGAUGGGAU	5005
274	93	UACUCAAGCUGAUUUGAUG	CAUCAAAUCAGCUUGAGUA	5006
759	94	ACCAGGUGGUGGUUAAUAA	UUAUUAACCACCACCUGGU	5007
1439	95	GCUGCAACUAAACAGGAAG	CUUCCUGUUUAGUUGCAGC	5008
1801	96	UGGAUUGAUUCGAAAUCUU	AAGAUUUCGAAUCAAUCCA	5009
1500	97	CAGAUGAUAUAAAUGUGGU	ACCACAUUUAUAUCAUCUG	5010
848	98	AUGGUGUCUGCUAUUGUAC	GUACAAUAGCAGACACCAU	5011
2268	99	CACAAGAUUACAAGAAACG	CGUUUCUUGUAAUCUUGUG	5012
882	100	CAAAUGAUGUAGAAACAGC	GCUGUUUCUACAUCAUUUG	5013
2266	101	GCCACAAGAUUACAAGAAA	UUUCUUGUAAUCUUGUGGC	5014
880	102	UACAAAUGAUGUAGAAACA	UGUUUCUACAUCAUUUGUA	5015
1810	103	UCGAAAUCUUGCCCUUUGU	ACAAAGGGCAAGAUUUCGA	5016
685	104	GAUUAACUAUCAAGAUGAU	AUCAUCUUGAUAGUUAAUC	5017
1007	105	CCAGUGGAUUCUGUGUUGU	ACAACACAGAAUCCACUGG	5018
1789	106	AAAGGCUACUGUUGGAUUG	CAAUCCAACAGUAGCCUUU	5019
499	107	ACAAGUAGCUGAUAUUGAU	AUCAAUAUCAGCUACUUGU	5020
2470	108	GAUGGAACAUGAGAUGGGU	ACCCAUCUCAUGUUCCAUC	5021
694	109	UCAAGAUGAUGCAGAACUU	AAGUUCUGCAUCAUCUUGA	5022
278	110	CAAGCUGAUUUGAUGGAGU	ACUCCAUCAAAUCAGCUUG	5023
1415	111	UGGACUCUCAGGAAUCUUU	AAAGAUUCCUGAGAGUCCA	5024
2046	112	UAAAUACCAUUCCAUUGUU	AACAAUGGAAUGGUAUUUA	5025
1057	113	AUUACAUCAAGAAGGAGCU	AGCUCCUUCUUGAUGUAAU	5026
1422	114	UCAGGAAUCUUUCAGAUGC	GCAUCUGAAAGAUUCCUGA	5027
684	115	UGAUUAACUAUCAAGAUGA	UCAUCUUGAUAGUUAAUCA	5028
2197	116	ACUUCACUCUAGGAAUGAA	UUCAUUCCUAGAGUGAAGU	5029
666	117	AACAUGCAGUUGUAAACUU	AAGUUUACAACUGCAUGUU	5030
279	118	AAGCUGAUUUGAUGGAGUU	AACUCCAUCAAAUCAGCUU	5031
1492	119	UCUGGGUUCAGAUGAUAUA	UAUAUCAUCUGAACCCAGA	5032
2195	120	UUACUUCACUCUAGGAAUG	CAUUCCUAGAGUGAAGUAA	5033
1424	121	AGGAAUCUUUCAGAUGCUG	CAGCAUCUGAAAGAUUCCU	5034
661	122	GCUGAAACAUGCAGUUGUA	UACAACUGCAUGUUUCAGC	5035

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1882	123	GUUGCUUGUUCGUGCACAU	AUGUGCACGAACAAGCAAC	5036
1866	124	GGAAGAAAUAGUUGAAGGU	ACCUUCAACUAUUUCUUCC	5037
2259	125	AGGACAAGCCACAAGAUUA	UAAUCUUGUGGCUUGUCCU	5038
832	126	CAUGCGUUCUCCUCAGAUG	CAUCUGAGGAGAACGCAUG	5039
2346	127	GAUGAUCCCAGCUACCGUU	AACGGUAGCUGGGAUCAUC	5040
1653	128	AGCCUGCCAUCUGUGCUCU	AGAGCACAGAUGGCAGGCU	5041
2389	129	UGGAUAUCGCCAGGAUGAU	AUCAUCCUGGCGAUAUCCA	5042
1669	130	UCUUCGUCAUCUGACCAGC	GCUGGUCAGAUGACGAAGA	5043
2123	131	UGUGAACUUGCUCAGGACA	UGUCCUGAGCAAGUUCACA	5044
1521	132	CCUGUGCAGCUGGAAUUCU	AGAAUUCCAGCUGCACAGG	5045
2125	133	UGAACUUGCUCAGGACAAG	CUUGUCCUGAGCAAGUUCA	5046
2503	134	UGCUGACUAUCCAGUUGAU	AUCAACUGGAUAGUCAGCA	5047
1502	135	GAUGAUAUAAAUGUGGUCA	UGACCACAUUUAUAUCAUC	5048
2502	136	GUGCUGACUAUCCAGUUGA	UCAACUGGAUAGUCAGCAC	5049
2506	137	UGACUAUCCAGUUGAUGGG	CCCAUCAACUGGAUAGUCA	5050
2127	138	AACUUGCUCAGGACAAGGA	UCCUUGUCCUGAGCAAGUU	5051
2505	139	CUGACUAUCCAGUUGAUGG	CCAUCAACUGGAUAGUCAG	5052
617	140	GCUCAUCCCACUAAUGUCC	GGACAUUAGUGGGAUGAGC	5053
2504	141	GCUGACUAUCCAGUUGAUG	CAUCAACUGGAUAGUCAGC	5054
1503	142	AUGAUAUAAAUGUGGUCAC	GUGACCACAUUUAUAUCAU	5055
618	143	CUCAUCCCACUAAUGUCCA	UGGACAUUAGUGGGAUGAG	5056
2074	144	GCUUUAUUCUCCCAUUGAA	UUCAAUGGGAGAAUAAAGC	5057
2499	145	CUGGUGCUGACUAUCCAGU	ACUGGAUAGUCAGCACCAG	5058
1406	146	AACUGUCUUUGGACUCUCA	UGAGAGUCCAAAGACAGUU	5059
582	147	AGGGCAUGCAGAUCCCAUC	GAUGGGAUCUGCAUGCCCU	5060
1505	148	GAUAUAAAUGUGGUCACCU	AGGUGACCACAUUUAUAUC	5061
1432	149	UUCAGAUGCUGCAACUAAA	UUUAGUUGCAGCAUCUGAA	5062
1968	150	AAGAAAUAGUUGAAGGUUG	CAACCUUCAACUAUUUCUU	5063
2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGG	5064
954	152	UGGCCAUCUUUAAGUCUGG	CCAGACUUAAAGAUGGCCA	5065
505	153	AGCUGAUAUUGAUGGACAG	CUGUCCAUCAAUAUCAGCU	5066
2011	154	UCGGGAUGUUCACAACCGA	UGCCUUGUGAACAUCCCGA	5067
1339	155	UGUAGAAGCUGGUGGAAUG	CAUUCCACCAGCUUCUACA	5068
1242	156	UAAAUAUAAUGAGGACCUA	UAGGUCCUCAUUAUAUUUA	5069
567	157	CUGAGACAUUAGAUGAGGG	CCCUCAUCUAAUGUCUCAG	5070
1240	158	AGUAAAUAUAAUGAGGACC	GGUCCUCAUUAUAUUUACU	5071
438	159	UGGAUACCUCCCAAGUCCU	AGGACUUGGGAGGUAUCCA	5072

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2445	160	AGGAUGCCUUGGGUAUGGA	UCCAUACCCAAGGCAUCCU	5073
860	161	AUUGUACGUACCAUGCAGA	UCUGCAUGGUACGUACAAU	5074
1413	162	UUUGGACUCUCAGGAAUCU	AGAUUCCUGAGAGUCCAAA	5075
1800	163	UUGGAUUGAUUCGAAAUCU	AGAUUUCGAAUCAAUCCAA	5076
2037	164	UCAGAGGACUAAAUACCAU	AUGGUAUUUAGUCCUCUGA	5077
2443	165	CCAGGAUGCCUUGGGUAUG	CAUACCCAAGGCAUCCUGG	5078
2471	166	AUGGAACAUGAGAUGGGUG	CACCCAUCUCAUGUUCCAU	5079
1792	167	GGCUACUGUUGGAUUGAUU	AAUCAAUCCAACAGUAGCC	5080
2547	168	AGGACCUCAUGGAUGGGCU	AGCCCAUCCAUGAGGUCCU	5081
1662	169	UCUGUGCUCUUCGUCAUCU	AGAUGACGAAGAGCACAGA	5082
288	170	UGAUGGAGUUGGACAUGGC	GCCAUGUCCAACUCCAUCA	5083
579	171	AUGAGGGCAUGCAGAUCCC	GGGAUCUGCAUGCCCUCAU	5084
2508	172	ACUAUCCAGUUGAUGGGCU	AGCCCAUCAACUGGAUAGU	5085
580	173	UGAGGGCAUGCAGAUCCCA	UGGGAUCUGCAUGCCCUCA	5086
2388	174	UUGGAUAUCGCCAGGAUGA	UCAUCCUGGCGAUAUCCAA	5087
2543	175	GCCCAGGACCUCAUGGAUG	CAUCCAUGAGGUCCUGGGC	5088
708	176	AACUUGCCACACGUGCAAU	AUUGCACGUGUGGCAAGUU	5089
447	177	CCCAAGUCCUGUAUGAGUG	CACUCAUACAGGACUUGGG	5090
654	178	CACAGAUGCUGAAACAUGC	GCAUGUUUCAGCAUCUGUG	5091
912	179	CUGGGACCUUGCAUAACCU	AGGUUAUGCAAGGUCCCAG	5092
1009	180	AGUGGAUUCUGUGUUGUUU	AAACAACACAGAAUCCACU	5093
1354	181	AAUGCAAGCUUUAGGACUU	AAGUCCUAAAGCUUGCAUU	5094
1969	182	AGAAAUAGUUGAAGGUUGU	ACAACCUUCAACUAUUUCU	5095
1958	183	UCCGCAUGGAAGAAAUAGU	ACUAUUUCUUCCAUGCGGA	5096
557	184	GCUAUGUUCCCUGAGACAU	AUGUCUCAGGGAACAUAGC	5097
403	185	UCUGAGUGGUAAAGGCAAU	AUUGCCUUUACCACUCAGA	5098
1356	186	UGCAAGCUUUAGGACUUCA	UGAAGUCCUAAAGCUUGCA	5099
517	187	UGGACAGUAUGCAAUGACU	AGUCAUUGCAUACUGUCCA	5100
1238	188	UUAGUAAAUAUAAUGAGGA	UCCUCAUUAUAUUUACUAA	5101
843	189	CUCAGAUGGUGUCUGCUAU	AUAGCAGACACCAUCUGAG	5102
496	190	AGAACAAGUAGCUGAUAUU	AAUAUCAGCUACUUGUUCU	5103
2387	191	CUUGGAUAUCGCCAGGAUG	CAUCCUGGCGAUAUCCAAG	5104
1660	192	CAUGUGUGCUCUUCGUCAU	AUGACGAAGAGCACAGAUG	5105
2497	193	CCCUGGUGCUGACUAUCCA	UGGAUAGUCAGCACCAGGG	5106
1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGU	5107
2353	195	UCUUGGACUUGAUAUUGGU	ACCAAUAUCAAGUCCAAGA	5108

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCC	5109
878	197	AAUACAAAUGAUGUAGAAA	UUUCUACAUCAUUUGUAUU	5110
647	198	GAACCAUCACAGAUGCUGA	UCAGCAUCUGUGAUGGUUC	5111
1998	199	UUCACAUCCUAGCUCGGGA	UCCCGAGCUAGGAUGUGAA	5112
588	200	UGCAGAUCCCAUCUACACA	UGUGUAGAUGGGAUCUGCA	5113
2042	201	GGACUAAAAUACCAUUCCAU	AUGGAAUGGUAUUUAGUCC	5114
855	202	CUGCUAUUGUACGUACCAU	AUGGUACGUACAAUAGCAG	5115
2038	203	CAGAGGACUAAAAUACCAUU	AAUGGUAUUUAGUCCUCUG	5116
1786	204	GAUAAAGGCUACUGUUGGA	UCCAACAGUAGCCUUUAUC	5117
1501	205	AGAUGAUAUAAAUGUGGUC	GACCACAUUUAUAUCAUCU	5118
1834	206	AAAUCAUGCACCUUUGCGU	ACGCAAAGGUGCAUGAUUU	5119
1157	207	ACGACAGACUGCCUUCAAA	UUUGAAGGCAGUCUGUCGU	5120
1239	208	UAGUAAAUAUAAUGAGGAC	GUCCUCAUUAUAUUUACUA	5121
1248	209	UAAUGAGGACCUAUACUUA	UAAGUAUAGGUCCUCAUUA	5122
660	210	UGCUGAAACAUGCAGUUGU	ACAACUGCAUGUUUCAGCA	5123
285	211	AUUUGAUGGAGUUGGACAU	AUGUCCAACUCCAUCAAAU	5124
1582	212	CUGCCAAGUGGGUGGUAUA	UAUACCACCCACUUGGCAG	5125
1735	213	UGGACUACCAGUUGUGGUU	AACCACAACUGGUAGUCCA	5126
771	214	UUAAUAAGGCUGCAGUUAU	AUAACUGCAGCCUUAUUAA	5127
1060	215	ACAUCAAGAAGGAGCUAAA	UUUAGCUCCUUCUUGAUGU	5128
2390	216	GGAUAUCGCCAGGAUGAUC	GAUCAUCCUGGCGAUAUCC	5129
2186	217	CUGACAGAGUUACUUCACU	AGUGAAGUAACUCUGUCAG	5130
1632	218	GUGACAGGGAAGACAUCAC	GUGAUGUCUUCCCUGUCAC	5131
619	219	UCAUCCCACUAAUGUCCAG	CUGGACAUUAGUGGGAUGA	5132
1656	220	CUGCCAUCUGUGCUCUUCG	CGAAGAGCACAGAUGGCAG	5133
1506	221	AUAUAAAUGUGGUCACCUG	CAGGUGACCACAUUUAUAU	5134
2494	222	CCACCCUGGUGCUGACUAU	AUAGUCAGCACGAGGGUGG	5135
1666	223	UGCUCUUCGUCAUCUGACC	GGUCAGAUGACGAAGAGCA	5136
1635	224	ACAGGGAAGACAUCACUGA	UCAGUGAUGUCUUCCCUGU	5137
294	225	AGUUGGACAUGGCCAUGGA	UCCAUGGCCAUGUCCAACU	5138
641	226	UUGGCUGAACCAUCACAGA	UCUGUGAUGGUUCAGCCAA	5139
576	227	UAGAUGAGGGCAUGCAGAU	AUCUGCAUGCCCUCAUCUA	5140
577	228	AGAUGAGGGCAUGCAGAUC	GAUCUGCAUGCCCUCAUCU	5141
1661	229	AUCUGUGCUCUUCGUCAUC	GAUGACGAAGAGCACAGAU	5142
707	230	GAACUUGCCACACGUGCAA	UUGCACGUGUGGCAAGUUC	5143
1659	231	CCAUCUGUGCUCUUCGUCA	UGACGAAGAGCACAGAUGG	5144
1185	232	AUGGCAACCAAGAAAGCAA	UUGCUUUCUUGGUUGCCAU	5145

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
664	233	GAAACAUGCAGUUGUAAAC	GUUUACAACUGCAUGUUUC	5146
1749	234	UGGUUAAGCUCUUACACCC	GGGUGUAAGAGCUUAACCA	5147
1234	235	AGCUUUAGUAAAUAUAAUG	CAUUAUAUUUACUAAAGCU	5148
691	236	CUAUCAAGAUGAUGCAGAA	UUCUGCAUCAUCUUGAUAG	5149
1387	237	AAGUCAACGUGUUGUUCAG	CUGAACAAGACGUUGACUU	5150
1382	238	GAUCCAAGUCAACGUCUUG	CAAGACGUUGACUUGGAUC	5151
828	239	CUAUCAUGCGUUCUCCUCA	UGAGGAGAACGCAUGAUAG	5152
1244	240	AAUAUAAUGAGGACCUAUA	UAUAGGUCCUCAUUAUAUU	5153
1304	241	GUGCUAUCUGUCUGCUCUA	UAGAGCAGACAGAUAGCAC	5154
812	242	GAAGCUUCCAGACACGCUA	UAGCGUGUCUGGAAGCUUC	5155
1558	243	UAAUUAUAAGAACAAGAUG	CAUCUUGUUCUUAUAAUUA	5156
879	244	AUACAAAUGAUGUAGAAAC	GUUUCUACAUCAUUUGUAU	5157
1311	245	CUGUCUGCUCUAGUAAUAA	UUAUUACUAGAGCAGACAG	5158
856	246	UGCUAUUGUACGUACCAUG	CAUGGUACGUACAAUAGCA	5159
1296	247	UGCUGAAGGUGCUAUCUGU	ACAGAUAGCACCUUCAGCA	5160
960	248	UCUUUAAGUCUGGAGGCAU	AUGCCUCCAGACUUAAAGA	5161
2049	249	AUACCAUUCCAUUGUUUGU	ACAAACAAUGGAAUGGUAU	5162
1791	250	AGGCUACUGUUGGAUUGAU	AUCAAUCCAACAGUAGCCU	5163
783	251	CAGUUAUGGUCCAUCAGCU	AGCUGAUGGACCAUAACUG	5164
1569	252	ACAAGAUGAUGGUCUGCCA	UGGCAGACCAUCAUCUUGU	5165
2224	253	GACAUAUGCAGCUGCUGUU	AACAGCAGCUGCAUAUGUC	5166
934	254	CCAUCAUCGUGAGGGCUUA	UAAGCCCUCACGAUGAUGG	5167
1378	255	GACAGAUCCAAGUCAACGU	ACGUUGACUUGGAUCUGUC	5168
659	256	GAGACAUUAGAUGAGGGCA	UGCCCUCAUCUAAUGUCUC	5169
1722	257	UUCGCCUUCACUAUGGACU	AGUCCAUAGUGAAGGCGAA	5170
1483	258	UGUUCAGCUUCUGGGUUCA	UGAACCCAGAAGCUGAACA	5171
2352	259	AUCUUGGACUUGAUAUUGG	CCAAUAUCAAGUCCAAGAU	5172
719	260	CGUGCAAUCCCUGAACUGA	UCAGUUCAGGGAUUGCACG	5173
762	261	AGGUGGUGGUUAAUAAGGC	GCCUUAUUAACCACCACCU	5174
599	262	UCUACACAGUUUGAUGCUG	CAGCAUCAAACUGUGUAGA	5175
1704	263	AGAUGGCCCAGAAUGCAGU	ACUGCAUUCUGGGCCAUCU	5176
2270	264	CAAGAUUACAAGAAACGGC	GCCGUUUCUUGUAAUCUUG	5177
662	265	CUGAAACAUGCAGUUGUAA	UUACAACUGCAUGUUUCAG	5178
396	266	CUCCUUCUCUGAGUGGUAA	UUACCACUCAGAGAAGGAG	5179
1199	267	AGCAAGCUCAUCAUACUGG	CCAGUAUGAUGAGCUUGCU	5180
1560	268	AUUAUAAGAACAAGAUGAU	AUCAUCUUGUUCUUAUAAU	5181

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1310	269	UCUGUCUGCUCUAGUAAUA	UAUUACUAGAGCAGACAGA	5182
1233	270	AAGCUUUAGUAAAUAUAAU	AUUAUAUUUACUAAAGCUU	5183
1330	271	GCCGGCUAUUGUAGAAGCU	AGCUUCUACAAUAGCCGGC	5184
1312	272	UGUCUGCUCUAGUAAUAAG	CUUAUUACUAGAGCAGACA	5185
1556	273	AAUAAUUAUAAGAACAAGA	UCUUGUUCUUAUAAUUAUU	5186
2438	274	UAUGGCCAGGAUGCCUUGG	CCAAGGCAUCCUGGCCAUA	5187
1826	275	UGUCCCGCAAAUCAUGCAC	GUGCAUGAUUUGCGGGACA	5188
1397	276	CUUGUUCAGAACUGUCUUU	AAAGACAGUUCUGAACAAG	5189
3181	277	GCUGUGAUACGAUGCUUCA	UGAAGCAUCGUAUCACAGC	5190
1912	278	GCGCCGUACGUCCAUGGGU	ACCCAUGGACGUACGGCGC	5191
846	279	AGAUGGUGUCUGCUAUUGU	ACAAUAGCAGACACCAUCU	5192
1404	280	AGAACUGUCUUUGGACUCU	AGAGUCCAAAGACAGUUCU	5193
586	281	CAUGCAGAUCCCAUCUACA	UGUAGAUGGGAUCUGCAUG	5194
1469	282	CUCCUUGGGACUCUUGUUC	GAACAAGAGUCCCAAGGAG	5195
380	283	GGUGCCACUACCACAGCUC	GAGCUGUGGUAGUGGCACC	5196
1345	284	AGCUGGUGGAAUGCAAGCU	AGCUUGCAUUCCACCAGCU	5197
1863	285	CCAUUCCACGACUAGUUCA	UGAACUAGUCGUGGAAUGG	5198
635	286	CAGCGUUUGGCUGAACCAU	AUGGUUCAGCCAAACGCGU	5199
959	287	AUGUUUAAGUCUGGAGGCA	UGCCUCCAGACUUAAAGAU	5200
2440	288	UGGCCAGGAUGCCUUGGGU	ACCCAAGGCAUCCUGGCCA	5201
877	289	GAAUACAAAUGAUGUAGAA	UUCUACAUCAUUUGUAUUC	5202
2556	290	UGGAUGGGCUGCCUCCAGG	CCUGGAGGCAGCCCAUCCA	5203
1916	291	CGUACGUCCAUGGGUGGGA	UCCCACCCAUGGACGUACG	5204
850	292	GGUGUCUGCUAUUGUACGU	ACGUACAAUAGCAGACACC	5205
1303	293	GGUGCUAUCUGUCUGCUCU	AGAGCAGACAGAUAGCACC	5206
1726	294	CCUUCACUAUGGACUACCA	UGGUAGUCCAUAGUGAAGG	5207
1477	295	GACUCUUGUUCAGCUUCUG	CAGAAGCUGAACAAGAGUC	5208
598	296	AUCUACACAGUUUGAUGCU	AGCAUCAAACUGUCUAGAU	5209
2062	297	GUUUGUGCAGCUGCUUUAU	AUAAAGCAGCUGCACAAAC	5210
2278	298	CAAGAAACGGCUUUCAGUU	AACUGAAAGCCGUUUCUUG	5211
1877	299	GUUCAGUUGCUUGUUCGUG	CACGAACAAGCAACUGAAC	5212
1499	300	UCAGAUGAUAUAAAUGUGG	CCACAUUUAUAUCAUCUGA	5213
1136	301	AAUGUUAAAUUCUUGGCUA	UAGCCAAGAAUUUAACAUU	5214
1494	302	UGGGUUCAGAUGAUAUAAA	UUUAUAUCAUCUGAACCCA	5215
1972	303	AAUAGUUGAAGGUUGUACC	GGUACAACCUUCAACUAUU	5216
668	304	CAUGCAGUUGUAAACUUGA	UCAAGUUUACAACUGCAUG	5217
2945	305	AAUCUGAAUAAAGUGUAAC	GUUACACUUUAUUCAGAUU	5218

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2492	306	CACCACCCUGGUGCUGACU	AGUCAGCACCAGGGUGGUG	5219
293	307	GAGUUGGACAUGGCCAUGG	CCAUGGCCAUGUCCAACUC	5220
1905	308	AUACCCAGCGCCGUACGUC	GACGUACGGCGCUGGGUAU	5221
944	309	GAGGGCUUACUGGCCAUCU	AGAUGGCCAGUAAGCCCUC	5222
581	310	GAGGGCAUGCAGAUCCCAU	AUGGGAUCUGCAUGCCCUC	5223
1454	311	GAAGGGAUGGAAGGUCUCC	GGAGACCUUCCAUCCCUUC	5224
2254	312	GUCUGAGGACAAGCCACAA	UUGUGGCUUGUCCUCAGAC	5225
1837	313	UCAUGCACCUUUGCGUGAG	CUCACGCAAAGGUGCAUGA	5226
1425	314	GGAAUCUUUCAGAUGCUGC	GCAGCAUCUGAAAGAUUCC	5227
1372	315	UCACCUGACAGAUCCAAGU	ACUUGGAUCUGUCAGGUGA	5228
1298	316	CUGAAGGUGCUAUCUGUCU	AGACAGAUAGCACCUUCAG	5229
1674	317	GUCAUCUGACCAGCCGACA	UGUCGGCUGGUCAGAUGAC	5230
1864	318	CAUUCCACGACUAGUUCAG	CUGAACUAGUCGUGGAAUG	5231
2404	319	UGAUCCUAGCUAUCGUUCU	AGAACGAUAGCUAGGAUCA	5232
1992	320	GAGCCCUUCACAUCCUAGC	GCUAGGAUGUGAAGGGCUC	5233
578	321	GAUGAGGGCAUGCAGAUCC	GGAUCUGCAUGCCCUCAUC	5234
3091	322	AUGGGUAGGGUAAAUCAGU	ACUGAUUUACCCUACCCAU	5235
720	323	GUGCAAUCCCUGAACUGAC	GUCAGUUCAGGGAUUGCAC	5236
2054	324	AUUCCAUUGUUUGUGCAGC	GCUGCACAAACAAUGGAAU	5237
374	325	CAUUCUGGUGCCACUACCA	UGGUAGUGGCACCAGAAUG	5238
868	326	UACCAUGCAGAAUACAAAU	AUUUGUAUUCUGCAUGGUA	5239
1716	327	AUGCAGUUCGCCUUCACUA	UAGUGAAGGCGAACUGCAU	5240
950	328	UUACUGGCCAUCUUUAAGU	ACUUAAAGAUGGCCAGUAA	5241
1489	329	GCUUCUGGGUUCAGAUGAU	AUCAUCUGAACCCAGAAGC	5242
1451	330	CAGGAAGGGAUGGAAGGUC	GACCUUCCAUCCCUUCCUG	5243
1181	331	GCUUAUGGCAACCAAGAAA	UUUCUUGGUUGCCAUAAGC	5244
1633	332	UGACAGGGAAGACAUCACU	AGUGAUGUCUUCCCUGUCA	5245
2394	333	AUCGCCAGGAUGAUCCUAG	CUAGGAUCAUCCUGGCGAU	5246
1322	334	AGUAAUAAGCCGGCUAUUG	CAAUAGCCGGCUUAUUACU	5247
884	335	AAUGAUGUAGAAACAGCUC	GAGCUGUUUCUACAUCAUU	5248
2255	336	UCUGAGGACAAGCCACAAG	CUUGUGGCUUGUCCUCAGA	5249
1466	337	GGUCUCCUUGGGACUCUUG	CAAGAGUCCCAAGGAGACC	5250
1399	338	UGUUCAGAACUGUCUUUGG	CCAAAGACAGUUCUGAACA	5251
378	339	CUGGUGCCACUACCACAGC	GCUGUGGUAGUGGCACCAG	5252
1921	340	GUCCAUGGGUGGGACACAG	CUGUGUCCCACCCAUGGAC	5253
1085	341	GUGCGUUUAGCUGGUGGGC	GCCCACCAGCUAAACGCAC	5254

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
865	342	ACGUACCAUGCAGAAUACA	UGUAUUCUGCAUGGUACGU	5255
2015	343	GAUGUUCACAACCGAAUUG	CAAUUCGGUUGUGAACAUC	5256
1195	344	AGAAAGCAAGCUCAUCAUA	UAUGAUGAGCUUGCUUUCU	5257
1484	345	GUUCAGCUUCUGGGUUCAG	CUGAACCCAGAAGCUGAAC	5258
1855	346	GCAGGGUGCCAUUCCACGA	UCGUGGAAUGGCACCCUGC	5259
1341	347	UAGAAGCUGGUGGAAUGCA	UGCAUUCCACCAGCUUCUA	5260
1963	348	CAUGGAAGAAAUAGUUGAA	UUCAACUAUUUCUUCCAUG	5261
2362	349	UGAUAUUGGUGCCCAGGGA	UCCCUGGGCACCAAUAUCA	5262
584	350	GGCAUGCAGAUCCCAUCUA	UAGAUGGGAUCUGCAUGCC	5263
1613	351	CGUACUGUCCUUCGGGCUG	CAGCCCGAAGGACAGUACG	5264
1155	352	UUACGACAGACUGCCUUCA	UGAAGGCAGUCUGUCGUAA	5265
334	353	UAGUCACUGGCAGCAACAG	CUGUUGCUGCCAGUGACUA	5266
1031	354	GCCAUUACAACUCUCCACA	UGUGGAGAGUUGUAAUGGC	5267
1725	355	GCCUUCACUAUGGACUACC	GGUAGUCCAUAGUGAAGGC	5268
2018	356	GUUCACAACCGAAUUGUUA	UAACAAUUCGGUUGUGAAC	5269
914	357	GGGACCUUGCAUAACCUUU	AAAGGUUAUGCAAGGUCCC	5270
2264	358	AAGCCACAAGAUUACAAGA	UCUUGUAAUCUUGUGGCUU	5271
343	359	GCAGCAACAGUCUUACCUG	CAGGUAAGACUGUUGCUGC	5272
1056	360	UAUUACAUCAAGAAGGAGC	GCUCCUUCUUGAUGUAAUA	5273
772	361	UAAUAAGGCUGCAGUUAUG	CAUAACUGCAGCCUUAUUA	5274
763	362	GGUGGUGGUUAAUAAGGCU	AGCCUUAUUAACCACCACC	5275
628	363	UAAUGUCCAGCGUUUGGCU	AGCCAAACGCUGGACAUUA	5276
399	364	CUUCUCUGAGUGGUAAAGG	CCUUUACCACUCAGAGAAG	5277
1682	365	ACCAGCCGACACCAAGAAG	CUUCUUGGUGUCGGCUGGU	5278
441	366	AUACCUCCCAAGUCCUGUA	UACAGGACUUGGGAGGUAU	5279
1729	367	UCACUAUGGACUACCAGUU	AACUGGUAGUCCAUAGUGA	5280
1902	368	AGGAUACCCAGCGCCGUAC	GUACGGCGCUGGGUAUCCU	5281
1637	369	AGGGAAGACAUCACUGAGC	GCUCAGUGAUGUCUUCCCU	5282
2391	370	GAUAUCGCCAGGAUGAUCC	GGAUCAUCCUGGCGAUAUC	5283
561	371	AAGUAGCUGAUAUUGAUGG	CCAUCAAUAUCAGCUACUU	5284
1358	372	CAAGCUUUAGGACUUCACC	GGUGAAGUCCUAAAGCUUG	5285
1821	373	CCCUUUGUCCCGCAAAUCA	UGAUUUGCGGGACAAAGGG	5286
575	374	UUAGAUGAGGGCAUGCAGA	UCUGCAUGCCCUCAUCUAA	5287
528	375	CAAUGACUCGAGCUCAGAG	CUCAGAGCUCGAGUCAUUG	5288
2433	376	GUGGAUAUGGCCAGGAUGC	GCAUCCUGGCCAUAUCCAC	5289
1497	377	GUUCAGAUGAUAUAAAUGU	ACAUUUAUAUCAUCUGAAC	5290
2134	378	UCAGGACAAGGAAGCUGCA	UGCAGCUUCCUUGUCCUGA	5291

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2160	379	UUGAAGCUGAGGGAGCCAC	GUGGCUCCCUCAGCUUCAA	5292
291	380	UGGAGUUGGACAUGGCCAU	AUGGCCAUGUCCAACUCCA	5293
657	381	AGAUGCUGAAACAUGCAGU	ACUGCAUGUUUCAGCAUCU	5294
1575	382	UGAUGGUCUGCCAAGUGGG	CCCACUUGGCAGACCAUCA	5295
667	383	ACAUGCAGUUGUAAACUUG	CAAGUUUACAACUGCAUGU	5296
2190	384	CAGAGUUACUUCACUCUAG	CUAGAGUGAAGUAACUCUG	5297
532	385	GACUCGAGCUCAGAGGGUA	UACCCUCUGAGCUCGAGUC	5298
953	386	CUGGCCAUCUUUAAGUCUG	CAGACUUAAAGAUGGCCAG	5299
3188	387	UACGAUGCUUCAAGAGAAA	UUUCUCUUGAAGCAUCGUA	5300
2301	388	UGACCAGCUCUCUCUUCAG	CUGAAGAGAGAGCUGGUCA	5301
2310	389	CUCUCUUCAGAACAGAGCC	GGCUCUGUUCUGAAGAGAG	5302
2287	390	GCUUUCAGUUGAGCUGACC	GGUCAGCUCAACUGAAAGC	5303
1927	391	GGGUGGGACACAGCAGCAA	UUGCUGCUGUGUCCCACCC	5304
712	392	UGCCACACGUGCAAUCCCU	AGGGAUUGCACGUGUGGCA	5305
2121	393	UCUGUGAACUUGCUCAGGA	UCCUGAGCAAGUUCACAGA	5306
2898	394	UGAGUAAUGGUGUAGAACA	UGUUCUACACCAUUACUCA	5307
1799	395	GUUGGAUUGAUUCGAAAUC	GAUUUCGAAUCAAUCCAAC	5308
1036	396	UACAACUCUCCCACAACCUU	AAGGUUGUGGAGAGUUGUA	5309
449	397	CAAGUCCUGUAUGAGUGGG	CCCACUCAUACAGGACUUG	5310
1452	398	AGGAAGGGAUGGAAGGUCU	AGACCUUCCAUCCCUUCCU	5311
1203	399	AGCUCAUCAUACUGGCUAG	CUAGCCAGUAUGAUGAGCU	5312
1357	400	GCAAGCUUUAGGACUUCAC	GUGAAGUCCUAAAGCUUGC	5313
1512	401	AUGUGGUCACCUGUGCAGC	GCUGCACAGGUGACCACAU	5314
275	402	ACUCAAGCUGAUUUGAUGG	CCAUCAAAUCAGCUUGAGU	5315
299	403	GACAUGGCCAUGGAACCAG	CUGGUUCCAUGGCCAUGUC	5316
1241	404	GUAAAUAUAAUGAGGACCU	AGGUCCUCAUUAUAUUUAC	5317
1961	405	CGCAUGGAAGAAAUAGUUG	CAACUAUUUCUUCCAUGCG	5318
1436	406	GAUGCUGCAACUAAACAGG	CCUGUUUAGUUGCAGCAUC	5319
2469	407	UGAUGGAACAUGAGAUGGG	CCCAUCUCAUGUUCCAUCA	5320
760	408	CCAGGUGGUGGUUAAUAAG	CUUAUUAACCACCACCUGG	5321
2257	409	UGAGGACAAGCCACAAGAU	AUCUUGUGGCUUGUCCUCA	5322
952	410	ACUGGCCAUCUUUAAGUCU	AGACUUAAAGAUGGCCAGU	5323
2283	411	AACGGCUUUCAGUUGAGCU	AGCUCAACUGAAAGCCGUU	5324
1794	412	CUACUGUUGGAUUGAUUCG	CGAAUCAAUCCAACAGUAG	5325
1745	413	GUUGUGGUUAAGCUCUUAC	GUAAGAGCUUAACCACAAC	5326
1211	414	AUACUGGCUAGUGGUGGAC	GUCCACCACUAGCCAGUAU	5327

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2549	415	GACCUCAUGGAUGGGCUGC	GCAGCCCAUCCAUGAGGUC	5328
2007	416	UAGCUCGGGAUGUUCACAA	UUGUGAACAUCCCGAGCUA	5329
2474	417	GAACAUGAGAUGGGUGGCC	GGCCACCCAUCUCAUGUUC	5330
1712	418	CAGAAUGCAGUUCGCCUUC	GAAGGCGAACUGCAUUCUG	5331
1919	419	ACGUCCAUGGGUGGGACAC	GUGUCCCACCCAUGGACGU	5332
1000	420	UGGUUCACCAGUGGAUUCU	AGAAUCCACUGGUGAACCA	5333
2392	421	AUAUCGCCAGGAUGAUCCU	AGGAUCAUCCUGGCGAUAU	5334
1449	422	AACAGGAAGGGAUGGAAGG	CCUUCCAUCCCUUCCUGUU	5335
2294	423	GUUGAGCUGACCAGCUCUC	GAGAGCUGGUCAGCUCAAC	5336
1135	424	AAAUGUUAAAUUCUUGGCU	AGCCAAGAAUUUAACAUUU	5337
1333	425	GGCUAUUGUAGAAGCUGGU	ACCAGCUUCUACAAUAGCC	5338
1743	426	CAGUUGUGGUUAAGCUCUU	AAGAGCUUAACCACAACUG	5339
600	427	CUACACAGUUUGAUGCUGC	GCAGCAUCAAACUGUGUAG	5340
970	428	UGGAGGCAUUCCUGCCCUG	CAGGGCAGGAAUGCCUCCA	5341
3137	429	GGACAGUUUACCAGUUGCC	GGCAACUGGUAAACUGUCC	5342
372	430	UCCAUUCUGGUGCCACUAC	GUAGUGGCACCAGAAUGGA	5343
1761	431	UACACCCACCAUCCCACUG	CAGUGGGAUGGUGGGUGUA	5344
1650	432	CUGAGCCUGCCAUCUGUGC	GCACAGAUGGCAGGCUCAG	5345
972	433	GAGGCAUUCCUGCCCUGGU	ACCAGGGCAGGAAUGCCUC	5346
1147	434	CUUGGCUAUUACGACAGAC	GUCUGUCGUAAUAGCCAAG	5347
565	435	CCCUGAGACAUUAGAUGAG	CUCAUCUAAUGUCUCAGGG	5348
525	436	AUGCAAUGACUCGAGCUCA	UGAGCUCGAGUCAUUGCAU	5349
1599	437	UAGAGGCUCUUGUGCGUAC	GUACGCACAAGAGCCUCUA	5350
2199	438	UUCACUCUAGGAAUGAAGG	CCUUCAUUCCUAGAGUGAA	5351
2261	439	GACAAGCCACAAGAUUACA	UGUAAUCUUGUGGCUUGUC	5352
705	440	CAGAACUUGCCACACGUGC	GCACGUGUGGCAAGUUCUG	5353
916	441	GACCUUGCAUAACCUUUCC	GGAAAGGUUAUGCAAGGUC	5354
385	442	CACUACCACAGCUCCUUCU	AGAAGGAGCUGUGGUAGUG	5355
3076	443	CUAUUUGGGAUAUGUAUGG	CCAUACAUAUCCCAAAUAG	5356
1396	444	UCUUGUUCAGAACUGUCUU	AAGACAGUUCUGAACAAGA	5357
2447	445	GAUGCCUUGGGUAUGGACC	GGUCCAUACCCAAGGCAUC	5358
1338	446	UUGUAGAAGCUGGUGGAAU	AUUCCACCAGCUUCUACAA	5359
2215	447	AGGUGUGGCGACAUAUGCA	UGCAUAUGUCGCCACACCU	5360
722	448	GCAAUCCCUGAACUGACAA	UUGUCAGUUCAGGGAUUGC	5361
1316	449	UGCUCUAGUAAUAAGCCGG	CCGGCUUAUUACUAGAGCA	5362
1687	450	CCGACACCAAGAAGCAGAG	CUCUGCUUCUUGGUGUCGG	5363
697	451	AGAUGAUGCAGAACUUGCC	GGCAAGUUCUGCAUCAUCU	5364

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2517	452	UUGAUGGGCUGCCAGAUCU	AGAUCUGGCAGCCCAUCAA	5365
1685	453	AGCCGACACCAAGAAGCAG	CUGCUUCUUGGUGUCGGCU	5366
3090	454	UAUGGGUAGGGUAAAUCAG	CUGAUUUACCCUACCCAUA	5367
1205	455	CUCAUCAUACUGGCUAGUG	CACUAGCCAGUAUGAUGAG	5368
1153	456	UAUUACGACAGACUGCCUU	AAGGCAGUCUGUCGUAAUA	5369
723	457	CAAUCCCUGAACUGACAAA	UUUGUCAGUUCAGGGAUUG	5370
1468	458	UCUCCUUGGGACUCUUGUU	AACAAGAGUCCCAAGGAGA	5371
2480	459	GAGAUGGGUGGCCACCACC	GGUGGUGGCCACCCAUCUC	5372
1856	460	CAGGGUGCCAUUCCACGAC	GUCGUGGAAUGGCACCCUG	5373
2193	461	AGUUACUUCACUCUAGGAA	UUCCUAGAGUGAAGUAACU	5374
2355	462	UUGGACUUGAUAUUGGUGC	GCACCAAUAUCAAGUCCAA	5375
1995	463	CCCUUCACAUCCUAGCUCG	CGAGCUAGGAUGUGAAGGG	5376
821	464	AGACACGCUAUCAUGCGUU	AACGCAUGAUAGCGUGUCU	5377
1715	465	AAUGCAGUUCGCCUUCACU	AGUGAAGGCGAACUGCAUU	5378
1182	466	CUUAUGGCAACCAAGAAAG	CUUUCUUGGUUGCCAUAAG	5379
445	467	CUCCCAAGUCCUGUAUGAG	CUCAUACAGGACUUGGGAG	5380
1759	468	CUUACACCCACCAUCCCAC	GUGGGAUGGUGGGUGUAAG	5381
1461	469	RGGAAGGUCUCCUUGGGAC	GUCCCAAGGAGACCUUCCA	5382
1993	470	AGCCCUUCACAUCCUAGCU	AGCUAGGAUGUGAAGGGCU	5383
2558	471	GAUGGGCUGCCUCCAGGUG	CACCUGGAGGCAGCCCAUC	5384
1488	472	AGCUUCUGGGUUCAGAUGA	UCAUCUGAACCCAGAAGCU	5385
1652	473	GAGCCUGCCAUCUGUGCUC	GAGCACAGAUGGCAGGCUC	5386
963	474	UUAAGUCUGGAGGCAUUCC	GGAAUGCCUCCAGACUUAA	5387
1520	475	ACCUGUGCAGCUGGAAUUC	GAAUUCCAGCUGCACAGGU	5388
1828	476	UCCCGCAAAUCAUGCACCU	AGGUGCAUGAUUUGCGGGA	5389
2214	477	AAGGUGUGGCGACAUAUGC	GCAUAUGUCGCCACACCUU	5390
2155	478	AGCUAUUGAAGCUGAGGGA	UCCCUCAGCUUCAAUAGCU	5391
332	479	GUUAGUCACUGGCAGCAAC	GUUGCUGCCAGUGACUAAC	5392
1878	480	UUCAGUUGCUUGUUCGUGC	GCACGAACAAGCAACUGAA	5393
1573	481	GAUGAUGGUCUGCCAAGUG	CACUUGGCAGACCAUCAUC	5394
1446	482	CUAAACAGGAAGGGAUGGA	UCCAUCCCUUCCUGUUUAG	5395
1868	483	CCACGACUAGUUCAGUUGC	GCAACUGAACUAGUCGUGG	5396
1873	484	ACUAGUUCAGUUGCUUGUU	AACAAGCAACUGAACUAGU	5397
1902	485	GUUCACCAGUGGAUUCUGU	ACAGAAUCCACUGGUGAAC	5398
408	486	GUGGUAAAGGCAAUCCUGA	UCAGGAUUGCCUUUACCAC	5399
287	487	UUGAUGGAGUUGGACAUGG	CCAUGUCCAACUCCAUCAA	5400

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2128	488	ACUUGCUCAGGACAAGGAA	UUCCUUGUCCUGAGCAAGU	5401
2513	489	CCAGUUGAUGGGCUGCCAG	CUGGCAGCCCAUCAACUGG	5402
1196	490	GAAAGCAAGCUCAUCAUAC	GUAUGAUGAGCUUGCUUUC	5403
573	491	ACAUUAGAUGAGGGCAUGC	GCAUGCCCUCAUCUAAUGU	5404
622	492	UCCCACUAAUGUCCAGCGU	ACGCUGGACAUUAGUGGGA	5405
1187	493	GGCAACCAAGAAAGCAAGC	GCUUGCUUUCUUGGUUGCC	5406
1971	494	AAAUAGUUGAAGGUUGUAC	GUACAACCUUCAACUAUUU	5407
3083	495	GGAUAUGUAUGGGUAGGGU	ACCCUACCCAUACAUAUCC	5408
2944	496	UAAUCUGAAUAAAGUGUAA	UUACACUUUAUUCAGAUUA	5409
1894	497	UGCACAUCAGGAUACCCAG	CUGGGUAUCCUGAUGUGCA	5410
1323	498	GUAAUAAGCCGGCUAUUGU	ACAAUAGCCGGCUUAUUAC	5411
1202	499	AAGCUCAUCAUACUGGCUA	UAGCCAGUAUGAUGAGCUU	5412
718	500	ACGUGCAAUCCCUGAACUG	CAGUUCAGGGAUUGCACGU	5413
1744	501	AGUUGUGGUUAAGCUCUUA	UAAGAGCUUAACCACAACU	5414
756	502	AGGACCAGGUGGUGGUUAA	UUAACCACCACCUGGUCCU	5415
1317	503	GCUCUAGUAAUAAGCCGGC	GCCGGCUUAUUACUAGAGC	5416
284	504	GAUUUGAUGGAGUUGGACA	UGUCCAACUCCAUCAAAUC	5417
886	505	UGAUGUAGAAACAGCUCGU	ACGAGCUCUUUCUACAUCA	5418
2430	506	CUGGUGGAUAUGGCCAGGA	UCCUGGCCAUAUCCACCAG	5419
1207	507	CAUCAUACUGGCUAGUGGU	ACCACUAGCCAGUAUGAUG	5420
592	508	GAUCCCAUCUACACAGUUU	AAACUGUGUAGAUGGGAUC	5421
824	509	CACGCUAUCAUGCGUUCUC	GAGAACGCAUGAUAGCGUG	5422
519	510	GACAGUAUGCAAUGACUCG	CGAGUCAUUGCAUACUGUC	5423
3166	511	AAGUUGUUGUAACCUGCUG	CAGCAGGUUACAACAACUU	5424
1151	512	GCUAUUACGACAGACUGCC	GGCAGUCUGUCGUAAUAGC	5425
2566	513	GCCUCCAGGUGACAGCAAU	AUUGCUGUCACCUGGAGGC	5426
453	514	UCCUGUAUGAGUGGGAACA	UGUUCCCACUCAUACAGGA	5427
587	515	AUGCAGAUCCCAUCUACAC	GUGUAGAUGGGAUCUGCAU	5428
930	516	UUUCCCAUCAUCGUGAGGG	CCCUCACGAUGAUGGGAAA	5429
1585	517	CCAAGUGGGUGGUAUAGAG	CUCUAUACCACCCACUUGG	5430
915	518	GGACCUUGCAUAACCUUUC	GAAAGGUUAUGCAAGGUCC	5431
446	519	UCCCAAGUCCUGUAUGAGU	ACUCAUACAGGACUUGGGA	5432
1869	520	CACGACUAGUUCAGUUGCU	AGCAACUGAACUAGUCGUG	5433
1960	521	CCGCAUGGAAGAAAUAGUU	AACUAUUUCUUCCAUGCGG	5434
1708	522	GGCCCAGAAUGCAGUUCGC	GCGAACUGCAUUCUGGGCC	5435
306	523	CCAUGGAACCAGACAGAAA	UUUCUGUCUGGUUCCAUGG	5436
2281	524	GAAACGGCUUUCAGUUGAG	CUCAACUGAAAGCCGUUUC	5437

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
3082	525	GGGAUAUGUAUGGGUAGGG	CCCUACCCAUACAUAUCCC	5438
1473	526	UUGGGACUCUUGUUCAGCU	AGCUGAACAAGAGUCCCAA	5439
559	527	UAUGUUCCCUGAGACAUUA	UAAUGUCUCAGGGAACAUA	5440
1416	528	GGACUCUCAGGAAUCUUUC	GAAAGAUUCCUGAGAGUCC	5441
2145	529	AAGCUGCAGAAGCUAUUGA	UCAAUAGCUUCUGCAGCUU	5442
1994	530	GCCCUUCACAUCCUAGCUC	GAGCUAGGAUGUGAAGGGC	5443
1702	531	AGAGAUGGCCCAGAAUGCA	UGCAUUCUGGGCCAUCUCU	5444
417	532	GCAAUCCUGAGGAAGAGGA	UCCUCUUCCUCAGGAUUGC	5445
2444	533	CAGGAUGCCUUGGGUAUGG	CCAUACCCAAGGCAUCCUG	5446
555	534	CUGCUAUGUUCCCUGAGAC	GUCUCAGGGAACAUAGCAG	5447
2019	535	UUCACAACCGAAUUGUUAU	AUAACAAUUCGGUUGUGAA	5448
1197	536	AAAGCAAGCUCAUCAUACU	AGUAUGAUGAGCUUGCUUU	5449
415	537	AGGCAAUCCUGAGGAAGAG	CUCUUCCUCAGGAUUGCCU	5450
2061	538	UGUUUGUGCAGCUGCUUUA	UAAAGCAGCUGCACAAACA	5451
1352	539	GGAAUGCAAGCUUUAGGAC	GUCCUAAAGCUUGCAUUCC	5452
1331	540	CCGGCUAUUGUAGAAGCUG	CAGCUUCUACAAUAGCCGG	5453
1325	541	AAUAAGCCGGCUAUUGUAG	CUACAAUAGCCGGCUUAUU	5454
1486	542	UCAGCUUCUGGGUUCAGAU	AUCUGAACCCAGAAGCUGA	5455
454	543	CCUGUAUGAGUGGGAACAG	CUGUUCCCACUCAUACAGG	5456
490	544	CACUCAAGAACAAGUAGCU	AGCUACUUGUUCUUGAGUG	5457
1996	545	CCUUCACAUCCUAGCUCGG	CCGAGCUAGGAUGUGAAGG	5458
1839	546	AUGCACCUUUGCGUGAGCA	UGCUCACGCAAAGGUGCAU	5459
1888	547	UGUUCGUGCACAUCAGGAU	AUCCUGAUGUGCACGAACA	5460
1879	548	UCAGUUGCUUGUUCGUGCA	UGCACGAACAAGCAACUGA	5461
1829	549	CCCGCAAAUCAUGCACCUU	AAGGUGCAUGAUUUGCGGG	5462
281	550	GCUGAUUUGAUGGAGUUGG	CCAACUCCAUCAAAUCAGC	5463
1598	551	AUAGAGGCUCUUGUGCGUA	UACGCACAAGAGCCUCUAU	5464
2135	552	CAGGACAAGGAAGCUGCAG	CUGCAGCUUCCUUGUCCUG	5465
1755	553	AGCUCUUACACCCACCAUC	GAUGGUGGGUGUAAGAGCU	5466
651	554	CAUCACAGAUGCUGAAACA	UGUUUCAGCAUCUGUGAUG	5467
1335	555	CUAUUGUAGAAGCUGGUGG	CCACCAGCUUCUACAAUAG	5468
2541	556	AUGCCCAGGACCUCAUGGA	UCCAUGAGGUCCUGGGCAU	5469
531	557	UGACUCGAGCUCAGAGGGU	ACCCUCUGAGCUCGAGUCA	5470
606	558	AGUUUGAUGCUGCUCAUCC	GGAUGAGCAGCAUCAAACU	5471
1620	559	UCCUUCGGGCUGGUGACAG	CUGUCACCAGCCCGAAGGA	5472
2211	560	AUGAAGGUGUGGCGACAUA	UAUGUCGCCACACCUUCAU	5473

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2293	561	AGUUGAGCUGACCAGCUCU	AGAGCUGGUCAGCUCAACU	5474
455	562	CUGUAUGAGUGGGAACAGG	CCUGUUCCCACUCAUACAG	5475
540	563	CUCAGAGGGUACGAGCUGC	GCAGCUCGUACCCUCUGAG	5476
416	564	GGCAAUCCUGAGGAAGAGG	CCUCUUCCUCAGGAUUGCC	5477
1210	565	CAUACUGGCUAGUGGUGGA	UCCACCACUAGCCAGUAUG	5478
2262	566	ACAAGCCACAAGAUUACAA	UUGUAAUCUUGUGGCUUGU	5479
1604	567	GCUCUUGUGCGUACUGUCC	GGACAGUACGCACAAGAGC	5480
435	568	AUGUGGAUACCUCCCAAGU	ACUUGGGAGGUAUCCACAU	5481
2060	569	UUGUUUGUGCAGCUGCUUU	AAAGCAGCUGCACAAACAA	5482
2225	570	ACAUAUGCAGCUGCUGUUU	AAACAGCAGCUGCAUAUGU	5483
481	571	UCAGUCCUUCACUCAAGAA	UUCUUGAGUGAAGGACUGA	5484
917	572	ACCUUGCAUAACCUUUCCC	GGGAAAGGUUAUGCAAGGU	5485
2221	573	GGCGACAUAUGCAGCUGCU	AGCAGCUGCAUAUGUCGCC	5486
849	574	UGGUGUCUGCUAUUGUACG	CGUACAAUAGCAGACACCA	5487
562	575	GUUCCCUGAGACAUUAGAU	AUCUAAUGUCUCAGGGAAC	5488
1787	576	AUAAAGGCUACUGUUGGAU	AUCCAACAGUAGCCUUUAU	5489
1860	577	GUGCCAUUCCACGACUAGU	ACUAGUCGUGGAAUGGCAC	5490
1590	578	UGGGUGGUAUAGAGGCUCU	AGAGCCUCUAUACCACCCA	5491
955	579	GGCCAUCUUUAAGUCUGGA	UCCAGACUUAAAGAUGGCC	5492
2365	580	UAUUGGUGCCCAGGGAGAA	UUCUCCCUGGGCACCAAUA	5493
634	581	CUCGAGCUCAGAGGGUACG	CGUACCCUCUGAGCUCGAG	5494
706	582	AGAACUUGCCACACGUGCA	UGCACGUGUGGCAAGUUCU	5495
1740	583	UACCAGUUGUGGUUAAGCU	AGCUUAACCACAACUGGUA	5496
638	584	CGUUUGGCUGAACCAUCAC	GUGAUGGUUCAGCCAAACG	5497
1334	585	GCUAUUGUAGAAGCUGGUG	CACCAGCUUCUACAAUAGC	5498
971	586	GGAGGCAUUCCUGCCCUGG	CCAGGGCAGGAAUGCCUCC	5499
2493	587	ACCACCCUGGUGCUGACUA	UAGUCAGCACCAGGGUGGU	5500
1814	588	AAUCUUGCCCUUUGUCCCG	CGGGACAAAGGGCAAGAUU	5501
1088	589	CGUUUAGCUGGUGGGCUGC	GCAGCCCACCAGCUAAACG	5502
2292	590	CAGUUGAGCUGACCAGCUC	GAGCUGGUCAGCUCAACUG	5503
1504	591	UGAUAUAAAUGUGGUCACC	GGUGACCACAUUUAUAUCA	5504
404	592	CUGAGUGGUAAAGGCAAUC	GAUUGCCUUUACCACUCAG	5505
1301	593	AAGGUGCUAUCUGUCUGCU	AGCAGACAGAUAGCACCUU	5506
2004	594	UCCUAGCUCGGGAUGUUCA	UGAACAUCCCGAGCUAGGA	5507
277	595	UCAAGCUGAUUUGAUGGAG	CUCCAUCAAAUCAGCUUGA	5508
2304	596	CCAGCUCUCUCUUCAGAAC	GUUCUGAAGAGAGAGCUGG	5509
300	597	ACAUGGCCAUGGAACCAGA	UCUGGUUCCAUGGCCAUGU	5510

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1906	598	UACCCAGCGCCGUACGUCC	GGACGUACGGCGCUGGGUA	5511
1973	599	AUAGUUGAAGGUUGUACCG	CGGUACAACCUUCAACUAU	5512
1360	600	AGCUUUAGGACUUCACCUG	CAGGUGAAGUCCUAAAGCU	5513
2094	601	ACAUCCAAAGAGUAGCUGC	GCAGCUACUCUUUGGAUGU	5514
920	602	UUGCAUAACCUUUCCCAUC	GAUGGGAAAGGUUAUGCAA	5515
1707	603	UGGCCCAGAAUGCAGUUCG	CGAACUGCAUUCUGGGCCA	5516
1808	604	AUUCGAAAUCUUGCCCUUU	AAAGGGCAAGAUUUCGAAU	5517
1326	605	AUAAGCCGGCUAUUGUAGA	UCUACAAUAGCCGGCUUAU	5518
1158	606	CGACAGACUGCCUUCAAAU	AUUUGAAGGCAGUCUGUCG	5519
781	607	UGCAGUUAUGGUCCAUCAG	CUGAUGGACCAUAACUGCA	5520
607	608	GUUUGAUGCUGCUCAUCCC	GGGAUGAGCAGCAUCAAAC	5521
627	609	CUAAUGUCCAGCGUUUGGC	GCCAAACGCUGGACAUUAG	5522
500	610	CAAGUAGCUGAUAUUGAUG	CAUCAAUAUCAGCUACUUG	5523
2185	611	UCUGACAGAGUUACUUCAC	GUGAAGUAACUCUGUCAGA	5524
1592	612	GGUGGUAUAGAGGCUCUUG	CAAGAGCCUCUAUACCACC	5525
758	613	GACCAGGUGGUGGUUAAUA	UAUUAACCACCACCUGGUC	5526
2551	614	CCUCAUGGAUGGGCUGCCU	AGGCAGCCCAUCCAUGAGG	5527
1409	615	UGUCUUUGGACUCUCAGGA	UCCUGAGAGUCCAAAGACA	5528
497	616	GAACAAGUAGCUGAUAUUG	CAAUAUCAGCUACUUGUUC	5529
381	617	GUGCCACUACCACAGCUCC	GGAGCUGUGGUAGUGGCAC	5530
1841	618	GCACCUUUGCGUGAGCAGG	CCUGCUCACGCAAAGGUGC	5531
1368	619	GACUUCACCUGACAGAUCC	GGAUCUGUCAGGUGAAGUC	5532
2047	620	AAAUACCAUUCCAUUGUUU	AAACAAUGGAAUGGUAUUU	5533
492	621	CUCAAGAACAAGUAGCUGA	UCAGCUACUUGUUCUUGAG	5534
2118	622	UCCUCUGUGAACUUGCUCA	UGAGCAAGUUCACAGAGGA	5535
968	623	UCUGGAGGCAUUCCUGCCC	GGGCAGGAAUGCCUCCAGA	5536
965	624	AAGUCUGGAGGCAUUCCUG	CAGGAAUGCCUCCAGACUU	5537
1977	625	UUGAAGGUUGUACCGGAGC	GCUCCGGUACAACCUUCAA	5538
2001	626	ACAUCCUAGCUCGGGAUGU	ACAUCCCGAGCUAGGAUGU	5539
1191	627	ACCAAGAAAGCAAGCUCAU	AUGAGCUUGCUUUCUUGGU	5540
640	628	UUUGGCUGAACCAUCACAG	CUGUGAUGGUUCAGCCAAA	5541
715	629	CACACGUGCAAUCCCUGAA	UUCAGGGAUUGCACGUGUG	5542
1204	630	GCUCAUCAUACUGGCUAGU	ACUAGCCAGUAUGAUGAGC	5543
3093	631	GGGUAGGGUAAAUCAGUAA	UUACUGAUUUACCCUACCC	5544
1371	632	UUCACCUGACAGAUCCAAG	CUUGGAUCUGUCAGGUGAA	5545
409	633	UGGUAAAGGCAAUCCUGAG	CUCAGGAUUGCCUUUACCA	5546

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2405	634	GAUCCUAGCUAUCGUUCUU	AAGAACGAUAGCUAGGAUC	5547
1671	635	UUCGUCAUCUGACCAGCCG	CGGCUGGUCAGAUGACGAA	5548
1427	636	AAUCUUUCAGAUGCUGCAA	UUGCAGCAUCUGAAAGAUU	5549
1717	637	UGCAGUUCGCCUUCACUAU	AUAGUGAAGGCGAACUGCA	5550
2400	638	AGGAUGAUCCUAGCUAUCG	CGAUAGCUAGGAUCAUCCU	5551
2305	639	CAGCUCUCUCUUCAGAACA	UGUUCUGAAGAGAGAGCUG	5552
1928	640	GGUGGGACACAGCAGCAAU	AUUGCUGCUGUGUCCCACC	5553
2399	641	CAGGAUGAUCCUAGCUAUC	GAUAGCUAGGAUCAUCCUG	5554
426	642	AGGAAGAGGAUGUGGAUAC	GUAUCCACAUCCUCUUCCU	5555
1309	643	AUCUGUCUGCUCUAGUAAU	AUUACUAGAGCAGACAGAU	5556
925	644	UAACCUUUCCCAUCAUCGU	ACGAUGAUGGGAAAGGUUA	5557
2072	645	CUGCUUUAUUCUCCCAUUG	CAAUGGGAGAAUAAAGCAG	5558
2939	646	AAUUGUAAUCUGAAUAAAG	CUUUAUUCAGAUUACAAUU	5559
1480	647	UCUUGUUCAGCUUCUGGGU	ACCCAGAAGCUGAACAAGA	5560
1889	648	GUUCGUGCACAUCAGGAUA	UAUCCUGAUGUGCACGAAC	5561
699	649	AUGAUGCAGAACUUGCCAC	GUGGCAAGUUCUGCAUCAU	5562
506	650	GCUGAUAUUGAUGGACAGU	ACUGUCCAUCAAUAUCAGC	5563
1750	651	GGUUAAGCUCUUACACCCA	UGGGUGUAAGAGCUUAACC	5564
1820	652	GCCCUUUGUCCCGCAAAUC	GAUUUGCGGGACAAAGGGC	5565
541	653	UCAGAGGGUACGAGCUGCU	AGCAGCUCGUACCCUCUGA	5566
665	654	AAACAUGCAGUUGUAAACU	AGUUUACAACUGCAUGUUU	5567
1817	655	CUUGCCCUUUGUCCCGCAA	UUGCGGGACAAAGGGCAAG	5568
2275	656	UUACAAGAAACGGCUUUCA	UGAAAGCCGUUUCUUGUAA	5569
2426	657	CACUCUGGUGGAUAUGGCC	GGCCAUAUCCACCAGAGUG	5570
958	658	CAUCUUUAAGUCUGGAGGC	GCCUCCAGACUUAAAGAUG	5571
1657	659	UGCCAUCUGUGCUCUUCGU	ACGAAGAGCACAGAUGGCA	5572
1146	660	UCUUGGCUAUUACGACAGA	UCUGUCGUAAUAGCCAAGA	5573
3078	661	AUUUGGGAUAUGUAUGGGU	ACCCAUACAUAUCCCAAAU	5574
1008	662	CAGUGGAUUCUGUGUUGUU	AACAACACAGAAUCCACUG	5575
1621	663	CCUUCGGGCUGGUGACAGG	CCUGUCACCAGCCCGAAGG	5576
1932	664	GGACACAGCAGCAAUUUGU	ACAAAUUGCUGCUGUGUCC	5577
1909	665	CCAGCGCCGUACGUCCAUG	CAUGGACGUACGGCGCUGG	5578
2279	666	AAGAAACGGCUUUCAGUUG	CAACUGAAAGCCGUUUCUU	5579
574	667	AUUAGAUGAGGGCAUGCAG	CUGCAUGCCCUCAUCUAAU	5580
2303	668	ACCAGCUCUCUCUUCAGAA	UUCUGAAGAGAGAGCUGGU	5581
784	669	AGUUAUGGUCCAUCAGCUU	AAGCUGAUGGACCAUAACU	5582
2507	670	GACUAUCCAGUUGAUGGGC	GCCCAUCAACUGGAUAGUC	5583

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
995	671	AUGCUUGGUUCACCAGUGG	CCACUGGUGAACCAAGCAU	5584
2006	672	CUAGCUCGGGAUGUUCACA	UGUGAACAUCCCGAGCUAG	5585
1757	673	CUCUUACACCCACCAUCCC	GGGAUGGUGGGUGUAAGAG	5586
2129	674	CUUGCUCAGGACAAGGAAG	CUUCCUUGUCCUGAGCAAG	5587
2272	675	AGAUUACAAGAAACGGCUU	AAGCCGUUUCUUGUAAUCU	5588
389	676	ACCACAGCGGCUUCUCUGA	UCAGAGAAGGAGCUGUGGU	5589
1435	677	AGAUGCUGCAACUAAACAG	CUGUUUAGUUGCAGCAUCU	5590
1752	678	UUAAGCUCUUACACCCACC	GGUGGGUGUAAGAGCUUAA	5591
773	679	AAUAAGGCUGCAGUUAUGG	CCAUAACUGCAGCCUUAUU	5592
3080	680	UUGGGAUAUGUAUGGGUAG	CUACCCAUACAUAUCCCAA	5593
3174	681	GUAACCUGCUGUGAUACGA	UCGUAUCACAGCAGGUUAC	5594
1578	682	UGGUCUGCCAAGUGGGUGG	CCACCCACUUGGCAGACCA	5595
398	683	CCUUCUCUGAGUGGUAAAG	CUUUACCACUCAGAGAAGG	5596
2153	684	GAAGCUAUUGAAGCUGAGG	CCUCAGCUUCAAUAGCUUC	5597
702	685	AUGCAGAACUUGCCACACG	CGUGUGGCAAGUUCUGCAU	5598
503	686	GUAGCUGAUAUUGAUGGAC	GUCCAUCAAUAUCAGCUAC	5599
276	687	CUCAAGCUGAUUUGAUGGA	UCCAUCAAAUCAGCUUGAG	5600
1962	688	GCAUGGAAGAAAUAGUUGA	UCAACUAUUUCUUCCAUGC	5601
1347	689	CUGGUGGAAUGCAAGCUUU	AAAGCUUGCAUUCCACCAG	5602
2544	690	CCCAGGACCUCAUGGAUGG	CCAUCCAUGAGGUCCUGGG	5603
3079	691	UUUGGGAUAUGUAUGGGUA	UACCCAUACAUAUCCCAAA	5604
3164	692	CAAAGUUGUUGUAACCUGC	GCAGGUUACAACAACUUUG	5605
2026	693	CCGAAUUGUUAUCAGAGGA	UCCUCUGAUAACAAUUCGG	5606
2938	694	UAAUUGUAAUCUGAAUAAA	UUUAUUCAGAUUACAAUUA	5607
2940	695	AUUGUAAUCUGAAUAAAGU	ACUUUAUUCAGAUUACAAU	5608
2027	696	CGAAUUGUUAUCAGAGGAC	GUCCUCUGAUAACAAUUCG	5609
448	697	CCAAGUCCUGUAUGAGUGG	CCACUCAUACAGGACUUGG	5610
1329	698	AAGCCGGCUAUUGUAGAAG	CUUCUACAAUAGCCGGCUU	5611
2406	699	AUCCUAGCUAUCGUUCUUU	AAAGAACGAUAGCUAGGAU	5612
924	700	AUAACCUUUCCCAUCAUCG	CGAUGAUGGGAAAGGUUAU	5613
1584	701	GCCAAGUGGGUGGUAUAGA	UCUAUACCACCCACUUGGC	5614
1871	702	CGACUAGUUCAGUUGCUUG	CAAGCAACUGAACUAGUCG	5615
999	703	UUGGUUCACCAGUGGAUUC	GAAUCCACUGGUGAACCAA	5616
1400	704	GUUCAGAACUGUCUUUGGA	UCCAAAGACAGUUCUGAAC	5617
3189	705	UGCUGUGAUACGAUGCUUC	GAAGCAUCGUAUCACAGCA	5618
2569	706	UCCAGGUGACAGCAAUCAG	CUGAUUGCUGUCACCUGGA	5619

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
787	707	UAUGGUCCAUCAGCUUUCU	AGAAAGCUGAUGGACCAUA	5620
1861	708	UGCCAUUCCACGACUAGUU	AACUAGUCGUGGAAUGGCA	5621
1190	709	AACCAAGAAAGCAAGCUCA	UGAGCUUGCUUUCUUGGUU	5622
1557	710	AUAAUUAUAAGAACAAGAU	AUCUUGUUCUUAUAAUUAU	5623
1751	711	GUUAAGCUCUUACACCCAC	GUGGGUGUAAGAGCUUAAC	5624
2897	712	UUGAGUAAUGGUGUAGAAC	GUUCUACACCAUUACUCAA	5625
2217	713	GUGUGGCGACAUAUGCAGC	GCUGCAUAUGUCGCCACAC	5626
2302	714	GACCAGCUCUCUCUUCAGA	UCUGAAGAGAGAGCUGGUC	5627
1984	715	UUGUACCGGAGCCCUUCAC	GUGAAGGGCUCCGGUACAA	5628
302	716	AUGGCCAUGGAACCAGACA	UGUCUGGUUCCAUGGCCAU	5629
2431	717	UGGUGGAUAUGGCCAGGAU	AUCCUGGCCAUAUCCACCA	5630
2183	718	CCUCUGACAGAGUUACUUC	GAAGUAACUCUGUCAGAGG	5631
2403	719	AUGAUCCUAGCUAUCGUUC	GAACGAUAGCUAGGAUCAU	5632
788	720	AUGGUCCAUCAGCUUUCUA	UAGAAAGCUGAUGGACCAU	5633
1479	721	GGACUCUUGUUCAGCUUCU	AGAAGCUGAACAAGAGUCC	5634
827	722	GCUAUCAUGCGUUCUCCUC	GAGGAGAACGCAUGAUAGC	5635
2299	723	GCUGACCAGCUCUCUCUUC	GAAGAGAGAGCUGGUCAGC	5636
1891	724	UCGUGCACAUCAGGAUACC	GGUAUCCUGAUGUGCACGA	5637
2196	725	UACUUCACUCUAGGAAUGA	UCAUUCCUAGAGUGAAGUA	5638
663	726	UGAAACAUGCAGUUGUAAA	UUUACAACUGCAUGUUUCA	5639
1028	727	UAUGCCAUUACAACUCUCC	GGAGAGUUGUAAUGGCAUA	5640
2032	728	UGUUAUCAGAGGACUAAAU	AUUUAGUCCUCUGAUAACA	5641
1459	729	GAUGGAAGGUCUCCUUGGG	CCCAAGGAGACCUUCCAUC	5642
2095	730	CAUCCAAAGAGUAGCUGCA	UGCAGCUACUCUUUGGAUG	5643
1686	731	GCCGACACCAAGAAGCAGA	UCUGCUUCUUGGUGUCGGC	5644
1412	732	CUUUGGACUCUCAGGAAUC	GAUUCCUGAGAGUCCAAAG	5645
2473	733	GGAACAUGAGAUGGGUGGC	GCCACCCAUCUCAUGUUCC	5646
1080	734	UGGCAGUGCGUUUAGCUGG	CCAGCUAAACGCACUGCCA	5647
2143	735	GGAAGCUGCAGAAGCUAUU	AAUAGCUUCUGCAGCUUCC	5648
2203	736	CUCUAGGAAUGAAGGUGUG	CACACCUUCAUUCCUAGAG	5649
548	737	GUACGAGCUGCUAUGUUCC	GGAACAUAGCAGCUCGUAC	5650
1867	738	UCCACGACUAGUUCAGUUG	CAACUGAACUAGUCGUGCA	5651
842	739	CCUCAGAUGGUGUCUGCUA	UAGCAGACACCAUCUGAGG	5652
2120	740	CUCUGUGAACUUGCUCAGG	CCUGAGCAAGUUCACAGAG	5653
752	741	GCAGUUAUGGUCCAUCAGC	GCUGAUGGACCAUAACUGC	5654
1758	742	UCUUACACCCACCAUCCCA	UGGGAUGGUGGGUGUAAGA	5655
2396	743	CGCCAGGAUGAUCCUAGCU	AGCUAGGAUCAUCCUGGCG	5656

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1373	744	CACCUGACAGAUCCAAGUC	GACUUGGAUCUGUCAGGUG	5657
1518	745	UCACCUGUGCAGCUGGAAU	AUUCCAGCUGCACAGGUGA	5658
2557	746	GGAUGGGCUGCCUCCAGGU	ACCUGGAGGCAGCCCAUCC	5659
1987	747	UACCGGAGCCCUUCACAUC	GAUGUGAAGGGCUCCGGUA	5660
568	748	UGAGACAUUAGAUGAGGGC	GCCCUCAUCUAAUGUCUCA	5661
2201	749	CACUCUAGGAAUGAAGGUG	CACCUUCAUUCCUAGAGUG	5662
609	750	UUGAUGCUGCUCAUCCCAC	GUGGGAUGAGCAGCAUCAA	5663
400	751	UUCUCUGAGUGGUAAAGGC	GCCUUUACCACUCAGAGAA	5664
331	752	UGUUAGUCACUGGCAGCAA	UUGCUGCCAGUGACUAACA	5665
1967	753	GAAGAAAUAGUUGAAGGUU	AACCUUCAACUAUUUCUUC	5666
2198	754	CUUCACUCUAGGAAUGAAG	CUUCAUUCCUAGAGUGAAG	5667
1493	755	CUGGGUUCAGAUGAUAUAA	UUAUAUCAUCUGAACCCAG	5668
2260	756	GGACAAGCCACAAGAUUAC	GUAAUCUUGUGGCUUGUCC	5669
2496	757	ACCCUGGUGCUGACUAUCC	GGAUAGUCAGCACCAGGGU	5670
2361	758	UUGAUAUUGGUGCCCAGGG	CCCUGGGCACCAAUAUCAA	5671
443	759	ACCUCCCAAGUCCUGUAUG	CAUACAGGACUUGGGAGGU	5672
523	760	GUAUGCAAUGACUCGAGCU	AGCUCGAGUCAUUGCAUAC	5673
1742	761	CCAGUUGUGGUUAAGCUCU	AGAGCUUAACCACAACUGG	5674
530	762	AUGACUCGAGCUCAGAGGG	CCCUCUGAGCUCGAGUCAU	5675
3169	763	UUGUUGUAACCUGCUGUGA	UCACAGCAGGUUACAACAA	5676
1385	764	CCAAGUCAACGUCUUGUUC	GAACAAGACGUUGACUUGG	5677
2036	765	AUCAGAGGACUAAAUACCA	UGGUAUUUAGUCCUCUGAU	5678
3088	766	UGUAUGGGUAGGGUAAAUC	GAUUUACCCUACCCAUACA	5679
1850	767	CGUGAGCAGGGUGCCAUUC	GAAUGGCACCCUGCUCACG	5680
2518	768	UGAUGGGCUGCCAGAUCUG	CAGAUCUGGCAGCCCAUCA	5681
1886	769	CUUGUUCGUGCACAUCAGG	CCUGAUGUGCACGAACAAG	5682
650	770	CCAUCACAGAUGCUGAAAC	GUUUCAGCAUCUGUGAUGG	5683
3139	771	ACAGUUUACCAGUUGCCUU	AAGGCAACUGGUAAACUGU	5684
2025	772	ACCGAAUUGUUAUCAGAGG	CCUCUGAUAACAAUUCGGU	5685
1082	773	GCAGUGCGUUUAGCUGGUG	CACCAGCUAAACGCACUGC	5686
2475	774	AACAUGAGAUGGGUGGCCA	UGGCCACCCAUCUCAUGUU	5687
1375	775	CCUGACAGAUCCAAGUCAA	UUGACUUGGAUCUGUCAGG	5688
2013	776	GGGAUGUUCACAACCGAAU	AUUCGGUUGUGAACAUCCC	5689
1802	777	GGAUUGAUUCGAAAUCUUG	CAAGAUUUCGAAUCAAUCC	5690
2144	778	GAAGCUGCAGAAGCUAUUG	CAAUAGCUUCUGCAGCUUC	5691
529	779	AAUGACUCGAGCUCAGAGG	CCUCUGAGCUCGAGUCAUU	5692

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1482	780	UUGUUCAGCUUCUGGGUUC	GAACCCAGAAGCUGAACAA	5693
1546	781	CCUCACUUGCAAUAAUUAU	AUAAUUAUUGCAAGUGAGG	5694
845	782	CAGAUGGUGUCUGCUAUUG	CAAUAGCAGACACCAUCUG	5695
487	783	CUUCACUCAAGAACAAGUA	UACUUGUUCUUGAGUGAAG	5696
652	784	AUCACAGAUGCUGAAACAU	AUGUUUCAGCAUCUGUGAU	5697
1720	785	AGUUCGCCUUCACUAUGGA	UCCAUAGUGAAGGCGAACU	5698
951	786	UACUGGCCAUCUUUAAGUC	GACUUAAAGAUGGCCAGUA	5699
1232	787	CAAGCUUUAGUAAAUAUAA	UUAUAUUUACUAAAGCUUG	5700
2265	788	AGCCACAAGAUUACAAGAA	UUCUUGUAAUCUUGUGGCU	5701
1698	789	AAGCAGAGAUGGCCCAGAA	UUCUGGGCCAUCUCUGCUU	5702
701	790	GAUGCAGAACUUGCCACAC	GUGUGGCAAGUUCUGCAUC	5703
1428	791	AUCUUUCAGAUGCUGCAAC	GUUGCAGCAUCUGAAAGAU	5704
1930	792	UGGGACACAGCAGCAAUUU	AAAUUGCUGCUGUGUCCCA	5705
1379	793	ACAGAUCCAAGUCAACGUC	GACGUUGACUUGGAUCUGU	5706
1936	794	ACAGCAGCAAUUUGUGGAG	CUCCACAAAUUGCUGCUGU	5707
1441	795	UGCAACUAAACAGGAAGGG	CCCUUCCUGUUUAGUUGCA	5708
2132	796	GCUCAGGACAAGGAAGCUG	CAGCUUCCUUGUCCUGAGC	5709
2043	797	GACUAAAUACCAUUCCAUU	AAUGGAAUGGUAUUUAGUC	5710
608	798	UUUGAUGCUGCUCAUCCCA	UGGGAUGAGCAGCAUCAAA	5711
341	799	UGGCAGCAACAGUCUUACC	GGUAAGACUGUUGCUGCCA	5712
1194	800	AAGAAAGCAAGCUCAUCAU	AUGAUGAGCUUGCUUUCUU	5713
2350	801	UGAUCUUGGACUUGAUAUU	AAUAUCAAGUCCAAGAUCA	5714
2948	802	CUGAAUAAAGUGUAACAAU	AUUGUUACACUUUAUUCAG	5715
2044	803	ACUAAAUACCAUUCCAUUG	CAAUGGAAUGGUAUUUAGU	5716
621	804	AUCCCACUAAUGUCCAGCG	CGCUGGACAUUAGUGGGAU	5717
384	805	CCACUACCACAGCUCCUUC	GAAGGAGCUGUGGUAGUGG	5718
1898	806	CAUCAGGAUACCCAGCGCC	GGCGCUGGGUAUCCUGAUG	5719
653	807	UCACAGAUGCUGAAACAUG	CAUGUUUCAGCAUCUGUGA	5720
1846	808	UUUGCGUGAGCAGGGUGCC	GGCACCCUGCUCACGCAAA	5721
2348	809	GCUGAUCUUGGACUUGAUA	UAUCAAGUCCAAGAUCAGC	5722
1150	810	GGCUAUUACGACAGACUGC	GCAGUCUGUCGUAAUAGCC	5723
298	811	GGACAUGGCCAUGGAACCA	UGGUUCCAUGGCCAUGUCC	5724
1568	812	AACAAGAUGAUGGUCUGCC	GGCAGACCAUCAUCUUGUU	5725
1058	813	UUACAUCAAGAAGGAGCUA	UAGCUCCUUCUUGAUGUAA	5726
1835	814	AAUCAUGCACCUUUGCGUG	CACGCAAAGGUGCAUGAUU	5727
1832	815	GCAAAUCAUGCACCUUUGC	GCAAAGGUGCAUGAUUUGC	5728
406	816	GAGUGGUAAAGGCAAUCCU	AGGAUUGCCUUUACCACUC	5729

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1723	817	UCGCCUUCACUAUGGACUA	UAGUCCAUAGUGAAGGCGA	5730
371	818	AUCCAUUCUGGUGCCACUA	UAGUGGCACCAGAAUGGAU	5731
1899	819	AUCAGGAUACCCAGCGCCG	CGGCGCUGGGUAUCCUGAU	5732
522	820	AGUAUGCAAUGACUCGAGC	GCUCGAGUCAUUGCAUACU	5733
2285	821	CGGCUUUCAGUUGAGCUGA	UCAGCUCAACUGAAAGCCG	5734
779	822	GCUGCAGUUAUGGUCCAUC	GAUGGACCAUAACUGCAGC	5735
2896	823	AUUGAGUAAUGGUGUAGAA	UUCUACACCAUUACUCAAU	5736
2943	824	GUAAUCUGAAUAAAGUGUA	UACACUUUAUUCAGAUUAC	5737
513	825	UUGAUGGACAGUAUGCAAU	AUUGCAUACUGUCCAUCAA	5738
3084	826	GAUAUGUAUGGGUAGGGUA	UACCCUACCCAUACAUAUC	5739
1567	827	GAACAAGAUGAUGGUCUGC	GCAGACCAUCAUCUUGUUC	5740
2034	828	UUAUCAGAGGACUAAAUAC	GUAUUUAGUCCUCUGAUAA	5741
1003	829	UUCACCAGUGGAUUCUGUG	CACAGAAUCCACUGGUGAA	5742
1980	830	AAGGUUGUACCGGAGCCCU	AGGGCUCCGGUACAACCUU	5743
1340	831	GUAGAAGCUGGUGGAAUGC	GCAUUCCACCAGCUUCUAC	5744
1437	832	AUGCUGCAACUAAACAGGA	UCCUGUUUAGUUGCAGCAU	5745
2425	833	UCACUCUGGUGGAUAUGGC	GCCAUAUCCACCAGAGUGA	5746
282	834	CUGAUUUGAUGGAGUUGGA	UCCAACUCCAUCAAAUCAG	5747
1206	835	UCAUCAUACUGGCUAGUGG	CCACUAGCCAGUAUGAUGA	5748
1885	836	GCUUGUUCGUGCACAUCAG	CUGAUGUGCACGAACAAGC	5749
1314	837	UCUGCUCUAGUAAUAAGCC	GGCUUAUUACUAGAGCAGA	5750
1308	838	UAUCUGUCUGCUCUAGUAA	UUACUAGAGCAGACAGAUA	5751
1200	839	GCAAGCUCAUCAUACUGGC	GCCAGUAUGAUGAGCUUGC	5752
543	840	AGAGGGUACGAGCUGCUAU	AUAGCAGCUCGUACCCUCU	5753
1609	841	UGUGCGUACUGUCCUUCGG	CCGAAGGACAGUACGCACA	5754
1453	842	GGAAGGGAUGGAAGGUCUC	GAGACCUUCCAUCCCUUCC	5755
833	843	AUGCGUUCUCCUCAGAUGG	CCAUCUGAGGAGAACGCAU	5756
2188	844	GACAGAGUUACUUCACUCU	AGAGUGAAGUAACUCUGUC	5757
1148	845	UUGGCUAUUACGACAGACU	AGUCUGUCGUAAUAGCCAA	5758
1736	846	GGACUACCAGUUGUGGUUA	UAACCACAACUGGUAGUCC	5759
1401	847	UUCAGAACUGUCUUUGGAC	GUCCAAAGACAGUUCUGAA	5760
1677	848	AUCUGACCAGCCGACACCA	UGGUGUCGGCUGGUCAGAU	5761
1934	849	ACACAGCAGCAAUUUGUGG	CCACAAAUUGCUGCUGUGU	5762
388	850	UACCACAGCUCCUUCUCUG	CAGAGAAGGAGCUGUGGUA	5763
1920	851	CGUCCAUGGGUGGGACACA	UGUGUCCCACCCAUGGACG	5764
1747	852	UGUGGUUAAGCUCUUACAC	GUGUAAGAGCUUAACCACA	5765

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
861	853	UUGUACGUACCAUGCAGAA	UUCUGCAUGGUACGUACAA	5766
1904	854	GAUACCCAGCGCCGUACGU	ACGUACGGCGCUGGGUAUC	5767
831	855	UCAUGCGUUCUCCUCAGAU	AUCUGAGGAGAACGCAUGA	5768
1895	856	GCACAUCAGGAUACCCAGC	GCUGGGUAUCCUGAUGUGC	5769
2273	857	GAUUACAAGAAACGGCUUU	AAAGCCGUUUCUUGUAAUC	5770
1738	858	ACUACCAGUUGUGGUUAAG	CUUAACCACAACUGGUAGU	5771
1395	859	GUCUUGUUCAGAACUGUCU	AGACAGUUCUGAACAAGAC	5772
1675	860	UCAUCUGACCAGCCGACAC	GUGUCGGCUGGUCAGAUGA	5773
1845	861	CUUUGCGUGAGCAGGGUGC	GCACCCUGCUCACGCAAAG	5774
1408	862	CUGUCUUUGGACUCUCAGG	CCUGAGAGUCCAAAGACAG	5775
1059	863	UACAUCAAGAAGGAGCUAA	UUAGCUCCUUCUUGAUGUA	5776
1381	864	AGAUCCAAGUCAACGUCUU	AAGACGUUGACUUGGAUCU	5777
1386	865	CAAGUCAACGUCUUGUUCA	UGAACAAGACGUUGACUUG	5778
1470	866	UCCUUGGGACUCUUGUUCA	UGAACAAGAGUCCCAAGGA	5779
1349	867	GGUGGAAUGCAAGCUUUAG	CUAAAGCUUGCAUUCCACC	5780
1440	868	CUGCAACUAAACAGGAAGG	CCUUCCUGUUUAGUUGCAG	5781
1364	869	UUAGGACUUCACCUGACAG	CUGUCAGGUGAAGUCCUAA	5782
502	870	AGUAGCUGAUAUUGAUGGA	UCCAUCAAUAUCAGCUACU	5783
1246	871	UAUAAUGAGGACCUAUACU	AGUAUAGGUCCUCAUUAUA	5784
3178	872	CCUGCUGUGAUACGAUGCU	AGCAUCGUAUCACAGCAGG	5785
2483	873	AUGGGUGGCCACCACCCUG	CAGGGUGGUGGCCACCCAU	5786
1417	874	GACUCUCAGGAAUCUUUCA	UGAAAGAUUCCUGAGAGUC	5787
1893	875	GUGCACAUCAGGAUACCCA	UGGGUAUCCUGAUGUGCAC	5788
817	876	UUCCAGACACGCUAUCAUG	CAUGAUAGCGUGUCUGGAA	5789
711	877	UUGCCACACGUGCAAUCCC	GGGAUUGCACGUGUGGCAA	5790
1433	878	UCAGAUGCUGCAACUAAAC	GUUUAGUUGCAGCAUCUGA	5791
1362	879	CUUUAGGACUUCACCUGAC	GUCAGGUGAAGUCCUAAAG	5792
1838	880	CAUGCACCUUUGCGUGAGC	GCUCACGCAAAGGUGCAUG	5793
1037	881	ACAACUCUCCACAACCUUU	AAAGGUUGUGGAGAGUUGU	5794
1474	882	UGGGACUCUUGUUCAGCUU	AAGCUGAACAAGAGUCCCA	5795
997	883	GCUUGGUUCACCAGUGGAU	AUCCACUGGUGAACCAAGC	5796
931	884	UUCCCAUCAUCGUGAGGGC	GCCCUCACGAUGAUGGGAA	5797
1313	885	GUCUGCUCUAGUAAUAAGC	GCUUAUUACUAGAGCAGAC	5798
1487	886	CAGCUUCUGGGUUCAGAUG	CAUCUGAACCCAGAAGCUG	5799
1673	887	CGUCAUCUGACCAGCCGAC	GUCGGCUGGUCAGAUGACG	5800
561	888	UGUUCCCUGAGACAUUAGA	UCUAAUGUCUCAGGGAACA	5801
1188	889	GCAACCAAGAAAGCAAGCU	AGCUUGCUUUCUUGGUUGC	5802

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
292	890	GGAGUUGGACAUGGCCAUG	CAUGGCCAUGUCCAACUCC	5803
1958	891	GUCCGCAUGGAAGAAAUAG	CUAUUUCUUCCAUGCGGAC	5804
2349	892	CUGAUCUUGGACUUGAUAU	AUAUCAAGUCCAAGAUCAG	5805
1460	893	AUGGAAGGUCUCCUUGGGA	UCCCAAGGAGACCUUCCAU	5806
1576	894	GAUGGUCUGCCAAGUGGGU	ACCCACUUGGCAGACCAUC	5807
690	895	ACUAUCAAGAUGAUGCAGA	UCUGCAUCAUCUUGAUAGU	5808
655	896	ACAGAUGCUGAAACAUGCA	UGCAUGUUUCAGCAUCUGU	5809
2290	897	UUCAGUUGAGCUGACCAGC	GCUGGUCAGCUCAACUGAA	5810
1600	898	AGAGGCUCUUGUGCGUACU	AGUACGCACAAGAGCCUCU	5811
2432	899	GGUGGAUAUGGCCAGGAUG	CAUCCUGGCCAUAUCCACC	5812
710	900	CUUGCCACACGUGCAAUCC	GGAUUGCACGUGUGGCAAG	5813
1714	901	GAAUGCAGUUCGCCUUCAC	GUGAAGGCGAACUGCAUUC	5814
2005	902	CCUAGCUCGGGAUGUUCAC	GUGAACAUCCCGAGCUAGG	5815
1728	903	UUCACUAUGGACUACCAGU	ACUGGUAGUCCAUAGUGAA	5816
2482	904	GAUGGGUGGCCACCACCCU	AGGGUGGUGGCCACCCAUC	5817
768	905	UGGUUAAUAAGGCUGCAGU	ACUGCAGCCUUAUUAACCA	5818
693	906	AUCAAGAUGAUGCAGAACU	AGUUCUGCAUCAUCUUGAU	5819
3179	907	CUGCUGUGAUACGAUGCUU	AAGCAUCGUAUCACAGCAG	5820
2448	908	AUGCCUUGGGUAUGGACCC	GGGUCCAUACCCAAGGCAU	5821
3183	909	UGUGAUACGAUGCUUCAAG	CUUGAAGCAUCGUAUCACA	5822
1293	910	GAGUGCUGAAGGUGCUAUC	GAUAGCACCUUCAGCACUC	5823
544	911	GAGGGUACGAGCUGCUAUG	CAUAGCAGCUCGUACCCUC	5824
2937	912	UUAAUUGUAAUCUGAAUAA	UUAUUCAGAUUACAAUUAA	5825
1691	913	CACCAAGAAGCAGAGAUGG	CCAUCUCUGCUUCUUGGUG	5826
1353	914	GAAUGCAAGCUUUAGGACU	AGUCCUAAAGCUUGCAUUC	5827
1843	915	ACCUUUGCGUGAGCAGGGU	ACCCUGCUCACGCAAAGGU	5828
1302	916	AGGUGCUAUCUGUCUGCUC	GAGCAGACAGAUAGCACCU	5829
2130	917	UUGCUCAGGACAAGGAAGC	GCUUCCUUGUCCUGAGCAA	5830
2165	918	GCUGAGGGAGCCACAGCUC	GAGCUGUGGCUCCCUCAGC	5831
387	919	CUACCACAGCUCCUUCUCU	AGAGAAGGAGCUGUGGUAG	5832
2472	920	UGGAACAUGAGAUGGGUGG	CCACCCAUCUCAUGUUCCA	5833
857	921	GCUAUUGUACGUACCAUGC	GCAUGGUACGUACAAUAGC	5834
1816	922	UCUUGCCCUUUGUCCCGCA	UGCGGGACAAAGGGCAAGA	5835
15461	923	UUAUAAGACAAGAUGAUG	CAUCAUCUUGUUCUUAUAA	5836
811	924	GGAAGCUUCCAGACACGCU	AGCGUGUCUGGAAGCUUCC	5837
1327	925	UAAGCCGGCUAUUGUAGAA	UUCUACAAUAGCCGGCUUA	5838

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
757	926	GGACCAGGUGGUGGUUAAU	AUUAACCACCACCUGGUCC	5839
507	927	CUGAUAUUGAUGGACAGUA	UACUGUCCAUCAAUAUCAG	5840
3092	928	UGGGUAGGGUAAAUCAGUA	UACUGAUUUACCCUACCCA	5841
2359	929	ACUUGAUAUUGGUGCCCAG	CUGGGCACCAAUAUCAAGU	5842
1753	930	UAAGCUCUUACACCCACCA	UGGUGGGUGUAAGAGCUUA	5843
273	931	CUACUCAAGCUGAUUUGAU	AUCAAAUCAGCUUGAGUAG	5844
1859	932	GGUGCCAUUCCACGACUAG	CUAGUCGUGGAAUGGCACC	5845
296	933	UUGGACAUGGCCAUGGAAC	GUUCCAUGGCCAUGUCCAA	5846
615	934	CUGCUCAUCCCACUAAUGU	ACAUUAGUGGGAUGAGCAG	5847
301	935	CAUGGCCAUGGAACCAGAC	GUCUGGUUCCAUGGCCAUG	5848
1184	936	UAUGGCAACCAAGAAAGCA	UGCUUUCUUGGUUGCCAUA	5849
1006	937	ACCAGUGGAUUCUGUGUUG	CAACACAGAAUCCACUGGU	5850
2189	938	ACAGAGUUACUUCACUCUA	UAGAGUGAAGUAACUCUGU	5851
1635	939	UAGGACUUCACCUGACAGA	UCUGUCAGGUGAAGUCCUA	5852
2442	940	GCCAGGAUGCCUUGGGUAU	AUACCCAAGGCAUCCUGGC	5853
1249	941	AAUGAGGACCUAUACUUAC	GUAAGUAUAGGUCCUCAUU	5854
1144	942	AUUCUUGGCUAUUACGACA	UGUCGUAAUAGCCAAGAAU	5855
2075	943	CUUUAUUCUCCCAUUGAAA	UUUCAAUGGGAGAAUAAAG	5856
504	944	UAGCUGAUAUUGAUGGACA	UGUCCAUCAAUAUCAGCUA	5857
1405	945	GAACUGUCUUUGGACUCUC	GAGAGUCCAAAGACAGUUC	5858
333	946	UUAGUCACUGGCAGCAACA	UGUUGCUGCCAGUGACUAA	5859
1032	947	CCAUUACAACUCUCCACAA	UUGUGGAGAGUUGUAAUGG	5860
1748	948	GUGGUUAAGCUCUUACACC	GGUGUAAGAGCUUAACCAC	5861
283	949	UGAUUUGAUGGAGUUGGAC	GUCCAACUCCAUCAAAUCA	5862
1700	950	GCAGAGAUGGCCCAGAAUG	CAUUCUGGGCCAUCUCUGC	5863
1445	951	ACUAAACAGGAAGGGAUGG	CCAUCCCUUCCUGUUUAGU	5864
1133	952	ACAAAUGUUAAAUUCUUGG	CCAAGAAUUUAACAUUUGU	5865
527	953	GCAAUGACUCGAGCUCAGA	UCUGAGCUCGAGUCAUUGC	5866
2010	954	CUCGGGAUGUUCACAACCG	CGGUUGUGAACAUCCCGAG	5867
851	955	GUGUCUGCUAUUGUACGUA	UACGUACAAUAGCAGACAC	5868
436	956	UGUGGAUACCUCCCAAGUC	GACUUGGGAGGUAUCCACA	5869
2446	957	GGAUGCCUUGGGAUAGGAC	GUCCAUACCCAAGGCAUCC	5870
1142	958	AAAUUCUUGGCUAUUACGA	UCGUAAUAGCCAAGAAUUU	5871
549	959	UACGAGCUGCUAUGUUCCC	GGGAACAUAGCAGCUCGUA	5872
1083	960	CAGUGCGUUUAGCUGGUGG	CCACCAGCUAAACGCACUG	5873
695	961	CAAGAUGAUGCAGAACUUG	CAAGUUCUGCAUCAUCUUG	5874
885	962	AUGAUGUAGAAACAGCUCG	CGAGCUGUUUCUACAUCAU	5875

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2067	963	UGCAGCUGCUUUAUUCUCC	GGAGAAUAAAGCAGCUGCA	5876
390	964	CCACAGCUCCUUCUCUGAG	CUCAGAGAAGGAGCUGUGG	5877
1719	965	CAGUUCGCCUUCACUAUGG	CCAUAGUGAAGGCGAACUG	5878
813	966	AAGCUUCCAGACACGCUAU	AUAGCGUGUCUGGAAGCUU	5879
2289	967	UUUCAGUUGAGCUGACCAG	CUGGUCAGCUCAACUGAAA	5880
377	968	UCUGGUGCCACUACCACAG	CUGUGGUAGUGGCACCAGA	5881
826	969	CGCUAUCAUGCGUUCUCCU	AGGAGAACGCAUGAUAGCG	5882
1634	970	GACAGGGAAGACAUCACUG	CAGUGAUGUCUUCCCUGUC	5883
1208	971	AUCAUACUGGCUAGUGGUG	CACCACUAGCCAGUAUGAU	5884
1628	972	GCUGGUGACAGGGAAGACA	UGUCUUCCCUGUCACCAGC	5885
2003	973	AUCCUAGCUCGGGAUGUUC	GAACAUCCCGAGCUAGGAU	5886
452	974	GUCCUGUAUGAGUGGGAAC	GUUCCCACUCAUACAGGAC	5887
3081	975	UGGGAUAUGUAUGGGUAGG	CCUACCCAUACAUAUCCCA	5888
2354	976	CUUGGACUUGAUAUUGGUG	CACCAAUAUCAAGUCCAAG	5889
1822	977	CCUUUGUCCCGCAAAUCAU	AUGAUUUGCGGGACAAAGG	5890
1299	978	UGAAGGUGCUAUCUGUCUG	CAGACAGAUAGCACCUUCA	5891
486	979	CCUUCACUCAAGAACAAGU	ACUUGUUCUUGAGUGAAGG	5892
1463	980	GAAGGUCUCCUUGGGACUC	GAGUCCCAAGGAGACCUUC	5893
2280	981	AGAAACGGCUUUCAGUUGA	UCAACUGAAAGCCGUUUCU	5894
1907	982	ACCCAGCGCCGUACGUCCA	UGGACGUACGGCGCUGGGU	5895
923	983	CAUAACCUUUCCCAUCAUC	GAUGAUGGGAAAGGUUAUG	5896
1979	984	GAAGGUUGUACCGGAGCCC	GGGCUCCGGUACAACCUUC	5897
1827	985	GUCCCGCAAAUCAUGCACC	GGUGCAUGAUUUGCGGGAC	5898
1201	986	CAAGCUCAUCAUACUGGCU	AGCCAGUAUGAUGAGCUUG	5899
1913	987	CGCCGUACGUCCAUGGGUG	CACCCAUGGACGUACGGCG	5900
2191	988	AGAGUUACUUCACUCUAGG	CCUAGAGUGAAGUAACUCU	5901
295	989	GUUGGACAUGGCCAUGGAA	UUCCAUGGCCAUGUCCAAC	5902
1149	990	UGGCUAUUACGACAGACUG	CAGUCUGUCGUAAUAGCCA	5903
533	991	ACUCGAGCUCAGAGGGUAC	GUACCCUCUGAGCUCGAGU	5904
604	992	ACAGUUUGAUGCUGCUCAU	AUGAGCAGCAUCAAACUGU	5905
766	993	GGUGGUUAAUAAGGCUGCA	UGCAGCCUUAUUAACCACC	5906
1823	994	CUUUGUCCCGCAAAUCAUG	CAUGAUUUGCGGGACAAAG	5907
2048	995	AAUACCAUUCCAUUGUUUG	CAAACAAUGGAAUGGUAUU	5908
714	996	CCACACGUGCAAUCCCUGA	UCAGGGAUUGCACGUGUGG	5909
2439	997	AUGGCCAGGAUGCCUUGGG	CCCAAGGCAUCCUGGCCAU	5910
1903	998	GGAUACCCAGCGCCGUACG	CGUACGGCGCUGGGUAUCC	5911

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2395	999	UCGCCAGGAUGAUCCUAGC	GCUAGGAUCAUCCUGGCGA	5912
789	1000	UGGUCCAUCAGCUUUCUAA	UUAGAAAGCUGAUGGACCA	5913
3085	1001	AUAUGUAUGGGUAGGGUAA	UUACCCUACCCAUACAUAU	5914
1710	1002	CCCAGAAUGCAGUUCGCCU	AGGCGAACUGCAUUCUGGG	5915
1336	1003	UAUUGUAGAAGCUGGUGGA	UCCACCAGCUUCUACAAUA	5916
3089	1004	GUAUGGGUAGGGUAAAUCA	UGAUUUACCCUACCCAUAC	5917
2351	1005	GAUCUUGGACUUGAUAUUG	CAAUAUCAAGUCCAAGAUC	5918
916	1006	ACACGUGCAAUCCCUGAAC	GUUCAGGGAUUGCACGUGU	5919
1911	1007	AGCGCCGUACGUCCAUGGG	CCCAUGGACGUACGGCGCU	5920
1985	1008	UGUACCGGAGCCCUUCACA	UGUGAAGGGCUCCGGUACA	5921
2516	1009	GUUGAUGGGCUGCCAGAUC	GAUCUGGCAGCCCAUCAAC	5922
1762	1010	ACACCCACCAUCCCACUGG	CCAGUGGGAUGGUGGGUGU	5923
1156	1011	UACGACAGACUGCCUUCAA	UUGAAGGCAGUCUGUCGUA	5924
1887	1012	UUGUUCGUGCACAUCAGGA	UCCUGAUGUGCACGAACAA	5925
1833	1013	CAAAUCAUGCACCUUUGCG	CGCAAAGGUGCAUGAUUUG	5926
967	1014	GUCUGGAGGCAUUCCUGCC	GGCAGGAAUGCCUCCAGAC	5927
1730	1015	CACUAUGGACUACCAGUUG	CAACUGGUAGUCCAUAGUG	5928
829	1016	UAUCAUGCGUUCUCCUCAG	CUGAGGAGAACGCAUGAUA	5929
890	1017	GUAGAAACAGCUCGUGGUA	UACAACGAGCUGUUUCUAC	5930
2181	1018	CUCCUCUGACAGAGUUACA	AGUAACUCUGUCAGAGGAG	5931
2131	1019	UGCUCAGGACAAGGAAGCU	AGCUUCCUUGUCCUGAGCA	5932
1586	1020	CAAGUGGGUGGUAUAGAGG	CCUCUAUACCACCCACUUG	5933
765	1021	UGGUGGUUAAUAAGGCUGC	GCAGCCUUAUUAACCACCA	5934
1369	1022	ACUUCACCUGACAGAUCCA	UGGAUCUGUCAGGUGAAGU	5935
1724	1023	CGCCUUCACUAUGGACUAC	GUAGUCCAUAGUGAAGGCG	5936
834	1024	UGCGUUCUCCUCAGAUGGU	ACCAUCUGAGGAGAACGCA	5937
1983	1025	GUUGUACCGGAGCCCUUCA	UGAAGGGCUCCGGUACAAC	5938
1688	1026	CGACACCAAGAAGCAGAGA	UCUCUGCUUCUUGGUGUCG	5939
1004	1027	UCACCAGUGGAUUCUGUGU	ACACAGAAUCCACUGGUGA	5940
1631	1028	GGUGACAGGGAAGACAUCA	UGAUGUCUUCCCUGUCACC	5941
1319	1029	UCUAGUAAUAAGCCGGCUA	UAGCCGGCUUAUUACUAGA	5942
767	1030	GUGGUUAAUAAGGCUGCAG	CUGCAGCCUUAUUAACCAC	5943
841	1031	UCCUCAGAUGGUGUCUGCU	AGCAGACACCAUCUGAGGA	5944
516	1032	AUGGACAGUAUGCAAUGAC	GUCAUUGCAUACUGUCCAU	5945
1848	1033	UGCGUGAGCAGGGUGCCAU	AUGGCACCCUGCUCACGCA	5946
2202	1034	ACUCUAGGAAUGAAGGUGU	ACACCUUCAUUCCUAGAGU	5947
571	1035	GACAUUAGAUGAGGGCAUG	CAUGCCCUCAUCUAAUGUC	5948

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1629	1036	CUGGUGACAGGGAAGACAU	AUGUCUUCCCUGUCACCAG	5949
1806	1037	UGAUUCGAAAUCUUGCCCU	AGGGCAAGAUUUCGAAUCA	5950
1756	1038	GCUCUUACACCCACCAUCC	GGAUGGUGGGUGUAAGAGC	5951
1619	1039	GUCCUUCGGGCUGGUGACA	UGUCACCAGCCCGAAGGAC	5952
1616	1040	GUGCGUACUGUCCUUCGGG	CCCGAAGGACAGUACGCAC	5953
2500	1041	UGGUGCUGACUAUCCAGUU	AACUGGAUAGUCAGCACCA	5954
2156	1042	GCUAUUGAAGCUGAGGGAG	CUCCCUCAGCUUCAAUAGC	5955
1189	1043	CAACCAAGAAAGCAAGCUC	GAGCUUGCUUUCUUGGUUG	5956
2066	1044	GUGCAGCUGCUUUAUUCUC	GAGAAUAAAGCAGCUGCAC	5957
1307	1045	CUAUCUGUCUGCUCUAGUA	UACUAGAGCAGACAGAUAG	5958
1448	1046	AAACAGGAAGGGAUGGAAG	CUUCCAUCCCUUCCUGUUU	5959
1213	1047	ACUGGCUAGUGGUGGACCC	GGGUCCACCACUAGCCAGU	5960
2119	1048	CCUCUGUGAACUUGCUCAG	CUGAGCAAGUUCACAGAGG	5961
889	1049	UGUAGAAACAGCUCGUUGU	ACAACGAGCUGUUUCUACA	5962
1376	1050	CUGACAGAUCCAAGUCAAC	GUUGACUUGGAUCUGUCAG	5963
427	1051	GGAAGAGGAUGUGGAUACC	GGUAUCCACAUCCUCUUCC	5964
649	1052	ACCAUCACAGAUGCUGAAA	UUUCAGCAUCUGUGAUGGU	5965
1915	1053	CCGUACGUCCAUGGGUGGG	CCCACCCAUGGACGUACGG	5966
2053	1054	CAUUCCAUUGUUUGUGCAG	CUGCACAAACAAUGGAAUG	5967
2568	1055	CUCCAGGUGACAGCAAUCA	UGAUUGCUGUCACCUGGAG	5968
1739	1056	CUACCAGUUGUGGUUAAGC	GCUUAACCACAACUGGUAG	5969
1746	1057	UUGUGGUUAAGCUCUUACA	UGUAAGAGCUUAACCACAA	5970
1321	1058	UAGUAAUAAGCCGGCUAUU	AAUAGCCGGCUUAUUACUA	5971
482	1059	CAGUCCUUCACUCAAGAAC	GUUCUUGAGUGAAGGACUG	5972
280	1060	AGCUGAUUUGAUGGAGUUG	CAACUCCAUCAAAUCAGCU	5973
1468	1061	AGGUCUCCUUGGGACUCUU	AAGAGUCCCAAGGAGACCU	5974
1731	1062	ACUAUGGACUACCAGUUGU	ACAACUGGUAGUCCAUAGU	5975
1937	1063	CAGCAGCAAUUUGUGGAGG	CCUCCACAAAUUGCUGCUG	5976
1892	1064	CGUGCACAUCAGGAUACCC	GGGUAUCCUGAUGUGCACG	5977
836	1065	CGUUCUCCUCAGAUGGUGU	ACACCAUCUGAGGAGAACG	5978
521	1066	CAGUAUGCAAUGACUCGAG	CUCGAGUCAUUGCAUACUG	5979
1595	1067	GGUAUAGAGGCUCUUGUGC	GCACAAGAGCCUCUAUACC	5980
2511	1068	AUCCAGUUGAUGGGCUGCC	GGCAGCCCAUCAACUGGAU	5981
1583	1069	UGCCAAGUGGGUGGUAUAG	CUAUACCACCCACUUGGCA	5982
1897	1070	ACAUCAGGAUACCCAGCGC	GCGCUGGGUAUCCUGAUGU	5983
956	1071	GCCAUCUUUAAGUCUGGAG	CUCCAGACUUAAAGAUGGC	5984

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
926	1072	AACCUUUCCCAUCAUCGUG	CACGAUGAUGGGAAAGGUU	5985
1874	1073	CUAGUUCAGUUGCUUGUUC	GAACAAGCAACUGAACUAG	5986
488	1074	UUCACUCAAGAACAAGUAG	CUACUUGUUCUUGAGUGAA	5987
1695	1075	AAGAAGCAGAGAUGGCCCA	UGGGCCAUCUCUGCUUCUU	5988
2182	1076	UCCUCUGACAGAGUUACUU	AAGUAACUCUGUCAGAGGA	5989
2029	1077	AAUUGUUAUCAGAGGACUA	UAGUCCUCUGAUAACAAUU	5990
479	1078	UCUCAGUCCUUCACUCAAG	CUUGAGUGAAGGACUGAGA	5991
818	1079	UCCAGACACGCUAUCAUGC	GCAUGAUAGCGUGUCUGGA	5992
625	1080	CACUAAUGUCCAGCGUUUG	CAAACGCUGGACAUUAGUG	5993
3172	1081	UUGUAACCUGCUGUGAUAC	GUAUCACAGCAGGUUACAA	5994
1490	1082	CUUCUGGGUUCAGAUGAUA	UAUCAUCUGAACCCAGAAG	5995
1914	1083	GCCGUACGUCCAUGGGUGG	CCACCCAUGGACGUACGGC	5996
1974	1084	UAGUUGAAGGUUGUACCGG	CCGGUACAACCUUCAACUA	5997
2258	1085	GAGGACAAGCCACAAGAUU	AAUCUUGUGGCUUGUCCUC	5998
2170	1086	GGGAGCCACAGCUCCUCUG	CAGAGGAGCUGUGGCUCCC	5999
1370	1087	CUUCACCUGACAGAUCCAA	UUGGAUCUGUCAGGUGAAG	6000
1429	1088	UCUUUCAGAUGCUGCAACU	AGUUGCAGCAUCUGAAAGA	6001
3173	1089	UGUAACCUGCUGUGAUACG	CGUAUCACAGCAGGUUACA	6002
444	1090	CCUCCCAAGUGGUGUAUGA	UCAUACAGGACUUGGGAGG	6003
1081	1091	GGCAGUGCGUUUAGCUGGU	ACCAGCUAAACGCACUGCC	6004
1318	1092	CUCUAGUAAUAAGCCGGCU	AGCCGGCUUAUUACUAGAG	6005
329	1093	GCUGUUAGUCACUGGCAGC	GCUGCCAGUGACUAACAGC	6006
1389	1094	GUCAACGUCUUGUUCAGAA	UUCUGAACAAGACGUUGAC	6007
428	1095	GAAGAGGAUGUGGAUACCU	AGGUAUCCACAUCCUCUUC	6008
3175	1096	UAACCUGCUGUGAUACGAU	AUCGUAUCACAGCAGGUUA	6009
3117	1097	GUUAUUUGGAACCUUGUUU	AAACAAGGUUCCAAAUAAC	6010
2020	1098	UCACAACCGAAUUGUUAUC	GAUAACAAUUCGGUUGUGA	6011
1625	1099	CGGGCUGGUGACAGGGAAG	CUUCCCUGUCACCAGCCCG	6012
2022	1100	ACAACCGAAUUGUUAUCAG	CUGAUAACAAUUCGGUUGU	6013
624	1101	CCACUAAUGUCCAGCGUUU	AAACGCUGGACAUUAGUGG	6014
1648	1102	CACUGAGCCUGCCAUCUGU	ACAGAUGGCAGGCUCAGUG	6015
790	1103	GGUCCAUCAGCUUUCUAAA	UUUAGAAAGCUGAUGGACC	6016
3160	1104	AUCCCAAAGUUGUUGUAAC	GUUACAACAACUUUGGGAU	6017
1251	1105	UGAGGACCUAUACUUACGA	UCGUAAGUAUAGGUCCUCA	6018
2253	1106	UGUCUGAGGACAAGCCACA	UGUGGCUUGUCCUCAGACA	6019
2515	1107	AGUUGAUGGGCUGCCAGAU	AUCUGGCAGCCCAUCAACU	6020
1680	1108	UGACCAGCCGACACCAAGA	UCUUGGUGUCGGCUGGUCA	6021

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2169	1109	AGGGAGCCACAGCUCCUCU	AGAGGAGCUGUGGCUCCCU	6022
3165	1110	AAAGUUGUUGUAACCUGCU	AGCAGGUUACAACAACUUU	6023
780	1111	CUGCAGUUAUGGUCCAUCA	UGAUGGACCAUAACUGCAG	6024
1978	1112	UGAAGGUUGUACCGGAGCC	GGCUCCGGUACAACCUUCA	6025
563	1113	UUCCCUGAGACAUUAGAUG	CAUCUAAUGUCUCAGGGAA	6026
1622	1114	CUUCGGGCUGGUGACAGGG	CCCUGUCACCAGCCCGAAG	6027
2295	1115	UUGAGCUGACCAGCUCUCU	AGAGAGCUGGUCAGCUCAA	6028
2126	1116	GAACUUGCUCAGGACAAGG	CCUUGUCCUGAGCAAGUUC	6029
1683	1117	CCAGCCGACACCAAGAAGC	GCUUCUUGGUGUCGGCUGG	6030
1857	1118	AGGGUGCCAUUCCACGACU	AGUCGUGGAAUGGCACCCU	6031
2064	1119	UUGUGCAGCUGCUUUAUUC	GAAUAAAGCAGCUGCACAA	6032
489	1120	UCACUCAAGAACAAGUAGC	GCUACUUGUUCUUGAGUGA	6033
1346	1121	GCUGGUGGAAUGCAAGCUU	AAGCUUGCAUUCCACCAGC	6034
1442	1122	GCAACUAAACAGGAAGGGA	UCCCUUCCUGUUUAGUUGC	6035
1981	1123	AGGUUGUACCGGAGCCCUU	AAGGGCUCCGGUACAACCU	6036
777	1124	AGGCUGCAGUUAUGGUCCA	UGGACCAUAACUGCAGCCU	6037
589	1125	GCAGAUCCCAUCUACACAG	CUGUGUAGAUGGGAUCUGC	6038
2205	1126	CUAGGAAUGAAGGUGUGGC	GCCACACCUUCAUUCCUAG	6039
394	1127	AGCUCCUUCUCUGAGUGGU	ACCACUCAGAGAAGGAGCU	6040
1035	1128	UUACAACUCUCCACAACCU	AGGUUGUGGAGAGUUGUAA	6041
410	1129	GGUAAAGGCAAUCCUGAGG	CCUCAGGAUUGCCUUUACC	6042
1721	1130	GUUCGCCUUCACUAUGGAC	GUCCAUAGUGAAGGCGAAC	6043
1134	1131	CAAAUGUUAAAUUCUUGGC	GCCAAGAAUUUAACAUUUG	6044
3182	1132	CUGUGAUACGAUGCUUCAA	UUGAAGCAUCGUAUCACAG	6045
881	1133	ACAAAUGAUGUAGAAACAG	CUGUUUCUACAUCAUUUGU	6046
547	1134	GGUACGAGCUGCUAUGUUC	GAACAUAGCAGCUCGUACC	6047
2028	1135	GAAUUGUUAUCAGAGGACU	AGUCCUCUGAUAACAAUUC	6048
2023	1136	CAACCGAAUUGUUAUCAGA	UCUGAUAACAAUUCGGUUG	6049
3184	1137	GUGAUACGAUGCUUCAAGA	UCUUGAAGCAUCGUAUCAC	6050
413	1138	AAAGGCAAUCCUGAGGAAG	CUUCCUCAGGAUUGCCUUU	6051
2178	1139	CAGCUCCUCUGACAGAGUU	AACUCUGUCAGAGGAGCUG	6052
1577	1140	AUGGUCUGCCAAGUGGGUG	CACCCACUUGGCAGACCAU	6053
1793	1141	GCUACUGUUGGAUUGAUUC	GAAUCAAUCCAACAGUAGC	6054
526	1142	UGCAAUGACUCGAGCUCAG	CUGAGCUCGAGUCAUUGCA	6055
2358	1143	GACUUGAUAUUGGUGCCCA	UGGGCACCAAUAUCAAGUC	6056
1403	1144	CAGAACUGUCUUUGGACUC	GAGUCCAAAGACAGUUCUG	6057

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1875	1145	UAGUUCAGUUGCUUGUUCG	CGAACAAGCAACUGAACUA	6058
1160	1146	ACAGACUGCCUUCAAAUUU	AAAUUUGAAGGCAGUCUGU	6059
1591	1147	GGGUGGUAUAGAGGCUCUU	AAGAGCCUCUAUACCACCC	6060
1734	1148	AUGGACUACCAGUUGUGGU	ACCACAACUGGUAGUCCAU	6061
2030	1149	AUUGUUAUCAGAGGACUAA	UUAGUCCUCUGAUAACAAU	6062
775	1150	UAAGGCUGCAGUUAUGGUC	GACCAUAACUGCAGCCUUA	6063
1813	1151	AAAUCUUGCCCUUUGUCCC	GGGACAAAGGGCAAGAUUU	6064
1938	1152	AGCAGCAAUUUGUGGAGGG	CCCUCCACAAAUUGCUGCU	6065
2039	1153	AGAGGACUAAAUACCAUUC	GAAUGGUAUUUAGUCCUCU	6066
1297	1154	GCUGAAGGUGCUAUCUGUC	GACAGAUAGCACCUUCAGC	6067
456	1155	UGUAUGAGUGGGAACAGGG	CCCUGUUCCCACUCAUACA	6068
590	1156	CAGAUCCCAUCUACACAGU	ACUGUGUAGAUGGGAUCUG	6069
1933	1157	GACACAGCAGCAAUUUGUG	CACAAAUUGCUGCUGUGUC	6070
583	1158	GGGCAUGCAGAUCCCAUCU	AGAUGGGAUCUGCAUGCCC	6071
2540	1159	CAUGCCCAGGACCUCAUGG	CCAUGAGGUCCUGGGCAUG	6072
2162	1160	GAAGCUGAGGGAGCCACAG	CUGUGGCUCCCUCAGCUUC	6073
330	1161	CUGUUAGUCACUGGCAGCA	UGCUGCCAGUGACUAACAG	6074
1481	1162	CUUGUUCAGCUUCUGGGUU	AACCCAGAAGCUGAACAAG	6075
1344	1163	AAGCUGGUGGAAUGCAAGC	GCUUGCAUUCCACCAGCUU	6076
431	1164	GAGGAUGUGGAUACCUCCC	GGGAGGUAUCCACAUCCUC	6077
1508	1165	AUAAAUGUGGUCACCUGUG	CACAGGUGACCACAUUUAU	6078
1918	1166	UACGUCCAUGGGUGGGACA	UGUCCCACCCAUGGACGUA	6079
289	1167	GAUGGAGUUGGACAUGGCC	GGCCAUGUCCAACUCCAUC	6080
631	1168	UGUCCAGCGUUUGGCUGAA	UUCAGCCAAACGCUGGACA	6081
1853	1169	GAGCAGGGUGCCAUUCCAC	GUGGAAUGGCACCCUGCUC	6082
1243	1170	AAAUAUAAUGAGGACCUAU	AUAGGUCCUCAUUAUAUUU	6083
1212	1171	UACUGGCUAGUGGUGGACC	GGUCCACCACUAGCCAGUA	6084
996	1172	UGCUUGGUUCACCAGUGGA	UCCACUGGUGAACCAAGCA	6085
2256	1173	CUGAGGACAAGCCACAAGA	UCUUGUGGCUUGUCCUCAG	6086
1607	1174	CUUGUGCGUACUGUCCUUC	GAAGGACAGUACGCACAAG	6087
3116	1175	UGUUAUUUGGAACCUUGUU	AACAAGGUUCCAAAUAACA	6088
1179	1176	UAGCUUAUGGCAACCAAGA	UCUUGGUUGCCAUAAGCUA	6089
3185	1177	UGAUACGAUGCUUCAAGAG	CUCUUGAAGCAUCGUAUCA	6090
1594	1178	UGGUAUAGAGGCUCUUGUG	CACAAGAGCCUCUAUACCA	6091
887	1179	GAUGUAGAAACAGCUCGUU	AACGAGCUGUUUCUACAUC	6092
928	1180	CCUUUCCCAUCAUCGUGAG	CUCACGAUGAUGGGAAAGG	6093
835	1181	GCGUUCUCCUCAGAUGGUG	CACCAUCUGAGGAGAACGC	6094

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1900	1182	UCAGGAUACCCAGCGCCGU	ACGGCGCUGGGUAUCCUGA	6095
2284	1183	ACGGCUUUCAGUUGAGCUG	CAGCUCAACUGAAAGCCGU	6096
1976	1184	GUUGAAGGUUGUACCGGAG	CUCCGGUACAACCUUCAAC	6097
2393	1185	UAUCGCCAGGAUGAUCCUA	UAGGAUCAUCCUGGCGAUA	6098
1295	1186	GUGCUGAAGGUGCUAUCUG	CAGAUAGCACCUUCAGCAC	6099
1410	1187	GUCUUUGGACUCUCAGGAA	UUCCUGAGAGUCCAAAGAC	6100
1457	1188	GGGAUGGAAGGUCUCCUUG	CAAGGAGACCUUCCAUCCC	6101
2296	1189	UGAGCUGACCAGCUCUCUC	GAGAGAGCUGGUCAGCUCA	6102
929	1190	CUUUCCCAUCAUCGUGAGG	CCUCACGAUGAUGGGAAAG	6103
1359	1191	AAGCUUUAGGACUUCACCU	AGGUGAAGUCCUAAAGCUU	6104
1351	1192	UGGAAUGCAAGCUUUAGGA	UCCUAAAGCUUGCAUUCCA	6105
969	1193	CUGGAGGCAUUCCUGCCCU	AGGGCAGGAAUGCCUCCAG	6106
1876	1194	AGUUCAGUUGCUUGUUCGU	ACGAACAAGCAACUGAACU	6107
552	1195	GAGCUGCUAUGUUCCCUGA	UCAGGGAACAUAGCAGCUC	6108
2441	1196	GGCCAGGAUGCCUUGGGUA	UACCCAAGGCAUCCUGGCC	6109
2402	1197	GAUGAUCCUAGCUAUCGUU	AACGAUAGCUAGGAUCAUC	6110
1803	1198	GAUUGAUUCGAAAUCUUGC	GCAAGAUUUCGAAUCAAUC	6111
1701	1199	CAGAGAUGGCCCAGAAUGC	GCAUUCUGGGCCAUCUCUG	6112
1910	1200	CAGCGCCGUACGUCCAUGG	CCAUGGACGUACGGCGCUG	6113
888	1201	AUGUAGAAACAGCUCGUUG	CAACGAGCUGUUUCUACAU	6114
1294	1202	AGUGCUGAAGGUGCUAUCU	AGAUAGCACCUUCAGCACU	6115
1737	1203	GACUACCAGUUGUGGUUAA	UUAACCACAACUGGUAGUC	6116
1450	1204	ACAGGAAGGGAUGGAAGGU	ACCUUCCAUCCCUUCCUGU	6117
761	1205	CAGGUGGUGGUUAAUAAGG	CCUUAUUAACCACCACCUG	6118
776	1206	AAGGCUGCAGUUAUGGUCC	GGACCAUAACUGCAGCCUU	6119
1509	1207	UAAAUGUGGUCACCUGUGC	GCACAGGUGAGGACAUUUA	6120
1788	1208	UAAAGGCUACUGUUGGAUU	AAUCCAACAGUAGCCUUUA	6121
515	1209	GAUGGACAGUAUGCAAUGA	UCAUUGCAUACUGUCCAUC	6122
1491	1210	UUCUGGGUUCAGAUGAUAU	AUAUCAUCUGAACCCAGAA	6123
1614	1211	GUACUGUCCUUCGGGCUGG	CCAGCCCGAAGGACAGUAC	6124
998	1212	CUUGGUUCACCAGUGGAUU	AAUCCACUGGUGAACCAAG	6125
2158	1213	UAUUGAAGCUGAGGGAGCC	GGCUCCCUCAGCUUCAAUA	6126
3168	1214	GUUGUUGUAACCUGCUGUG	CACAGCAGGUUACAACAAC	6127
1854	1215	AGCAGGGUGCCAUUCCACG	CGUGGAAUGGCACCCUGCU	6128
2117	1216	GUCCUCUGUGAACUUGCUC	GAGCAAGUUCACAGAGGAC	6129
1678	1217	UCUGACCAGCCGACACCAA	UUGGUGUCGGCUGGUCAGA	6130

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
305	1218	GCCAUGGAACCAGACAGAA	UUCUGUCUGGUUCCAUGGC	6131
2154	1219	AAGCUAUUGAAGCUGAGGG	CCCUCAGCUUCAAUAGCUU	6132
1807	1220	GAUUCGAAAUCUUGCCCUU	AAGGGCAAGAUUUCGAAUC	6133
1881	1221	AGUUGCUUGUUCGUGCACA	UGUGCACGAACAAGCAACU	6134
1565	1222	AAGAACAAGAUGAUGGUCU	AGACCAUCAUCUUGUUCUU	6135
407	1223	AGUGGUAAAGGCAAUCCUG	CAGGAUUGCCUUUACCACU	6136
1434	1224	CAGAUGCUGCAACUAAACA	UGUUUAGUUGCAGCAUCUG	6137
566	1225	CCUGAGACAUUAGAUGAGG	CCUCAUCUAAUGUCUCAGG	6138
3161	1226	UCCCAAAGUUGUUGUAACC	GGUUACAACAACUUUGGGA	6139
1679	1227	CUGACCAGCCGACACCAAG	CUUGGUGUCGGCUGGUCAG	6140
2096	1228	AUCCAAAGAGUAGCUGCAG	CUGCAGCUACUCUUUGGAU	6141
630	1229	AUGUCCAGCGUUUGGCUGA	UCAGCCAAACGCUGGACAU	6142
1606	1230	UCUUGUGCGUACUGUCCUU	AAGGACAGUACGCACAAGA	6143
432	1231	AGGAUGUGGAUACCUCCCA	UGGGAGGUAUCCACAUCCU	6144
778	1232	GGCUGCAGUUAUGGUCCAU	AUGGACCAUAACUGCAGCC	6145
1999	1233	UCACAUCCUAGCUCGGGAU	AUCCCGAGCUAGGAUGUGA	6146
1692	1234	ACCAAGAAGCAGAGAUGGC	GCCAUCUCUGCUUCUUGGU	6147
2490	1235	GCCACCACCCUGGUGCUGA	UCAGCACCAGGGUGGUGGC	6148
623	1236	CCCACUAAUGUCCAGCGUU	AACGCUGGACAUUAGUGGG	6149
339	1237	ACUGGCAGCAACAGUCUUA	UAAGACUGUUGCUGCCAGU	6150
2946	1238	AUCUGAAUAAAGUGAUUCA	UGUUACACUUUAUUCAGAU	6151
1654	1239	GCCUGCCAUCUGUGCUCUU	AAGAGCACAGAUGGCAGGC	6152
1033	1240	CAUUACAACUCUCCACAAC	GUUGUGGAGAGUUGUAAUG	6153
840	1241	CUCCUCAGAUGGUGUCUGC	GCAGACACCAUCUGAGGAG	6154
1880	1242	CAGUUGCUUGUUCGUGCAC	GUGCACGAACAAGCAACUG	6155
420	1243	AUCCUGAGGAAGAGGAUGU	ACAUCCUCUUCCUCAGGAU	6156
1005	1244	CACCAGUGGAUUCUGUGUU	AACACAGAAUCCACUGGUG	6157
1193	1245	CAAGAAAGCAAGCUCAUCA	UGAUGAGCUUGCUUUCUUG	6158
919	1246	CUUGCAUAACCUUUCCCAU	AUGGGAAAGGUUAUGCAAG	6159
1727	1247	CUUCACUAUGGACUACCAG	CUGGUAGUCCAUAGUGAAG	6160
1883	1248	UUGCUUGUUCGUGCACAUC	GAUGUGCACGAACAAGCAA	6161
859	1249	UAUUGUACGUACCAUGCAG	CUGCAUGGUACGUACAAUA	6162
1812	1250	GAAAUCUUGCCCUUUGUCC	GGACAAAGGGCAAGAUUUC	6163
1605	1251	CUCUUGUGCGUACUGUCCU	AGGACAGUACGCACAAGAG	6164
2021	1252	CACAACCGAAUUGUUAUCA	UGAUAACAAUUCGGUUGUG	6165
2180	1253	GCUCCUCUGACAGAGUUAC	GUAACUCUGUCAGAGGAGC	6166
636	1254	AGCGUUUGGCUGAACCAUC	GAUGGUUCAGCCAAACGCU	6167

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2282	1255	AAACGGCUUUCAGUUGAGC	GCUCAACUGAAAGCCGUUU	6168
1824	1256	UUUGUCCCGCAAAUCAUGC	GCAUGAUUUGCGGGACAAA	6169
2204	1257	UCUAGGAAUGAAGGUGUGG	CCACACCUUCAUUCCUAGA	6170
450	1258	AAGUCCUGUAUGAGUGGGA	UCCCACUCAUACAGGACUU	6171
1001	1259	GGUUCACCAGUGGAUUCUG	CAGAAUCCACUGGUGAACC	6172
1579	1260	GGUCUGCCAAGUGGGUGGU	ACCACCCACUUGGCAGACC	6173
2179	1261	AGCUCCUCUGACAGAGUUA	UAACUCUGUCAGAGGAGCU	6174
376	1262	UUCUGGUGCCACUACCACA	UGUGGUAGUGGCACCAGAA	6175
556	1263	UGCUAUGUUCCCUGAGACA	UGUCUCAGGGAACAUAGCA	6176
1804	1264	AUUGAUUCGAAAUCUUGCC	GGCAAGAUUUCGAAUCAAU	6177
2552	1265	CUCAUGGAUGGGCUGCCUC	GAGGCAGCCCAUCCAUGAG	6178
2071	1266	GCUGCUUUAUUCUCCCAUU	AAUGGGAGAAUAAAGCAGC	6179
1836	1267	AUCAUGCACCUUUGCGUGA	UCACGCAAAGGUGCAUGAU	6180
336	1268	GUCACUGGCAGCAACAGUC	GACUGUUGCUGCCAGUGAC	6181
460	1269	UGAGUGGGAACAGGGAUUU	AAAUCCCUGUUCCCACUCA	6182
1559	1270	AAUUAUAAGAACAAGAUGA	UCAUCUUGUUCUUAUAAUU	6183
3136	1271	UGGACAGUUUACCAGUUGC	GCAACUGGUAAACUGUCCA	6184
1250	1272	AUGAGGACCUAUACUUACG	CGUAAGUAUAGGUCCUCAU	6185
1462	1273	GGAAGGUCUCCUUGGGACU	AGUCCCAAGGAGACCUUCC	6186
1965	1274	UGGAAGAAAUAGUUGAAGG	CCUUCAACUAUUUCUUCCA	6187
3114	1275	GGUGUUAUUUGGAACCUUG	CAAGGUUCCAAAUAACACC	6188
1665	1276	GUGCUCUUCGUCAUCUGAC	GUCAGAUGACGAAGAGCAC	6189
304	1277	GGCCAUGGAACCAGACAGA	UCUGUCUGGUUCCAUGGCC	6190
327	1278	CGGCUGUUAGUCACUGGCA	UGCCAGUGACUAACAGCCG	6191
1866	1279	UUCCACGACUAGUUCAGUU	AACUGAACUAGUCGUGGAA	6192
1699	1280	AGCAGAGAUGGCCCAGAAU	AUUCUGGGCCAUCUCUGCU	6193
2397	1281	GCCAGGAUGAUCCUAGCUA	UAGCUAGGAUCAUCCUGGC	6194
1658	1282	GCCAUCUGUGCUCUUCGUC	GACGAAGAGCACAGAUGGC	6195
891	1283	UAGAAACAGCUCGUUGUAC	GUACAACGAGCUGUUUCUA	6196
1572	1284	AGAUGAUGGUCUGCCAAGU	ACUUGGCAGACCAUCAUCU	6197
927	1285	ACCUUUCCCAUCAUCGUGA	UCACGAUGAUGGGAAAGGU	6198
290	1286	AUGGAGUUGGACAUGGCCA	UGGCCAUGUCCAACUCCAU	6199
1663	1287	CUGUGCUCUUCGUCAUCUG	CAGAUGACGAAGAGCACAG	6200
1562	1288	UAUAAGAACAAGAUGAUGG	CCAUCAUCUUGUUCUUAUA	6201
2947	1289	UCUGAAUAAAGUGUAACAA	UUGUUACACUUUAUUCAGA	6202
1711	1290	CCAGAAUGCAGUUCGCCUU	AAGGCGAACUGCAUUCUGG	6203

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1566	1291	AGAACAAGAUGAUGGUCUG	CAGACCAUCAUCUUGUUCU	6204
1815	1292	AUCUUGCCCUUUGUCCCGC	GCGGGACAAAGGGCAAGAU	6205
1087	1293	GCGUUUAGCUGGUGGGCUG	CAGCCCACCAGCUAAACGC	6206
1495	1294	GGGUUCAGAUGAUAUAAAU	AUUUAUAUCAUCUGAACCC	6207
1363	1295	UUUAGGACUUCACCUGACA	UGUCAGGUGAAGUCCUAAA	6208
391	1296	CACAGCUCCUUCUCUGAGU	ACUCAGAGAAGGAGCUGUG	6209
1392	1297	AACGUCUUGUUCAGAACUG	CAGUUCUGAACAAGACGUU	6210
1935	1298	CACAGCAGCAAUUUGUGGA	UCCACAAAUUGCUGCUGUG	6211
1872	1299	GACUAGUUCAGUUGCUUGU	ACAAGCAACUGAACUAGUC	6212
1159	1300	GACAGACUGCCUUCAAAUU	AAUUUGAAGGCAGUCUGUC	6213
2308	1301	CUCUCUCUUCAGAACAGAG	CUCUGUUCUGAAGAGAGAG	6214
632	1302	GUCCAGCGUUUGGCUGAAC	GUUCAGCCAAACGCUGGAC	6215
1564	1303	UAAGAACAAGAUGAUGGUC	GACCAUCAUCUUGUUCUUA	6216
1384	1304	UCCAAGUCAACGUCUUGUU	AACAAGACGUUGACUUGGA	6217
1690	1305	ACACCAAGAAGCAGAGAUG	CAUCUCUGCUUCUUGGUGU	6218
1421	1306	CUCAGGAAUCUUUCAGAUG	CAUCUGAAAGAUUCCUGAG	6219
1141	1307	UAAAUUCUUGGCUAUUACG	CGUAAUAGCCAAGAAUUUA	6220
1732	1308	CUAUGGACUACCAGUUGUG	CACAACUGGUAGUCCAUAG	6221
634	1309	CCAGCGUUUGGCUGAACCA	UGGUUCAGCCAAACGCUGG	6222
932	1310	UCCCAUCAUCGUGAGGGCU	AGCCCUCACGAUGAUGGGA	6223
1366	1311	AGGACUUCACCUGACAGAU	AUCUGUCAGGUGAAGUCCU	6224
1608	1312	UUGUGCGUACUGUCCUUCG	CGAAGGACAGUACGCACAA	6225
1923	1313	CCAUGGGUGGGACACAGCA	UGCUGUGUCCCACCCAUGG	6226
1458	1314	GGAUGGAAGGUCUCCUUGG	CCAAGGAGACCUUCCAUCC	6227
1908	1315	CCCAGCGCCGUACGUCCAU	AUGGACGUACGGCGCUGGG	6228
539	1316	GCUCAGAGGGUACGAGCUG	CAGCUCGUACCCUCUGAGC	6229
2016	1317	AUGUUCACAACCGAAUUGU	ACAAUUCGGUUGUGAACAU	6230
1884	1318	UGCUUGUUCGUGCACAUCA	UGAUGUGCACGAACAAGCA	6231
560	1319	AUGUUCCCUGAGACAUUAG	CUAAUGUCUCAGGGAACAU	6232
411	1320	GUAAAGGCAAUCCUGAGGA	UCCUCAGGAUUGCCUUUAC	6233
338	1321	CACUGGCAGCAACAGUCUU	AAGACUGUUGCUGCCAGUG	6234
830	1322	AUCAUGCGUUCUCCUCAGA	UCUGAGGAGAACGCAUGAU	6235
3086	1323	UAUGUAUGGGUAGGGUAAA	UUUACCCUACCCAUACAUA	6236
3115	1324	GUGUUAUUUGGAACCUUGU	ACAAGGUUCCAAAUAACAC	6237
2177	1325	ACAGCUCCUCUGACAGAGU	ACUCUGUCAGAGGAGCUGU	6238
1733	1326	UAUGGACUACCAGUUGUGG	CCACAACUGGUAGUCCAUA	6239
375	1327	AUUCUGGUGCCACUACCAC	GUGGUAGUGGCACCAGAAU	6240

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2565	1328	UGCCUCCAGGUGACAGCAA	UUGCUGUCACCUGGAGGCA	6241
442	1329	UACCUCCCAAGUGGUGUAU	AUACAGGACUUGGGAGGUA	6242
819	1330	CCAGACACGCUAUCAUGCG	CGCAUGAUAGCGUGUCUGG	6243
700	1331	UGAUGCAGAACUUGCCACA	UGUGGCAAGUUCUGCAUCA	6244
1089	1332	GUUUAGCUGGUGGGCUGCA	UGCAGCCCACCAGCUAAAC	6245
1580	1333	GUCUGCCAAGUGGGUGGUA	UACCACCCACUUGGCAGAC	6246
1982	1334	GGUUGUACCGGAGCCCUUC	GAAGGGCUCCGGUACAACC	6247
1986	1335	GUACCGGAGCCCUUCACAU	AUGUGAAGGGCUCCGGUAC	6248
418	1336	CAAGCCUGAGGAAGAGGAU	AUCCUCUUCCUCAGGAUUG	6249
1306	1337	GCUAUCUGUCUGCUCUAGA	ACUAGAGCAGACAGAUAGC	6250
1377	1338	UGACAGAUCCAAGUCAACG	CGUUGACUUGGAUCUGUCA	6251
2467	1339	CAUGAUGGAACAUGAGAUG	CAUCUCAUGUUCCAUCAUG	6252
1414	1340	UUGGACUCUCAGGAAUCUU	AAGAUUCCUGAGAGUCCAA	6253
1668	1341	CUCUUCGUCAUCUGACCAG	CUGGACAGAUGACGAAGAG	6254
1818	1342	UUGCCCUUUGUCCCGCAAA	UUUGCGGGACAAAGGGCAA	6255
16897	1343	GAAGCAGAGAUGGCCCAGA	UCUGGGCCAUCUCUGCUUC	6256
978	1344	CCUUGCAUAACCUUUCCCA	UGGGAAAGGUUAUGCAAGG	6257
605	1345	CAGUUUGAUGCUGCUCAUC	GAUGAGCAGCAUCAAACUG	6258
1374	1346	ACCUGACAGAUCCAAGUCA	UGACUUGGAUCUGUCAGGU	6259
1430	1347	CUUUCAGAUGCUGCAACUA	UAGUUGCAGCAUCUGAAAG	6260
3186	1348	GAUACGAUGCUUCAAGAGA	UCUCUUGAAGCAUCGUAUC	6261
1355	1349	AUGCAAGCUUUAGGACUUC	GAAGUCCUAAAGCUUGCAU	6262
433	1350	GGAUGUGGAUACCUCCCAA	UUGGGAGGUAUCCACAUCC	6263
1713	1351	AGAAUGCAGUUCGCCUUCA	UGAAGGCGAACUGCAUUCU	6264
1811	1352	CGAAAUCUUGCCCUUUGUC	GACAAAGGGCAAGAUUUCG	6265
491	1353	ACUCAAGAACAAGUAGCUG	CAGCUACUUGUUCUUGAGU	6266
2209	1354	GAAUGAAGGUGUGGCGACA	UGUCGCCACACCUUCAUUC	6267
1840	1355	UGCACCUUUGCGUGAGCAG	CUGCUCACGCAAAGGUGCA	6268
550	1356	ACGAGCUGCUAUGUUCCCU	AGGGAACAUAGCAGCUCGU	6269
429	1357	AAGAGGAUGUGGAUACCUC	GAGGUAUCCACAUCCUCUU	6270
2436	1358	GAUAUGGCCAGGAUGCCUU	AAGGCAUCCUGGCCAUAUC	6271
1597	1359	UAUAGAGGCUCUUGUGCGU	ACGCACAAGAGCCUCUAUA	6272
1496	1360	GGUUCAGAUGAUAUAAAUG	CAUUUAUAUCAUCUGAACC	6273
1456	1361	AGGGAUGGAAGGUCUCCUU	AAGGAGACCUUCCAUCCCU	6274
3159	1362	UAUCCCAAAGUUGUUGUAA	UUACAACAACUUUGGGAUA	6275
2309	1363	UCUCUCUUCAGAACAGAGC	GCUCUGUUCUGAAGAGAGA	6276

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
2300	1364	CUGACCAGCUCUCUCUUCA	UGAAGAGAGAGCUGGUCAG	6277
3177	1365	ACCUGCUGUGAUACGAUGC	GCAUCGUAUCACAGCAGGU	6278
1079	1366	AUGGCAGUGCGUUUAGCUG	CAGCUAAACGCACUGCCAU	6279
1383	1367	AUCCAAGUCAACGUCUUGU	ACAAGACGUUGACUUGGAU	6280
2563	1368	GCUGCCUCCAGGUGACAGC	GCUGUCACCUGGAGGCAGC	6281
1084	1369	AGUGCGUUUAGCUGGUGGG	CCCACCAGCUAAACGCACU	6282
1329	1370	AGCCGGCUAUUGUAGAAGC	GCUUCUACAAUAGCCGGCU	6283
573	1371	CAUUAGAUGAGGGCAUGCA	UGCAUGCCCUCAUCUAAUG	6284
2213	1372	GAAGGUGUGGCGACAUAUG	CAUAUGUCGCCACACCUUC	6285
1587	1373	AAGUGGGUGGUAUAGAGGC	GCCUCUAUACCACCCACUU	6286
2166	1374	CUGAGGGAGCCACAGCUCC	GGAGCUGUGGCUCCCUCAG	6287
637	1375	GCGUUUGGCUGAACCAUCA	UGAUGGUUCAGCCAAACGC	6288
397	1376	UCCUUCUCUGAGUGGUAAA	UUUACCACUCAGAGAAGGA	6289
1718	1377	GCAGUUCGCCUUCACUAUG	CAUAGUGAAGGCGAACUGC	6290
2357	1378	GGACUUGAUAUUGGUGCCC	GGGCACCAAUAUCAAGUCC	6291
639	1379	GUUUGGCUGAACCAUCACA	UGUGAUGGUUCAGCCAAAC	6292
585	1380	GCAUGCAGAUCCCAUCUAC	GUAGAUGGGAUCUGCAUGC	6293
2519	1381	GAUGGGCUGCCAGAUCUGG	CCAGAUCUGGCAGCCCAUC	6294
1367	1382	GGACUUCACCUGACAGAUC	GAUCUGUCAGGUGAAGUCC	6295
1391	1383	CAACGUCUUGUUCAGAACU	AGUUCUGAACAAGACGUUG	6296
509	1384	GAUAUUGAUGGACAGUAUG	CAUACUGUCCAUCAAUAUC	6297
303	1385	UGGCCAUGGAACCAGACAG	CUGUCUGGUUCCAUGGCCA	6298
494	1386	CAAGAACAAGUAGCUGAUA	UAUCAGCUACUUGUUCUUG	6299
328	1387	GGCUGUUAGUCACUGGCAG	CUGCCAGUGACUAACAGCC	6300
2058	1388	CAUUGUUUGUGCAGCUGCU	AGCAGCUGCACAAACAAUG	6301
1447	1389	UAAACAGGAAGGGAUGGAA	UUCCAUCCCUUCCUGUUUA	6302
1563	1390	AUAAGAACAAGAUGAUGGU	ACCAUCAUCUUGUUCUUAU	6303
1350	1391	GUGGAAUGCAAGCUUUAGG	CCUAAAGCUUGCAUUCCAC	6304
2208	1392	GGAAUGAAGGUGUGGCGAC	GUCGCCACACCUUCAUUCC	6305
1689	1393	GACACCAAGAAGCAGAGAU	AUCUCUGCUUCUUGGUGUC	6306
1407	1394	ACUGUCUUUGGACUCUCAG	CUGAGAGUCCAAAGACAGU	6307
2137	1395	GGACAAGGAAGCUGCAGAA	UUCUGCAGCUUCCUUGUCC	6308
854	1396	UCUGCUAUUGUACGUACCA	UGGUACGUACAAUAGCAGA	6309
2070	1397	AGCUGCUUUAUUCUCCCAU	AUGGGAGAAUAAAGCAGCU	6310
545	1398	AGGGUACGAGCUGCUAUGU	ACAUAGCAGCUCGUACCCU	6311
1640	1399	GAAGACAUCACUGAGCCUG	CAGGCUCAGUGAUGUCUUC	6312
2012	1400	CGGGAUGUUCACAACCGAA	UUCGGUUGUGAACAUCCCG	6313

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
1684	1401	CAGCCGACACCAAGAAGCA	UGCUUCUUGGUGUCGGCUG	6314
2017	1402	UGUUCACAACCGAAUUGUU	AACAAUUCGGUUGUGAACA	6315
2307	1403	GCUCUCUCUUCAGAACAGA	UCUGUUCUGAAGAGAGAGC	6316
844	1404	UCAGAUGGUGUCUGCUAUU	AAUAGCAGACACCAUCUGA	6317
405	1405	UGAGUGGUAAAGGCAAUCC	GGAUUGCCUUUACCACUCA	6318
379	1406	UGGUGCCACUACCACAGCU	AGCUGUGGUAGUGGCACCA	6319
1825	1407	UUGUCCCGCAAAUCAUGCA	UGCAUGAUUUGCGGGACAA	6320
2495	1408	CACCCUGGUGCUGACUAUC	GAUAGUCAGCACCAGGGUG	6321
629	1409	AAUGUCCAGCGUUUGGCUG	CAGCCAAACGCUGGACAUU	6322
2561	1410	GGGCUGCCUCCAGGUGACA	UGUCACCUGGAGGCAGCCC	6323
2192	1411	GAGUUACUUCACUCUAGGA	UCCUAGAGUGAAGUAACUC	6324
1809	1412	UUCGAAAUCUUGCCCUUUG	CAAAGGGCAAGAUUUCGAA	6325
1596	1413	GUAUAGAGGCUCUUGUGCG	CGCACAAGAGCCUCUAUAC	6326
2298	1414	AGCUGACCAGCUCUCUCUU	AAGAGAGAGCUGGUCAGCU	6327
858	1415	CUAUUGUACGUACCAUGCA	UGCAUGGUACGUACAAUAG	6328
524	1416	UAUGCAAUGACUCGAGCUC	GAGCUCGAGUCAUUGCAUA	6329
2542	1417	UGCCCAGGACCUCAUGGAU	AUCCAUGAGGUCCUGGGCA	6330
498	1418	AACAAGUAGCUGAUAUUGA	UCAAUAUCAGCUACUUGUU	6331
414	1419	AAGGCAAUCCUGAGGAAGA	UCUUCCUCAGGAUUGCCUU	6332
1570	1420	CAAGAUGAUGGUCUGCCAA	UUGGCAGACCAUCAUCUUG	6333
1030	1421	UGCCAUUACAACUCUCCAC	GUGGAGAGUUGUAAUGGCA	6334
3087	1422	AUGUAUGGGAUGGGUAAAU	AUUUACCCUACCCAUACAU	6335
1664	1423	UGUGCUCUUCGUCAUCUGA	UCAGAUGACGAAGAGCACA	6336
1790	1424	AAGGCUACUGUUGGAUUGA	UCAAUCCAACAGUAGCCUU	6337
1615	1425	UACUGUCCUUCGGGCUGGU	ACCAGCCCGAAGGACAGUA	6338
774	1426	AUAAGGCUGCAGUUAUGGU	ACCAUAACUGCAGCCUUAU	6339
1672	1427	UCGUCAUCUGACCAGCCGA	UCGGCUGGUCAGAUGACGA	6340
3171	1428	GUUGUAACCUGCUGUGAUA	UAUCACAGCAGGUUACAAC	6341
2271	1429	AAGAUUACAAGAAACGGCU	AGCCGUUUCUUGUAAUCUU	6342
1183	1430	UUAUGGCAACCAAGAAAGC	GCUUUCUUGGUUGCCAUAA	6343
2512	1431	UCCAGUUGAUGGGCUGCCA	UGGCAGCCCAUCAACUGGA	6344
1931	1432	GGGACACAGCAGCAAUUUG	CAAAUUGCUGCUGUGUCCC	6345
2468	1433	AUGAUGGAACAUGAGAUGG	CCAUCUCAUGUUCCAUCAU	6346
3077	1434	UAUUUGGGAUAUGUAUGGG	CCCAUACAUAUCCCAAAUA	6347
2069	1435	CAGCUGCUUUAUUCUCCCA	UGGGAGAAUAAAGCAGCUG	6348
272	1436	GCUACUCAAGCUGAUUUGA	UCAAAUCAGCUUGAGUAGC	6349

TABLE 1b-continued

Various c-CTNNB1 siNA sense and antisense sequences corresponding to the identified target sequences in Table 1a.

Target Site (human)	SEQ ID NO:	Sense Sequence	Antisense Sequence	SEQ ID NO:
564	1437	UCCCUGAGACAUUAGAUGA	UCAUCUAAUGUCUCAGGGA	6350
437	1438	GUGGAUACCUCCCAAGUCC	GGACUUGGGAGGUAUCCAC	6351
2206	1439	UAGGAAUGAAGGUGUGGCG	CGCCACACCUUCAUUCCUA	6352
2187	1440	UGACAGAGUUACUUCACUC	GAGUGAAGUAACUCUGUCA	6353
325	1441	AGCGGCUGUUAGUCACUGG	CCAGUGACUAACAGCCGCU	6354
3222	1442	AUGGUUCAGAAUUAAACUU	AAGUUUAAUUCUGAACCAU	6355
2024	1443	AACCGAAUUGUUAUCAGAG	CUCUGAUAACAAUUCGGUU	6356
1858	1444	GGGUGCCAUUCCACGACUA	UAGUCGUGGAAUGGCACCC	6357
1574	1445	AUGAUGGUCUGCCAAGUGG	CCACUUGGCAGACCAUCAU	6358
1896	1446	CACAUCAGGAUACCCAGCG	CGCUGGGUAUCCUGAUGUG	6359
2207	1447	AGGAAUGAAGGUGUGGCGA	UCGCCACACCUUCAUUCCU	6360
1300	1448	GAAGGUGCUAUCUGUCUGC	GCAGACAGAUAGCACCUUC	6361
1192	1449	CCAAGAAAGCAAGCUCAUC	GAUGAGCUUGCUUUCUUGG	6362
551	1450	CGAGCUGCUAUGUUCCCUG	CAGGGAACAUAGCAGCUCG	6363
2498	1451	CCUGGUGCUGACUAUCCAG	CUGGAUAGUCAGCACCAGG	6364
1305	1452	UGCUAUCUGUCUGCUCUAG	CUAGAGCAGACAGAUAGCA	6365
1337	1453	AUUGUAGAAGCUGGUGGAA	UUCCACCAGCUUCUACAAU	6366

For each oligonucleotide of a target sequence, the two individual, complementary strands of the siNA were synthesized separately using solid phase synthesis, then purified separately by reversed phase solid phase extraction (SPE). The complementary strands were annealed to form the double strand (duplex) and delivered in the desired concentration and buffer of choice.

Briefly, the single strand oligonucleotides were synthesized using phosphoramidite chemistry on an automated solid-phase synthesizer, using procedures as are generally known in the art (see for example U.S. application Ser. No. 12/064,014). A synthesis column was packed with solid support derivatized with the first nucleoside residue (natural or chemically modified). Synthesis was initiated by detritylation of the acid labile 5'-O-dimethoxytrityl group to release the 5'-hydroxyl. The column was then washed with a solvent, such as acetonitrile. An oxidizing solution, such as an iodine solution was pumped through the column to oxidize the phosphite triester linkage P(III) to its phosphotriester P(V) analog. Unreacted 5'-hydroxyl groups were capped using reagents such as acetic anhydride in the presence of 2,6-lutidine and N-methylimidazole. The elongation cycle was resumed with the detritylation step for the next phosphoramidite incorporation. This process was repeated until the desired sequence was synthesized. The synthesis concluded with the final 5'-terminus protecting group (trityl or 5'-O-dimethoxytrityl).

Upon completion of the synthesis, the solid-support and associated oligonucleotide were dried under argon pressure or vacuum. Aqueous base was added and the mixture was heated to effect cleavage of the succinyl linkage, removal of the cyanoethyl phosphate protecting group, and deprotection of the exocyclic amine protection.

The following process was performed on single strands that do not contain ribonucleotides. After treating the solid support with the aqueous base, the mixture was filtered to separate the solid support from the deprotected crude synthesis material. The solid support was then rinsed with water, which is combined with the filtrate. The resultant basic solution allows for retention of the 5'-O-dimethoxytrityl group to remain on the 5' terminal position (trityl-on).

For single strands that contain ribonucleotides, the following process was performed. After treating the solid support with the aqueous base, the mixture was filtered to separate the solid support from the deprotected crude synthesis material. The solid support was then rinsed with dimethylsulfoxide (DMSO), which was combined with the filtrate. Fluoride reagent, such as triethylamine trihydrofluoride, was added to the mixture, and the solution was heated. The reaction was quenched with suitable buffer to provide a solution of crude single strand with the 5'-O-dimethoxytrityl group on the final 5' terminal position.

The trityl-on solution of each crude single strand was purified using chromatographic purification, such as SPE RPC purification. The hydrophobic nature of the trityl group permits stronger retention of the desired full-length oligo than the non-tritylated truncated failure sequences. The failure sequences were selectively washed from the resin with a suitable solvent, such as low percent acetonitrile. Retained oligonucleotides were then detritylated on-column

with trifluoroacetic acid to remove the acid-labile trityl group. Residual acid was washed from the column, a salt exchange was performed, and a final desalting of the material commenced. The full-length oligo was recovered in a purified form with an aqueous-organic solvent. The final product was then analyzed for purity (HPLC), identity (Maldi-TOF MS), and yield (UV A_{260}). The oligos were dried via lyophilization or vacuum condensation.

Annealing: Based on the analysis of the product, the dried oligos were dissolved in appropriate buffers followed by mixing equal molar amounts (calculated using the theoretical extinction coefficient) of the sense and antisense oligonucleotide strands. The solution was then analyzed for purity of duplex by chromatographic methods and desired final concentration. If the analysis indicated an excess of either strand, then the additional non-excess strand was titrated until duplexing was complete. When analysis indicated that the target product purity has been achieved the material was delivered and ready for use.

Below is a table showing various modified siNAs synthesized using this protocol or that can be synthesized using this protocol or using methods known in the art.

TABLE 1c

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008247452-000C	535	1	UCGAGCUCAGAGGGUACGA	B ucGAGcucAGAGGGuAcGATT B	1454
R-008247452-000C	535	1	UCGAGCUCAGAGGGUACGA	UCGuAcccucuGAGcucGAUU	1455
R-008247449-000W	1601	2	GAGGCUCUUGUGCGUACUG	B GAGGcucuuGuGcGuAcuGTT B	1456
R-008247449-000W	1601	2	GAGGCUCUUGUGCGUACUG	CAGuAcGcAcAAGAGccucUU	1457
R-008247575-000Y	1709	3	GCCCAGAAUGCAGUUCGCC	B GcccAGAAuGcAGuucGccTT B	1458
R-008247575-000Y	1709	3	GCCCAGAAUGCAGUUCGCC	GGCGAAcuGcAuucuGGGcUU	1459
R-008247572-000X	536	4	CGAGCUCAGAGGGUACGAG	B cGAGcucAGAGGGuAcGAGTT B	1460
R-008247572-000X	536	4	CGAGCUCAGAGGGUACGAG	CUCGuAcccucuGAGcucGUU	1461
R-008247569-000R	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUU	1463
R-008247569-000R	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	1462
R-008247446-000V	853	6	GUCUGCUAUUGUACGUACC	B GucuGcuAuuGuAcGuAccTT B	1464
R-008247446-000V	853	6	GUCUGCUAUUGUACGUACC	GGUAcGuAcAAuAGcAGAcUU	1465
R-008247566-000P	1143	7	AAUUCUUGGCUAUUACGAC	GUCGuAAuAGccAAGAAuuUU	1467
R-008247566-000P	1143	7	AAUUCUUGGCUAUUACGAC	B AAuucuuGGcuAuuAcGAcTT B	1466
R-008247563-000N	2014	8	GGAUGUUCACAACCGAAUU	B GGAuGuucAcAAccGAAuuTT B	1468
R-008247563-000N	2014	8	GGAUGUUCACAACCGAAUU	AAUucGGuuGuGAAcAuccUU	1469
R-008247560-000M	520	9	ACAGUAUGCAAUGACUCGA	B AcAGuAuGcAAuGAcucGATT B	1470
R-008247560-000M	520	9	ACAGUAUGCAAUGACUCGA	UCGAGucAuuGcAuAcuGuUU	1471
R-008247443-000U	814	10	AGCUUCCAGACACGCUAUC	B AGcuuccAGAcAcGcuAucTT B	1472
R-008247443-000U	814	10	AGCUUCCAGACACGCUAUC	GAUAGcGuGucuGGAAGcuUU	1473
R-008247440-000T	852	11	UGUCUGCUAUUGUACGUAC	GUAcGuAcAAuAGcAGAcAUU	1475
R-008247440-000T	852	11	UGUCUGCUAUUGUACGUAC	B uGucuGcuAuuGuAcGuAcTT B	1474
R-008247557-000F	1796	12	ACUGUUGGAUUGAUUCGAA	UUCGAAucAAuccAAcAGuUU	1477
R-008247557-000F	1796	12	ACUGUUGGAUUGAUUCGAA	B AcuGuuGGAuuGAuucGAATT B	1476
R-008247437-000L	1901	13	CAGGAUACCCAGCGCCGUA	UACGGcGcuGGGuAuccuGUU	1479
R-008247437-000L	1901	13	CAGGAUACCCAGCGCCGUA	B CAGGAuAcccAGcGccGuATT B	1478
R-008247554-000E	822	14	GACACGCUAUCAUGCGUUC	B GAcAcGcuAucAuGcGuucTT B	1480
R-008247554-000E	822	14	GACACGCUAUCAUGCGUUC	GAAcGcAuGAuAGcGuGucUU	1481
R-008247551-000D	1795	15	UACUGUUGGAUUGAUUCGA	UGCAAucAAuccAAcAGuAUU	1483

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008247551-000D	1795	15	UACUGUUGGAUUGAUUCGA	B uAcuGuuGGAuuGauucGATT B	1482
R-008247548-000X	1145	16	UUCUUGGCUAUUACGACAG	B uucuuGGcuAuuAcGAcAGTT B	1484
R-008247548-000X	1145	16	UUCUUGGCUAUUACGACAG	CUGucGuAAuAGccAAGAAUU	1485
R-008247545-000W	823	17	ACACGCUAUCAUGCGUUCU	B AcAcGcuAucAuGcGuucuTT B	1486
R-008247545-000W	823	17	ACACGCUAUCAUGCGUUCU	AGAAcGcAuGAuAGcGuGuUU	1487
R-008247434-000K	820	18	CAGACACGCUAUCAUGCGU	B cAGAcAcGcuAucAuGcGuTT B	1488
R-008247434-000K	820	18	CAGACACGCUAUCAUGCGU	ACGcAuGAuAGcGuGucuGUU	1489
R-008247431-000J	1798	19	UGUUGGAUUGAUUCGAAAU	B uGuuGGAuuGAuucGAAAuTT B	1490
R-008247431-000J	1798	19	UGUUGGAUUGAUUCGAAAU	AUUucGAAucAAuccAAcAUU	1491
R-008247428-000C	1380	20	CAGAUCCAAGUCAACGUCU	B cAGAuccAAGucAAcGucuTT B	1492
R-008247428-000C	1380	20	CAGAUCCAAGUCAACGUCU	AGAcGuuGAcuuGGAucuGUU	1493
R-008247542-000V	1602	21	AGGCUCUUGUGCGUACUGU	B AGGcucuuGuGcGuAcuGuTT B	1494
R-008247542-000V	1602	21	AGGCUCUUGUGCGUACUGU	ACAGuAcGcAcAAGAGccuUU	1495
R-008247539-000N	1612	22	GCGUACUGUCCUUCGGGCU	B GcGuAcuGuccuucGGGcuTT B	1496
R-008247539-000N	1612	22	GCGUACUGUCCUUCGGGCU	AGCccGAAGGAcAGuAcGcUU	1497
R-008247425-000B	626	23	ACUAAUGUCCAGCGUUUGG	B AcuAAuGuccAGcGuuuGGTT B	1498
R-008247425-000B	626	23	ACUAAUGUCCAGCGUUUGG	CCAAAcGcuGGAcAuuAGuUU	1499
R-008247536-000M	2000	24	CACAUCCUAGCUCGGGAUG	B cAcAuccaAGcucGGGAuGTT B	1500
R-008247536-000M	2000	24	CACAUCCUAGCUCGGGAUG	CAUcccGAGcuAGGAuGuGUU	1501
R-008247422-000A	2665	25	GUUGCUGAGAGGGCUCGAG	B GuuGcuGAGAGGGcucGAGTT B	1502
R-008247422-000A	2665	25	GUUGCUGAGAGGGCUCGAG	CUCGAGcccucucAGcAAcUU	1503
R-008247533-000L	1676	26	CAUCUGACCAGCCGACACC	GGUGucGGcuGGucAGAuGUU	1505
R-008247533-000L	1676	26	CAUCUGACCAGCCGACACC	B cAucuGAccAGccGAcAccTT B	1504
R-008247530-000K	1611	27	UGCGUACUGUCCUUCGGGC	B uGcGuAcuGuccuucGGGcTT B	1506
R-008247530-000K	1611	27	UGCGUACUGUCCUUCGGGC	GCCcGAAGGAcAGuAcGcAUU	1507
R-008247419-000U	2269	28	ACAAGAUUACAAGAAACGG	B AcAAGAuuAcAAGAAAcGGTT B	1508
R-008247419-000U	2269	28	ACAAGAUUACAAGAAACGG	CCGuuucuuGuAAucuuGuUU	1509
R-008247527-000D	674	29	GUUGUAAACUUGAUUAACU	B GuuGuAAAcuuGauuAAcuTT B	1510
R-008247527-000D	674	29	GUUGUAAACUUGAUUAACU	AGUuAAucAAGuuuAcAAcUU	1511
R-008247602-000K	678	30	UAAACUUGAUUAACUAUCA	B uAAAcuuGauuAAcuAucATT B	1512
R-008247602-000K	678	30	UAAACUUGAUUAACUAUCA	UGAuAGuuAAucAAGuuuAUU	1513
R-008247599-000T	1245	31	AUAUAAUGAGGACCUAUAC	B AuAuAAuGAGGAccuAuacTT B	1514
R-008247599-000T	1245	31	AUAUAAUGAGGACCUAUAC	GUAuAGGuccucAuuAuAuUU	1515
R-008247596-000S	679	32	AAACUUGAUUAACUAUCAA	B AAAcuuGauuAAcuAucAATT B	1516
R-008247596-000S	679	32	AAACUUGAUUAACUAUCAA	UUGAuAGuuAAucAAGuuuUU	1517
R-008247593-000R	1970	33	GAAAUAGUUGAAGGUUGUA	B GAAAuAGuuGAAGGuuGuATT B	1518
R-008247593-000R	1970	33	GAAAUAGUUGAAGGUUGUA	UACAAccuucAAcuAuuucUU	1519

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008247590-000P	1247	34	AUAAUGAGGACCUAUACUU	AAGuAuAGGuccucAuuAuUU	1521
R-008247590-000P	1247	34	AUAAUGAGGACCUAUACUU	B AuAAuGAGGAccuAuAcuuTT B	1520
R-008247464-000M	1140	35	UUAAAUUCUUGGCUAUUAC	B uuAAAuucuuGgcuAuuAcTT B	1522
R-008247464-000M	1140	35	UUAAAUUCUUGGCUAUUAC	GUAAuAGccAAGAAuuuAAUU	1523
R-008247587-000H	676	36	UGUAAACUUGAUUAACUAU	B uGuAAAcuuGAuuAAcuAuTT B	1524
R-008247587-000H	676	36	UGUAAACUUGAUUAACUAU	AUAGuuAAucAAGuuuAcAUU	1525
R-008247461-000L	677	37	GUAAACUUGAUUAACUAUC	GAUAGuuAAucAAGuuuAcUU	1527
R-008247461-000L	677	37	GUAAACUUGAUUAACUAUC	B GuAAAcuuGAuuAAcuAucTT B	1526
R-008247458-000E	675	38	UUGUAAACUUGAUUAACUA	B uuGuAAAcuuGAuuAAcuATT B	1528
R-008247458-000E	675	38	UUGUAAACUUGAUUAACUA	UAGuuAAucAAGuuuAcAAUU	1529
R-008247584-000G	1235	39	GCUUUAGUAAAUAUAAUGA	B GcuuuAGuAAAuAuAAuGATT B	1530
R-008247584-000G	1235	39	GCUUUAGUAAAUAUAAUGA	UCAuuAuAuuuAcuAAAGcuUU	1531
R-008247581-000F	2488	40	UGGCCACCACCCUGGUGCU	B uGGccAccAcccuGGuGcuTT B	1532
R-008247581-000F	2488	40	UGGCCACCACCCUGGUGCU	AGCAccAGGGuGGuGGccAUU	1533
R-008247578-000Z	1236	41	CUUUAGUAAAUAUAAUGAG	B cuuuAGuAAAuAuAAuGAGTT B	1534
R-008247578-000Z	1236	41	CUUUAGUAAAUAUAAUGAG	CUCAuuAuAuuuAcuAAAGUU	1535
R-008247455-000D	1237	42	UUUAGUAAAUAUAAUGAGG	CCUcAuuAuAuuuAcuAAAUU	1537
R-008247455-000D	1237	42	UUUAGUAAAUAUAAUGAGG	B uuuAGuAAAuAuAAuGAGTT B	1536
R-008042883-001A	2555	43	GUAAAUCGUCCUUUAGGUA	B GuAAAucGuccuuuAGGuATT B	1538
R-008042883-001A	2555	43	GUAAAUCGUCCUUUAGGUA	UACcuAAAGGAcGAuuuAcUU	1539
R-008308583-000P	1545	44	ACCUCACUUGCAAUAAUUA	B AccucAcuuGcAAuAAuuATT B	1540
R-008308583-000P	1545	44	ACCUCACUUGCAAUAAUUA	UAAuuAuuGcAAGuGAGGuUU	1541
R-008308520-000J	2050	45	UACCAUUCCAUUGUUUGUG	B uAccAuuccAuuGuuuGuGTT B	1542
R-008308520-000J	2050	45	UACCAUUCCAUUGUUUGUG	CACAAAcAAuGGAAuGGuAUU	1543
R-008308622-000L	2097	46	UCCAAAGAGUAGCUGCAGG	CCUGcAGcuAcucuuuGGAUU	1545
R-008308622-000L	2097	46	UCCAAAGAGUAGCUGCAGG	B uccAAAGAGuAGcuGcAGGTT B	1544
R-008308652-000N	2510	47	UAUCCAGUUGAUGGGCUGC	B uAuccAGuuGAuGGGcuGcTT B	1546
R-008308652-000N	2510	47	UAUCCAGUUGAUGGGCUGC	GCAGcccAucAAcuGGAuAUU	1547
R-008308718-000F	871	48	CAUGCAGAAUACAAAUGAU	AUCAuuuGuAuucuGcAuGUU	1549
R-008308718-000F	871	48	CAUGCAGAAUACAAAUGAU	B cAuGcAGAAuAcAAAuGAuTT B	1548
R-008308694-000A	2098	49	CCAAAGAGUAGCUGCAGGG	CCCuGcAGcuAcucuuuGGUU	1551
R-008308694-000A	2098	49	CCAAAGAGUAGCUGCAGGG	B ccAAAGAGuAGcuGcAGGGTT B	1550
R-008308517-000C	1767	50	CACCAUCCCACUGGCCUCU	B cAccAucccAcuGGccucuTT B	1552
R-008308517-000C	1767	50	CACCAUCCCACUGGCCUCU	AGAGGccAGuGGGAuGGuGUU	1553
R-008308619-000E	869	51	ACCAUGCAGAAUACAAAUG	B AccAuGcAGAAuAcAAAuGTT B	1554
R-008308619-000E	869	51	ACCAUGCAGAAUACAAAUG	CAUuuGuAuucuGcAuGGuUU	1555

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008308514-000B	1641	52	AAGACAUCACUGAGCCUGC	B AAGAcAucAcuGAGccuGcTT B	1556
R-008308514-000B	1641	52	AAGACAUCACUGAGCCUGC	GCAGGcucAGuGAuGucuuUU	1557
R-008308616-000D	2582	53	AAUCAGCUGGCCUGGUUUG	B AAucAGcuGgccuGGuuuGTT B	1558
R-008308616-000D	2582	53	AAUCAGCUGGCCUGGUUUG	CAAAccAGGccAGcuGAuuUU	1559
R-008308580-000N	1544	54	AACCUCACUUGCAAUAAUU	AAUuAuuGcAAGuGAGGuuUU	1561
R-008308580-000N	1544	54	AACCUCACUUGCAAUAAUU	B AAccucAcuuGcAauAAuuTT B	1560
R-008308736-000Y	2550	55	ACCUCAUGGAUGGGCUGCC	B AccucAuGGAuGGGcuGccTT B	1562
R-008308736-000Y	2550	55	ACCUCAUGGAUGGGCUGCC	GGCAGcccAuccAuGAGGuUU	1563
R-008308613-000C	2051	56	ACCAUUCCAUUGUUUGUGC	GCAcAAAcAAuGGAAuGGuUU	1565
R-008308613-000C	2051	56	ACCAUUCCAUUGUUUGUGC	B AccAuuccAuuGuuuGuGcTT B	1564
R-008308577-000G	870	57	CCAUGCAGAAUACAAAUGA	UCAuuuGuAuucuGcAuGGUU	1567
R-008308577-000G	870	57	CCAUGCAGAAUACAAAUGA	B ccAuGcAGAAuAcAAAuGATT B	1566
R-008308691-000Z	1670	58	CUUCGUCAUCUGACCAGCC	B cuucGucAucuGAccAGccTT B	1568
R-008308691-000Z	1670	58	CUUCGUCAUCUGACCAGCC	GGCuGGucAGAuGAcGAAGUU	1569
R-008308649-000G	2122	59	CUGUGAACUUGCUCAGGAC	B cuGuGAAcuuGcucAGGAcTT B	1570
R-008308649-000G	2122	59	CUGUGAACUUGCUCAGGAC	GUCcuGAGcAAGuucAcAGUU	1571
R-008308553-000M	1642	60	AGACAUCACUGAGCCUGCC	B AGAcAucAcuGAGccuGccTT B	1572
R-008308553-000M	1642	60	AGACAUCACUGAGCCUGCC	GGCAGGcucAGuGAuGucuUU	1573
R-008308574-000F	2324	61	GAGCCAAUGGCUUGGAAUG	B GAGccAAuGGcuuGGAAuGTT B	1574
R-008308574-000F	2324	61	GAGCCAAUGGCUUGGAAUG	CAUuccAAGccAuuGGcucUU	1575
R-008308688-000T	1649	62	ACUGAGCCUGCCAUCUGUG	B AcuGAGccuGccAucuGuGTT B	1576
R-008308688-000T	1649	62	ACUGAGCCUGCCAUCUGUG	CACAGAuGGcAGGcucAGuUU	1577
R-008308550-000L	2159	63	AUUGAAGCUGAGGGAGCCA	B AuuGAAGcuGAGGGAGccATT B	1578
R-008308550-000L	2159	63	AUUGAAGCUGAGGGAGCCA	UGGcucccucAGcuucAAuUU	1579
R-008308511-000A	785	64	GUUAUGGUCCAUCAGCUUU	B GuuAuGGuccAucAGcuuuTT B	1580
R-008308511-000A	785	64	GUUAUGGUCCAUCAGCUUU	AAAGcuGAuGGAccAuAAcUU	1581
R-008308685-000S	1511	65	AAUGUGGUCACCUGUGCAG	B AAuGuGGucAccuGuGcAGTT B	1582
R-008308685-000S	1511	65	AAUGUGGUCACCUGUGCAG	CUGcAcAGGuGAccAcAuuUU	1583
R-008308610-000B	2586	66	AGCUGGCCUGGUUUGAUAC	B AGcuGGccuGGuuuGAuAcTT B	1584
R-008308610-000B	2586	66	AGCUGGCCUGGUUUGAUAC	GUAucAAAccAGGccAGcuUU	1585
R-008308571-000E	642	67	UGGCUGAACCAUCACAGAU	B uGGcuGAAccAucAcAGAuTT B	1586
R-008308571-000E	642	67	UGGCUGAACCAUCACAGAU	AUCuGuGAuGGuucAGccAUU	1587
R-008308715-000E	1763	68	CACCCACCAUCCCACUGGC	B cAcccAccAucccAcuGGcTT B	1588
R-008308715-000E	1763	68	CACCCACCAUCCCACUGGC	GCCAGuGGGAuGGuGGGuGUU	1589
R-008308682-000R	2328	69	CAAUGGCUUGGAAUGAGAC	GUCucAuuccAAGccAuuGUU	1591
R-008308682-000R	2328	69	CAAUGGCUUGGAAUGAGAC	B cAAuGGcuuGGAAuGAGAcTT B	1590
R-008308646-000F	1280	70	UGGACCACAAGCAGAGUGC	GCAcucuGcuuGuGGuccAUU	1593

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008308646-000F	1280	70	UGGACCACAAGCAGAGUGC	B u*GG*AccAc*AAG*cA*GA*G*u*G*cTT* B	1592
R-008308508-000U	2052	71	CCAUUCCAUUGUUUGUGCA	B ccAuuccAuu*G*uuu*G*u*G*c*ATT* B	1594
R-008308508-000U	2052	71	CCAUUCCAUUGUUUGUGCA	UGCAcAAAcAAuGGAAuGGUU	1595
R-008308547-000E	2546	72	CAGGACCUCAUGGAUGGGC	GCCcAuccAuGAGGuccuGUU	1597
R-008308547-000E	2546	72	CAGGACCUCAUGGAUGGGC	B c*AGG*AccucAu*GG*Au*GGG*c*TT* B	1596
R-008308505-000T	2124	73	GUGAACUUGCUCAGGACAA	UUGuccuGAGcAAGuucAcUU	1599
R-008308505-000T	2124	73	GUGAACUUGCUCAGGACAA	B *G*u*GA*AcuuGcuc*AGG*Ac*AATT* B	1598
R-008308733-000X	2545	74	CCAGGACCUCAUGGAUGGG	CCCAuccAuGAGGuccuGGUU	1601
R-008308733-000X	2545	74	CCAGGACCUCAUGGAUGGG	B cc*AGG*AccucAu*GG*Au*GGGTT* B	1600
R-008308544-000D	643	75	GGCUGAACCAUCACAGAUG	B *GG*cu*GA*AccAucAcA*GA*u*GTT* B	1602
R-008308544-000D	643	75	GGCUGAACCAUCACAGAUG	CAUcuGuGAuGGuucAGccUU	1603
R-008308643-000E	2501	76	GGUGCUGACUAUCCAGUUG	B *GG*u*G*cu*GA*cuAuccA*G*uu*GTT* B	1604
R-008308643-000E	2501	76	GGUGCUGACUAUCCAGUUG	CAAcuGGAuAGucAGcAccUU	1605
R-008308712-000D	2330	77	AUGGCUUGGAAUGAGACUG	B Au*GG*cuu*GGA*Au*GAG*Acu*GTT* B	1606
R-008308712-000D	2330	77	AUGGCUUGGAAUGAGACUG	CAGucucAuuccAAGccAuUU	1607
R-008308568-000Y	1638	78	GGGAAGACAUCACUGAGCC	GGCucAGuGAuGucuucccUU	1609
R-008308568-000Y	1638	78	GGGAAGACAUCACUGAGCC	B *GGGAAG*AcAucAcu*GAG*cc*TT* B	1608
R-008308640-000D	1630	79	UGGUGACAGGGAAGACAUC	B u*GG*u*GA*c*AGGGAAG*AcAuc*TT* B	1510
R-008308640-000D	1630	79	UGGUGACAGGGAAGACAUC	GAUGucuucccuGucAccAUU	1611
R-008308541-000C	616	80	UGCUCAUCCCACUAAUGUC	GAcAuuAGuGGGAuGAGcAUU	1613
R-008308541-000C	616	80	UGCUCAUCCCACUAAUGUC	B u*G*cucAucccAcuAAu*G*uc*TT* B	1612
R-008308679-000J	2509	81	CUAUCCAGUUGAUGGGCUG	B cuAucc*AG*uu*GA*u*GGG*cu*GTT* B	1614
R-008308679-000J	2509	81	CUAUCCAGUUGAUGGGCUG	CAGcccAucAAcuGGAuAGUU	1615
R-008308565-000X	2548	82	GGACCUCAUGGAUGGGCUG	B *GG*AccucAu*GG*Au*GGG*uu*GTT* B	1616
R-008308565-000X	2548	82	GGACCUCAUGGAUGGGCUG	CAGcccAuccAuGaGGuccUU	1617
R-008308538-000W	1773	83	CCCACUGGCCUCUGAUAAA	UUUAucAGAGGccAGuGGGUU	1619
R-008308538-000W	1773	83	CCCACUGGCCUCUGAUAAA	B cccAcu*GG*ccucu*GA*u*AAATT* B	1618
R-008308535-000V	2247	84	UCCGAAUGUCUGAGGACAA	UUGuccucAGAcAuucGGAUU	1621
R-008308535-000V	2247	84	UCCGAAUGUCUGAGGACAA	B ucc*GA*Au*G*ucu*GAGG*Ac*AATT* B	1620
R-008308637-000X	2331	85	UGGCUUGGAAUGAGACUGC	B u*GG*cuu*GGA*Au*GAG*Acu*G*c*TT* B	1622
R-008308637-000X	2331	85	UGGCUUGGAAUGAGACUGC	GCAGucucAuuccAAGccAUU	1623
R-008309111-000F	1498	86	UUCAGAUGAUAUAAAUGUG	CACAuuuAuAucAucuGAAUU	1625
R-008309111-000F	1498	86	UUCAGAUGAUAUAAAUGUG	B uuc*AG*Au*G*Au*A*uAAAu*G*u*GTT* B	1624
R-008309108-000Z	2267	87	CCACAAGAUUACAAGAAAC	B ccAc*AAG*AuuAc*AAG*AAAc*TT* B	1626
R-008309108-000Z	2267	87	CCACAAGAUUACAAGAAAC	GUUucuuGuAAucuuGuGGUU	1627
R-008308994-000E	1547	88	CUCACUUGCAAUAAUUAUA	UAUAAuuAuuGcAAGuGAGUU	1629

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008308994-000E	1547	88	CUCACUUGCAAUAAUUAUA	B cucAcuuGcAAuAAuuAuATT B	1628
R-008309075-000K	1549	89	CACUUGCAAUAAUUAUAAG	CUUAuAAuuAuuGcAAGuGUU	1631
R-008309075-000K	1549	89	CACUUGCAAUAAUUAUAAG	B cAcuuGcAAuAAuuAuAAGTT B	1630
R-008309045-000H	867	90	GUACCAUGCAGAAUACAAA	UUUGuAuucuGcAuGGuAcUU	1633
R-008309045-000H	867	90	GUACCAUGCAGAAUACAAA	B GuAccAuGcAGAAuAcAAATT B	1632
R-008309072-000J	1390	91	UCAACGUCUUGUUCAGAAC	B ucAAcGucuuGuucAGAAcTT B	1634
R-008309072-000J	1390	91	UCAACGUCUUGUUCAGAAC	GUUcuGAAcAAGAcGuuGAUU	1635
R-008309027-000R	593	92	AUCCCAUCUACACAGUUUG	CAAAcuGuGuAGAuGGGAuUU	1637
R-008309027-000R	593	92	AUCCCAUCUACACAGUUUG	B AucccAucuAcAcAGuuuGTT B	1636
R-008309009-000Y	274	93	UACUCAAGCUGAUUUGAUG	CAUcAAAucAGcuuGAGuAUU	1639
R-008309009-000Y	274	93	UACUCAAGCUGAUUUGAUG	B uAcucAAgcuGauuuGauGTT B	1638
R-008309024-000P	759	94	ACCAGGUGGUGGUUAAUAA	B AccAGGuGGuGGuuAAuAATT B	1640
R-008309024-000P	759	94	ACCAGGUGGUGGUUAAUAA	UUAuuAAccAccAccuGGuUU	1641
R-008309093-000C	1439	95	GCUGCAACUAAACAGGAAG	B GcuGcAAcuAAAcAGGAAGTT B	1642
R-008309093-000C	1439	95	GCUGCAACUAAACAGGAAG	CUUccuGuuuAGuuGcAGcUU	1643
R-008309069-000C	1801	96	UGGAUUGAUUCGAAAUCUU	B uGGAuuGAuucGAAAucuuTT B	1644
R-008309069-000C	1801	96	UGGAUUGAUUCGAAAUCUU	AAGAuuuucGAAucAAuccAUU	1645
R-008309021-000N	1500	97	CAGAUGAUAUAAAUGUGGU	B cAGAuGAuAuAAAuGuGGuTT B	1646
R-008309021-000N	1500	97	CAGAUGAUAUAAAUGUGGU	ACCAcAuuuAuAucAucuGUU	1647
R-008309066-000B	848	98	AUGGUGUCUGCUAUUGUAC	B AuGGuGucuGcuAuuGuAcTT B	1648
R-008309066-000B	848	98	AUGGUGUCUGCUAUUGUAC	GUAcAAuAGcAGAcAccAuUU	1649
R-008309105-000Y	2268	99	CACAAGAUUACAAGAAACG	CGUuucuuGuAAucuuGuGUU	1651
R-008309105-000Y	2268	99	CACAAGAUUACAAGAAACG	B cAcAAGAuuAcAAGAAAcGTT B	1650
R-008309042-000G	882	100	CAAAUGAUGUAGAAACAGC	GCUGuuucuAcAucAuuuGUU	1653
R-008309042-000G	882	100	CAAAUGAUGUAGAAACAGC	B cAAAuGAuGuAGAAAcAGcTT B	1652
R-008309063-000A	2266	101	GCCACAAGAUUACAAGAAA	UUUcuuGuAAucuuGuGGcUU	1655
R-008309063-000A	2266	101	GCCACAAGAUUACAAGAAA	B GccAcAAGAuuAcAAgAAATT B	1654
R-008309018-000G	880	102	UACAAAUGAUGUAGAAACA	B uAcAAAuGAuGuAGAAAcATT B	1656
R-008309018-000G	880	102	UACAAAUGAUGUAGAAACA	UGUuucuAcAucAuuuGuAUU	1657
R-008309039-000A	1810	103	UCGAAAUCUUGCCCUUUGU	ACAAAGGGcAAGAuuucGAUU	1659
R-008309039-000A	1810	103	UCGAAAUCUUGCCCUUUGU	B ucGAAAucuuGcccuuuGuTT B	1658
R-008309015-000F	685	104	GAUUAACUAUCAAGAUGAU	B GAuuAAcuAucAAGAuGAuTT B	1660
R-008309015-000F	685	104	GAUUAACUAUCAAGAUGAU	AUCAucuuGAuAGuuAAucUU	1661
R-008309060-000Z	1007	105	CCAGUGGAUUCUGUGUUGU	ACAAcAcAGAAuccAcuGGUU	1663
R-008309060-000Z	1007	105	CCAGUGGAUUCUGUGUUGU	B ccAGuGGAuucuGuGuuGuTT B	1662
R-008309057-000T	1789	106	AAAGGCUACUGUUGGAUUG	B AAAGGcuAcuGuuGGAuuGTT B	1664
R-008309057-000T	1789	106	AAAGGCUACUGUUGGAUUG	CAAuccAAcAGuAGccuuuUU	1665

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008309054-000S	499	107	ACAAGUAGCUGAUAUUGAU	AUCAAuAucAGcuAcuuGuUU	1667
R-008309054-000S	499	107	ACAAGUAGCUGAUAUUGAU	B AcAAGuAGcuGAuAuuGAuTT B	1666
R-008309090-000B	2470	108	GAUGGAACAUGAGAUGGGU	B GAuGGAAcAuGAGAuGGGuTT B	1668
R-008309090-000B	2470	108	GAUGGAACAUGAGAUGGGU	ACCcAucucAuGuuccAucUU	1669
R-008309051-000R	694	109	UCAAGAUGAUGCAGAACUU	B ucAAGAuGAuGcAGAAcuuTT B	1670
R-008309051-000R	694	109	UCAAGAUGAUGCAGAACUU	AAGuucuGcAucAucuuGAUU	1671
R-008309036-000Z	278	110	CAAGCUGAUUUGAUGGAGU	ACUccAucAAAucAGcuuGUU	1673
R-008309036-000Z	278	110	CAAGCUGAUUUGAUGGAGU	B cAAGcuGAuuuGAuGGAGuTT B	1672
R-008309102-000X	1415	111	UGGACUCUCAGGAAUCUUU	B uGGAcucucAGGAAucuuuTT B	1674
R-008309102-000X	1415	111	UGGACUCUCAGGAAUCUUU	AAAGAuuccuGAGAGuccAUU	1675
R-008308991-000D	2046	112	UAAAUACCAUUCCAUUGUU	AACAAuGGAAuGGuAuuuAUU	1677
R-008308991-000D	2046	112	UAAAUACCAUUCCAUUGUU	B uAAAuAccAuuccAuuGuuTT B	1676
R-008309006-000X	1057	113	AUUACAUCAAGAAGGAGCU	AGCuccuucuuGAuGuAAuUU	1679
R-008309006-000X	1057	113	AUUACAUCAAGAAGGAGCU	B AuuAcAucAAGAAGGAGcuTT B	1678
R-008309087-000V	1422	114	UCAGGAAUCUUUCAGAUGC	B ucAGGAAucuuucAGAuGcTT B	1680
R-008309087-000V	1422	114	UCAGGAAUCUUUCAGAUGC	GCAucuGAAAGAuuccuGAUU	1681
R-008309084-000U	684	115	UGAUUAACUAUCAAGAUGA	UCAucuuGAuAGuuAAucAUU	1683
R-008309084-000U	684	115	UGAUUAACUAUCAAGAUGA	B uGAuuAAcuAucAAGAuGATT B	1682
R-008309099-000E	2197	116	ACUUCACUCUAGGAAUGAA	B AcuucAcucuAGGAAuGAATT B	1684
R-008309099-000E	2197	116	ACUUCACUCUAGGAAUGAA	UUCAuuccuAGAGuGAAGuUU	1685
R-008309003-000W	666	117	AACAUGCAGUUGUAAACUU	B AAcAuGcAGuuGuAAAcuuTT B	1686
R-008309003-000W	666	117	AACAUGCAGUUGUAAACUU	AAGuuuAcAAcuGcAuGuuUU	1687
R-008309012-000E	279	118	AAGCUGAUUUGAUGGAGUU	AACuccAucAAAucAGcuuUU	1689
R-008309012-000E	279	118	AAGCUGAUUUGAUGGAGUU	B AAGcuGAuuuGAuGGAGuuTT B	1688
R-008309033-000Y	1492	119	UCUGGGUUCAGAUGAUAUA	B ucuGGGuucAGAuGAuAuATT B	1690
R-008309033-000Y	1492	119	UCUGGGUUCAGAUGAUAUA	UAUAucAucuGAAcccAGAUU	1691
R-008309081-000T	2195	120	UUACUUCACUCUAGGAAUG	CAUuccuAGAGuGAAGuAAUU	1693
R-008309081-000T	2195	120	UUACUUCACUCUAGGAAUG	B uuAcuucAcucuAGGAAuGTT B	1692
R-008309048-000J	1424	121	AGGAAUCUUUCAGAUGCUG	B AGGAAucuuucAGAuGcuGTT B	1694
R-008309048-000J	1424	121	AGGAAUCUUUCAGAUGCUG	CAGcAucuGAAAGAuuccuUU	1695
R-008309000-000V	661	122	GCUGAAACAUGCAGUUGUA	UACAAcuGcAuGuuucAGcUU	1697
R-008309000-000V	661	122	GCUGAAACAUGCAGUUGUA	B GcuGAAAcAuGcAGuuGuATT B	1696
R-008309078-000L	1882	123	GUUGCUUGUUCGUGCACAU	B GuuGcuuGuucGuGcAcAuTT B	1698
R-008309078-000L	1882	123	GUUGCUUGUUCGUGCACAU	AUGuGcAcGAAcAAGcAAcUU	1699
R-008309096-000D	1966	124	GGAAGAAAUAGUUGAAGGU	B ggAAGAAAuAGuuGAAGGuTT B	1700
R-008309096-000D	1966	124	GGAAGAAAUAGUUGAAGGU	ACCuucAAcuAuuucuuccUU	1701

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008308997-000F	2259	125	AGGACAAGCCACAAGAUUA	B *AGGAcAAGccAcAAGAuuATT* B	1702
R-008308997-000F	2259	125	AGGACAAGCCACAAGAUUA	UAAucuuGuGGcuuGuccuUU	1703
R-008309030-000X	832	126	CAUGCGUUCUCCUCAGAUG	B *cAuGcGuucuccucAGAuGTT* B	1704
R-008309030-000X	832	126	CAUGCGUUCUCCUCAGAUG	CAUcuGAGGAGAAcGcAuGUU	1705
R-008042849-001H	2346	127	GAUGAUCCCAGCUACCGUU	AACGGuAGcuGGGAucAucUU	1707
R-008042849-001H	2346	127	GAUGAUCCCAGCUACCGUU	B *GAuGAucccAGcuAccGuuTT* B	1706
R-008308601-000T	1653	128	AGCCUGCCAUCUGUGCUCU	B *AGccuGccAucuGuGcucuTT* B	1708
R-008308601-000T	1653	128	AGCCUGCCAUCUGUGCUCU	AGAGcAcAGAuGGcAGGcuUU	1709
R-008308562-000W	2389	129	UGGAUAUCGCCAGGAUGAU	B *uGGAuAucGccAGGAuGAuTT* B	1710
R-008308562-000W	2389	129	UGGAUAUCGCCAGGAUGAU	AUCAuccuGGcGAuAuccAUU	1711
R-008308709-000X	1669	130	UCUUCGUCAUCUGACCAGC	B *ucuucGucAucuGAccAGcTT* B	1712
R-008308709-000X	1669	130	UCUUCGUCAUCUGACCAGC	GCUGGucAGAuGAcGAAGAUU	1713
R-008308634-000W	2123	131	UGUGAACUUGCUCAGGACA	B *uGuGAAcuuGcucAGGAcATT* B	1714
R-008308634-000W	2123	131	UGUGAACUUGCUCAGGACA	UGUccuGAGcAAGuucAcAUU	1715
R-008308667-000Z	1521	132	CCUGUGCAGCUGGAAUUCU	B *ccuGuGcAGcuGGAAuucuTT* B	1716
R-008308667-000Z	1521	132	CCUGUGCAGCUGGAAUUCU	AGAAuuccAGcuGcAcAGGUU	1717
R-008308706-000W	2125	133	UGAACUUGCUCAGGACAAG	CUUGuccuGAGcAAGuucAUU	1719
R-008308706-000W	2125	133	UGAACUUGCUCAGGACAAG	B *uGAAcuuGcucAGGAcAAGTT* B	1718
R-008308724-000N	2503	134	UGCUGACAUACCAGUUGAU	B *uGcuGAcuAuccAGuuGAuTT* B	1720
R-008308724-000N	2503	134	UGCUGACAUACCAGUUGAU	AUCAAcuGGAuAGucAGcAUU	1721
R-008308703-000V	1502	135	GAUGAUAUAAAUGUGGUCA	UGAccAcAuuuAuAucAucUU	1723
R-008308703-000V	1502	135	GAUGAUAUAAAUGUGGUCA	B *GAuGAuAuAAAuGuGGucATT* B	1722
R-008308496-000Y	2502	136	GUGCUGACUAUCCAGUUGA	UCAAcuGGAuAGucAGcAcUU	1725
R-008308496-000Y	2502	136	GUGCUGACUAUCCAGUUGA	B *GuGcuGAcuAuccAGuuGATT* B	1724
R-008308625-000M	2506	137	UGACUAUCCAGUUGAUGGG	CCCAucAAcuGGAuAGucAUU	1727
R-008308625-000M	2506	137	UGACUAUCCAGUUGAUGGG	B *uGAcuAuccAGuuGAuGGGTT* B	1726
R-008308589-000S	2127	138	AACUUGCUCAGGACAAGGA	B *AAcuuGcucAGGAcAAGGATT* B	1728
R-008308589-000S	2127	138	AACUUGCUCAGGACAAGGA	UCCuuGuccuGAGcAAGuuUU	1729
R-008308586-000R	2505	139	CUGACUAUCCAGUUGAUGG	B *cuGAcuAuccAGuuGAuGGTT* B	1730
R-008308586-000R	2505	139	CUGACUAUCCAGUUGAUGG	CCAucAAcuGGAuAGucAGUU	1731
R-008308493-000X	617	140	GCUCAUCCCACUAAUGUCC	B *GcucAucccAcuaauGuccTT* B	1732
R-008308493-000X	617	140	GCUCAUCCCACUAAUGUCC	GGAcAuuAGuGGGAuGAGcUU	1733
R-008308697-000B	2504	141	GCUGACUAUCCAGUUGAUG	B *GcuGacuAuccAGuuGAuGTT* B	1734
R-008308697-000B	2504	141	GCUGACUAUCCAGUUGAUG	CAUcAAcuGGAuAGucAGcUU	1735
R-008308661-000X	1503	142	AUGAUAUAAAUGUGGUCAC	GUGAccAcAuuuAuAucAuUU	1737
R-008308661-000X	1503	142	AUGAUAUAAAUGUGGUCAC	B *AuGAuAuAAAuGuGGucAcTT* B	1736
R-008308526-000L	618	143	CUCAUCCCACUAAUGUCCA	UGGAcAuuAGuGGGAuGAGUU	1739

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008308526-000L	618	143	CUCAUCCCACUAAUGUCCA	B cucAucccAcuAAuGuccATT B	1738
R-008308556-000N	2074	144	GCUUUAUUCUCCCAUUGAA	B GcuuuAuucucccAuuGAATT B	1740
R-008308556-000N	2074	144	GCUUUAUUCUCCCAUUGAA	UUCAAuGGGAGAAuAAAGcUU	1741
R-008308523-000K	2499	145	CUGGUGCUGACUAUCCAGU	B cuGGuGcuGAcuAuccAGuTT B	1742
R-008308523-000K	2499	145	CUGGUGCUGACUAUCCAGU	ACUGGAuAGucAGcAccAGUU	1743
R-008362860-000A	1406	146	AACUGUCUUUGGACUCUCA	B AAcuGucuuuGGAcucucATT B	1744
R-008362860-000A	1406	146	AACUGUCUUUGGACUCUCA	UGAGAGuccAAAGAcAGuuUU	1745
R-008362809-000Z	582	147	AGGGCAUGCAGAUCCCAUC	GAUGGGAucuGcAuGcccuUU	1747
R-008362809-000Z	582	147	AGGGCAUGCAGAUCCCAUC	B AGGGcAuGcAGAucccAucTT B	1746
R-008362908-000A	1505	148	GAUAUAAAUGUGGUCACCU	B GAuAuAAAuGuGGucAccuTT B	1748
R-008362908-000A	1505	148	GAUAUAAAUGUGGUCACCU	AGGuGAccAcAuuuAuAucUU	1749
R-008362713-000E	1432	149	UUCAGAUGCUGCAACUAAA	UUUAGuuGcAGcAucuGAAUU	1751
R-008362713-000E	1432	149	UUCAGAUGCUGCAACUAAA	B uucAGAuGcuGcAAcuAAATT B	1750
R-008363073-000K	1968	150	AAGAAAUAGUUGAAGGUUG	B AAGAAAuAGuuGAAGGuuGTT B	1752
R-008363073-000K	1968	150	AAGAAAUAGUUGAAGGUUG	CAAccuucAAcuAuuucuuUU	1753
R-008362947-000L	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuTT B	1754
R-008362947-000L	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUU	1755
R-008363070-000J	954	152	UGGCCAUCUUUAAGUCUGG	CCAGAcuuAAAGAuGGccAUU	1757
R-008363070-000J	954	152	UGGCCAUCUUUAAGUCUGG	B uGGccAucuuuAAGucuGGTT B	1756
R-008362857-000U	505	153	AGCUGAUAUUGAUGGACAG	B AGcuGAuAuuGAuGGAcAGTT B	1758
R-008362857-000U	505	153	AGCUGAUAUUGAUGGACAG	CUGuccAucAAuAucAGcuUU	1759
R-008363067-000C	2011	154	UCGGGAUGUUCACAACCGA	B ucGGGAuGuucAcAAccGATT B	1760
R-008363067-000C	2011	154	UCGGGAUGUUCACAACCGA	UCGGuuGuGAAcAucccGAUU	1761
R-008362944-000K	1339	155	UGUAGAAGCUGGUGGAAUG	B uGuAGAAGcuGGuGGAAuGTT B	1762
R-008362944-000K	1339	155	UGUAGAAGCUGGUGGAAUG	CAUuccAccAGcuucuAcAUU	1763
R-008362761-000Z	1242	156	UAAAUAUAAUGAGGACCUA	B uAAAuAuAAuGAGGAccuATT B	1764
R-008362761-000Z	1242	156	UAAAUAUAAUGAGGACCUA	UAGGuccucAuuAuAuuuAUU	1765
R-008362758-000T	567	157	CUGAGACAUUAGAUGAGGG	B cuGAGAcAuuAGAuGAGGGTT B	1766
R-008362758-000T	567	157	CUGAGACAUUAGAUGAGGG	CCCucAucuAAuGucucAGUU	1767
R-008363007-000Y	1240	158	AGUAAAUAUAAUGAGGACC	B AGuAAAuAuAAuGAGGAccTT B	1768
R-008363007-000Y	1240	158	AGUAAAUAUAAUGAGGACC	GGUccucAuuAuAuuuAcuUU	1769
R-008362854-000T	438	159	UGGAUACCUCCCAAGUCCU	B uGGAuAccucccAAGuccuTT B	1770
R-008362854-000T	438	159	UGGAUACCUCCCAAGUCCU	AGGAcuuGGGAGGuAuccAUU	1771
R-008362755-000S	2445	160	AGGAUGCCUUGGGUAUGGA	UCCAuAcccAAGGcAuccuUU	1773
R-008362755-000S	2445	160	AGGAUGCCUUGGGUAUGGA	B AGGAuGccuuGGGuAuGGATT B	1772
R-008363064-000B	860	161	AUUGUACGUACCAUGCAGA	B AuuGuAcGuAccAuGcAGATT B	1774

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008363064-000B	860	161	AUUGUACGUACCAUGCAGA	UCUGcAuGGuAcGuAcAAuUU	1775
R-008362752-000R	1413	162	UUUGGACUCUCAGGAAUCU	B uuuGGAcucucAGGAAucuTT B	1776
R-008362752-000R	1413	162	UUUGGACUCUCAGGAAUCU	AGAuuccuGAGAGuccAAAUU	1777
R-008363061-000A	1800	163	UUGGAUUGAUUCGAAAUCU	AGAuuucGAAucAAuccAAUU	1779
R-008363061-000A	1800	163	UUGGAUUGAUUCGAAAUCU	B uuGGAuuGAuucGAAAucuTT B	1778
R-008363004-000X	2037	164	UCAGAGGACUAAAUACCAU	AUGGuAuuuAGuccucuGAUU	1781
R-008363004-000X	2037	164	UCAGAGGACUAAAUACCAU	B ucAGAGGAcuAAAuAccAuTT B	1780
R-008362851-000S	2443	165	CCAGGAUGCCUUGGGUAUG	B ccAGGAuGccuuGGGuAuGTT B	1782
R-008362851-000S	2443	165	CCAGGAUGCCUUGGGUAUG	CAUAcccAAGGcAuccuGGUU	1783
R-008363001-000W	2471	166	AUGGAACAUGAGAUGGGUG	B AuGGAAcAuGAGAuGGGuGTT B	1784
R-008363001-000W	2471	166	AUGGAACAUGAGAUGGGUG	CACccAucucAuGuuccAuUU	1785
R-008362905-000Z	1792	167	GGCUACUGUUGGAUUGAUU	B GGcuAcuGuuGGAuuGAuuTT B	1786
R-008362905-000Z	1792	167	GGCUACUGUUGGAUUGAUU	AAUcAAuccAAcAGuAGccUU	1787
R-008362902-000Y	2547	168	AGGACCUCAUGGAUGGGCU	B AGGAccucAuGGAuGGGcuTT B	1788
R-008362902-000Y	2547	168	AGGACCUCAUGGAUGGGCU	AGCccAuccAuGAGGuccuUU	1789
R-008362998-000G	1662	169	UCUGUGCUCUUCGUCAUCU	AGAuGAcGAAGAGcAcAGAUU	1791
R-008362998-000G	1662	169	UCUGUGCUCUUCGUCAUCU	B ucuGuGcucuucGucAucuTT B	1790
R-008362848-000K	288	170	UGAUGGAGUUGGACAUGGC	GCCAuGuccAAcuccAucAUU	1793
R-008362848-000K	288	170	UGAUGGAGUUGGACAUGGC	B uGAuGGAGuuGGAcAuGGcTT B	1792
R-008362710-000D	579	171	AUGAGGGCAUGCAGAUCCC	GGGAucuGcAuGcccucAuUU	1795
R-008362710-000D	579	171	AUGAGGGCAUGCAGAUCCC	B AuGAGGGcAuGcAGAucccTT B	1794
R-008362707-000X	2508	172	ACUAUCCAGUUGAUGGGCU	AGCccAucAAcuGGAuAGuUU	1797
R-008362707-000X	2508	172	ACUAUCCAGUUGAUGGGCU	B AcuAuccAGuuGauGGGcuTT B	1796
R-008362806-000Y	580	173	UGAGGGCAUGCAGAUCCCA	B uGAGGGcAuGcAGAucccATT B	1798
R-008362806-000Y	580	173	UGAGGGCAUGCAGAUCCCA	UGGGAucuGcAuGcccucAUU	1799
R-008362803-000X	2388	174	UUGGAUAUCGCCAGGAUGA	B uuGGAuAucGccAGGAuGATT B	1800
R-008362803-000X	2388	174	UUGGAUAUCGCCAGGAUGA	UCAuccuGGcGAuAuccAAUU	1801
R-008362899-000F	2543	175	GCCCAGGACCUCAUGGAUG	B GcccAGGAccucAuGGAuGTT B	1802
R-008362899-000F	2543	175	GCCCAGGACCUCAUGGAUG	CAUccAuGAGGuccuGGGcUU	1803
R-008362749-000J	708	176	AACUUGCCACACGUGCAAU	B AAcuuGccAcAcGuGcAAuTT B	1804
R-008362749-000J	708	176	AACUUGCCACACGUGCAAU	AUUGcACGuGuGGcAAGuuUU	1805
R-008362845-000J	447	177	CCCAAGUCCUGUAUGAGUG	B cccAAGuccuGuAuGAGuGTT B	1806
R-008362845-000J	447	177	CCCAAGUCCUGUAUGAGUG	CACucAuAcAGGAcuuGGGUU	1807
R-008362842-000H	654	178	CACAGAUGCUGAAACAUGC	GCAuGuuucAGcAucuGuGUU	1809
R-008362842-000H	654	178	CACAGAUGCUGAAACAUGC	B cAcAGAuGcuGAAAcAuGcTT B	1808
R-008362896-000E	912	179	CUGGGACCUUGCAUAACCU	B cuGGGAccuuGcAuAAccuTT B	1810
R-008362896-000E	912	179	CUGGGACCUUGCAUAACCU	AGGuuAuGcAAGGucccAGUU	1811

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008363058-000U	1009	180	AGUGGAUUCUGUGUUGUUU	AAAcAAcAcAGAAuccAcuUU	1813
R-008363058-000U	1009	180	AGUGGAUUCUGUGUUGUUU	B AGuGGAuucuGuGuuGuuuTT B	1812
R-008362941-000J	1354	181	AAUGCAAGCUUUAGGACUU	B AAuGcAAGcuuuAGGAcuuTT B	1814
R-008362941-000J	1354	181	AAUGCAAGCUUUAGGACUU	AAGuccuAAAGcuuGcAuuUU	1815
R-008362839-000B	1969	182	AGAAAUAGUUGAAGGUUGU	B AGAAAuAGuuGAAGGuuGuTT B	1816
R-008362839-000B	1969	182	AGAAAUAGUUGAAGGUUGU	ACAAccuucAAcuAuuucuUU	1817
R-008363055-000T	1959	183	UCCGCAUGGAAGAAAUAGU	ACUAuuucuuccAuGcGGAUU	1819
R-008363055-000T	1959	183	UCCGCAUGGAAGAAAUAGU	B uccGcAuGGAAGAAAuAGuTT B	1818
R-008362836-000A	557	184	GCUAUGUUCCCUGAGACAU	B GcuAuGuucccuGAGAcAuTT B	1820
R-008362836-000A	557	184	GCUAUGUUCCCUGAGACAU	AUGucucAGGGAAcAuAGcUU	1821
R-008363052-000S	403	185	UCUGAGUGGUAAAGGCAAU	AUUGccuuuAccAcucAGAUU	1823
R-008363052-000S	403	185	UCUGAGUGGUAAAGGCAAU	B ucuGAGuGGuAAAGGcAAuTT B	1822
R-008363049-000K	1356	186	UGCAAGCUUUAGGACUUCA	B uGcAAGcuuuAGGAcuucATT B	1824
R-008363049-000K	1356	186	UGCAAGCUUUAGGACUUCA	UGAAGuccuAAAGcuuGcAUU	1825
R-008362893-000D	517	187	UGGACAGUAUGCAAUGACU	B uGGAcAGuAuGcAAuGAcuTT B	1826
R-008362893-000D	517	187	UGGACAGUAUGCAAUGACU	AGUcAuuGcAuAcuGuccAUU	1827
R-008362890-000C	1238	188	UUAGUAAAUAUAAUGAGGA	UCCucAuuAuAuuuAcuAAUU	1829
R-008362890-000C	1238	188	UUAGUAAAUAUAAUGAGGA	B uuAGuAAAuAuAAuGAGGATT B	1828
R-008362995-000F	843	189	CUCAGAUGGUGUCUGCUAU	B cucAGAuGGuGucuGcuAuTT B	1830
R-008362995-000F	843	189	CUCAGAUGGUGUCUGCUAU	AUAGcAGAcAccAucuGAGUU	1831
R-003262992-000E	496	190	AGAACAAGUAGCUGAUAUU	B AGAAcAAGuAGcuGAuAuuTT B	1832
R-003262992-000E	496	190	AGAACAAGUAGCUGAUAUU	AAUAucAGcuAcuuGuucuUU	1833
R-008363046-000J	2387	191	CUUGGAUAUCGCCAGGAUG	B cuuGGAuAucGccAGGAuGTT B	1834
R-008363046-000J	2387	191	CUUGGAUAUCGCCAGGAUG	CAUccuGGcGAuAuccAAGUU	1835
R-008362704-000W	1660	192	CAUCUGUGCUCUUCGUCAU	AUGAcGAAGAGcAcAGAuGUU	1837
R-008362704-000W	1660	192	CAUCUGUGCUCUUCGUCAU	B cAucuGuGcucuucGucAuTT B	1836
R-008362938-000C	2497	193	CCCUGGUGCUGACUAUCCA	B cccuGGuGcuGAcuAuccATT B	1838
R-008362938-000C	2497	193	CCCUGGUGCUGACUAUCCA	UGGAuAGucAGcAccAGGGUU	1839
R-008363043-000H	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	1840
R-008363043-000H	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUU	1841
R-008362746-000H	2353	195	UCUUGGACUUGAUAUUGGU	B ucuuGGAcuuGauAuuGGuTT B	1842
R-008362746-000H	2353	195	UCUUGGACUUGAUAUUGGU	ACCAAuAucAAGuccAAGAUU	1843
R-008362743-000G	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	1844
R-008362743-000G	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUU	1845
R-008362887-000W	1238	188	UUAGUAAAUAUAAUGAGGA	B UUAGUAAAUAUAAUGAGGATT B	1846
R-008362887-000W	1238	188	UUAGUAAAUAUAAUGAGGA	UCCUCAUUAUAUUUACUAAUU	1847

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008363040-000G	2125	133	UGAACUUGCUCAGGACAAG	B UGAACUUGCUCAGGACAAGTT B	1848
R-008363040-000G	2125	133	UGAACUUGCUCAGGACAAG	CUUGUCCUGAGCAAGUUCAUU	1849
R-008362935-000B	843	189	CUCAGAUGGUGUCUGCUAU	AUAGCAGACACCAUCUGAGUU	1851
R-008362935-000B	843	189	CUCAGAUGGUGUCUGCUAU	B CUCAGAUGGUGUCUGCUAUTT B	1850
R-008362740-000F	496	190	AGAACAAGUAGCUGAUAUU	AAUAUCAGCUACUUGUUCUUU	1853
R-008362740-000F	496	190	AGAACAAGUAGCUGAUAUU	B AGAACAAGUAGCUGAUAUUTT B	1852
R-008362884-000V	2074	144	GCUUUAUUCUCCCAUUGAA	UUCAAUGGGAGAAUAAAGCUU	1855
R-008362884-000V	2074	144	GCUUUAUUCUCCCAUUGAA	B GCUUUAUUCUCCCAUUGAATT B	1854
R-008362701-000V	2503	134	UGCUGACUAUCCAGUUGAU	B UGCUGACUAUCCAGUUGAUTT B	1856
R-008362701-000V	2503	134	UGCUGACUAUCCAGUUGAU	AUCAACUGGAUAGUCAGCAUU	1857
R-008362698-000C	2387	191	CUUGGAUAUCGCCAGGAUG	B CUUGGAUAUCGCCAGGAUGTT B	1858
R-008362698-000C	2387	191	CUUGGAUAUCGCCAGGAUG	CAUCCUGGCGAUAUCCAAGUU	1859
R-008362800-000W	1660	192	CAUCUGUGCUCUUCGUCAU	AUGACGAAGAGCACAGAUGUU	1861
R-008362800-000W	1660	192	CAUCUGUGCUCUUCGUCAU	B CAUCUGUGCUCUUCGUCAUTT B	1860
R-008362737-000Z	2497	193	CCCUGGUGCUGACUAUCCA	B CCCUGGUGCUGACUAUCCATT B	1862
R-008362737-000Z	2497	193	CCCUGGUGCUGACUAUCCA	UGGAUAGUCAGCACCAGGGUU	1863
R-008363037-000A	1503	142	AUGAUAUAAAUGUGGUCAC	B AUGAUAUAAAUGUGGUCACTT B	1864
R-008363037-000A	1503	142	AUGAUAUAAAUGUGGUCAC	GUGACCACAUUUAUAUCAUUU	1865
R-008362734-000Y	2506	137	UGACUAUCCAGUUGAUGGG	CCCAUCAACUGGAUAGUCAUU	1867
R-008362734-000Y	2506	137	UGACUAUCCAGUUGAUGGG	B UGACUAUCCAGUUGAUGGGTT B	1866
R-008362797-000D	2052	71	CCAUUCCAUUGUUUGUGCA	UGCACAAACAAUGGAAUGGUU	1869
R-008362797-000D	2052	71	CCAUUCCAUUGUUUGUGCA	B CCAUUCCAUUGUUUGUGCATT B	1868
R-008362731-000X	2389	129	UGGAUAUCGCCAGGAUGAU	B UGGAUAUCGCCAGGAUGAUTT B	1870
R-008362731-000X	2389	129	UGGAUAUCGCCAGGAUGAU	AUCAUCCUGGCGAUAUCCAUU	1871
R-008362794-000C	1406	146	AACUGUCUUUGGACUCUCA	B AACUGUCUUUGGACUCUCATT B	1872
R-008362794-000C	1406	146	AACUGUCUUUGGACUCUCA	UGAGAGUCCAAAGACAGUUUU	1873
R-008362833-000Z	1796	12	ACUGUUGGAUUGAUUCGAA	B ACUGUUGGAUUGAUUCGAATT B	1874
R-008362833-000Z	1796	12	ACUGUUGGAUUGAUUCGAA	UUCGAAUCAAUCCAACAGUUU	1875
R-008362989-000Y	2505	139	CUGACUAUCCAGUUGAUGG	B CUGACUAUCCAGUUGAUGGTT B	1876
R-008362989-000Y	2505	139	CUGACUAUCCAGUUGAUGG	CCAUCAACUGGAUAGUCAGUU	1877
R-008362791-000B	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAATT B	1878
R-008362791-000B	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUU	1879
R-008362881-000U	643	75	GGCUGAACCAUCACAGAUG	B GGCUGAACCAUCACAGAUGTT B	1880
R-008362881-000U	643	75	GGCUGAACCAUCACAGAUG	CAUCUGUGAUGGUUCAGCCUU	1881
R-008363034-000Z	582	147	AGGGCAUGCAGAUCCCAUC	GAUGGGAUCUGCAUGCCCUUU	1883
R-008363034-000Z	582	147	AGGGCAUGCAGAUCCCAUC	B AGGGCAUGCAGAUCCCAUCTT B	1882
R-008362830-000Y	2502	136	GUGCUGACUAUCCAGUUGA	B GUGCUGACUAUCCAGUUGATT B	1884

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008362830-000Y	2502	136	GUGCUGACUAUCCAGUUGA	UCAACUGGAUAGUCAGCACUU	1885
R-008362827-000S	1505	148	GAUAUAAAUGUGGUCACCU	AGGUGACCACAUUUAUAUCUU	1887
R-008362827-000S	1505	148	GAUAUAAAUGUGGUCACCU	B GAUAUAAAUGUGGUCACCUTT B	1886
R-008362728-000R	1432	149	UUCAGAUGCUGCAACUAAA	B UUCAGAUGCUGCAACUAAATT B	1888
R-008362728-000R	1432	149	UUCAGAUGCUGCAACUAAA	UUUAGUUGCAGCAUCUGAAUU	1889
R-008362986-000X	1968	150	AAGAAAUAGUUGAAGGUUG	CAACCUUCAACUAUUUCUUUU	1891
R-008362986-000X	1968	150	AAGAAAUAGUUGAAGGUUG	B AAGAAAUAGUUGAAGGUUGTT B	1890
R-008362878-000M	694	109	UCAAGAUGAUGCAGAACUU	B UCAAGAUGAUGCAGAACUUTT B	1892
R-008362878-000M	694	109	UCAAGAUGAUGCAGAACUU	AAGUUCUGCAUCAUCUUGAUU	1893
R-008362824-000R	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUU	1895
R-008362824-000R	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUTT B	1894
R-008362932-000A	2259	125	AGGACAAGCCACAAGAUUA	UAAUCUUGUGGCUUGUCCUUU	1897
R-008362932-000A	2259	125	AGGACAAGCCACAAGAUUA	B AGGACAAGCCACAAGAUUATT B	1896
R-008362788-000V	954	152	UGGCCAUCUUUAAGUCUGG	B UGGCCAUCUUUAAGUCUGGTT B	1898
R-008362788-000V	954	152	UGGCCAUCUUUAAGUCUGG	CCAGACUUAAAGAUGGCCAUU	1899
R-008362983-000W	2197	116	ACUUCACUCUAGGAAUGAA	B ACUUCACUCUAGGAAUAGAATT B	1900
R-008362983-000W	2197	116	ACUUCACUCUAGGAAUGAA	UUCAUUCCUAGAGUGAAGUUU	1901
R-008362929-000U	505	153	AGCUGAUAUUGAUGGACAG	B AGCUGAUAUUGAUGGACAGTT B	1902
R-008362929-000U	505	153	AGCUGAUAUUGAUGGACAG	CUGUCCAUCAAUAUCAGCUUU	1903
R-008362926-000T	2011	154	UCGGGAUGUUCACAACCGA	B UCGGGAUGUUCACAACCGATT B	1904
R-008362926-000T	2011	154	UCGGGAUGUUCACAACCGA	UCGGUUGUGAACAUCCCGAUU	1905
R-008362923-000S	1339	155	UGUAGAAGCUGGUGGAAUG	B UGUAGAAGCUGGUGGAAUGTT B	1906
R-008362923-000S	1339	155	UGUAGAAGCUGGUGGAAUG	CAUUCCACCAGCUUCUACAUU	1907
R-008362695-000B	1242	156	UAAAUAUAAUGAGGACCUA	B UAAAUAUAAUGAGGACCUATT B	1908
R-008362695-000B	1242	156	UAAAUAUAAUGAGGACCUA	UAGGUCCUCAUUAUAUUUAUU	1909
R-008362692-000A	499	107	ACAAGUAGCUGAUAUUGAU	B ACAAGUAGCUGAUAUUGAUTT B	1910
R-008362692-000A	499	107	ACAAGUAGCUGAUAUUGAU	AUCAAUAUCAGCUACUUGUUU	1911
R-008362689-000U	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUU	1913
R-008362689-000U	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUTT B	1912
R-008362785-000U	2353	195	UCUUGGACUUGAUAUUGGU	B UCUUGGACUUGAUAUUGGUTT B	1914
R-008362785-000U	2353	195	UCUUGGACUUGAUAUUGGU	ACCAAUAUCAAGUCCAAGAUU	1915
R-008363031-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUU	1917
R-008363031-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUTT B	1916
R-008362920-000R	878	197	AAUACAAAUGAUGUAGAAA	UUUCUACAUCAUUUGUAUUUU	1919
R-008362920-000R	878	197	AAUACAAAUGAUGUAGAAA	B AAUACAAAUGAUGUAGAAATT B	1918
R-008362917-000J	2046	112	UAAAUACCAUUCCAUUGUU	AACAAUGGAAUGGUAUUUAUU	1921

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008362917-000J	2046	112	UAAAUACCAUUCCAUUGUU	B UAAAUACCAUUCCAUUGUUTT B	1920
R-008362980-000V	647	198	GAACCAUCACAGAUGCUGA	UCAGCAUCUGUGAUGGUUCUU	1923
R-008362980-000V	647	198	GAACCAUCACAGAUGCUGA	B GAACCAUCACAGAUGCUGATT B	1922
R-008362725-000P	1998	199	UUCACAUCCUAGCUCGGGA	B UUCACAUCCUAGCUCGGGATT B	1924
R-008362725-000P	1998	199	UUCACAUCCUAGCUCGGGA	UCCCGAGCUAGGAUGUGAAUU	1925
R-008363028-000S	588	200	UGCAGAUCCCAUCUACACA	UGUGUAGAUGGGAUCUGCAUU	1927
R-008363028-000S	588	200	UGCAGAUCCCAUCUACACA	B UGCAGAUCCCAUCUACACATT B	1926
R-008362782-000T	2042	201	GGACUAAAUACCAUUCCAU	AUGGAAUGGUAUUUAGUCCUU	1929
R-008362782-000T	2042	201	GGACUAAAUACCAUUCCAU	B GGACUAAAUACCAUUCCAUTT B	1928
R-008362977-000N	855	202	CUGCUAUUGUACGUACCAU	B CUGCUAUUGUACGUACCAUTT B	1930
R-008362977-000N	855	202	CUGCUAUUGUACGUACCAU	AUGGUACGUACAAUAGCAGUU	1931
R-008362686-000T	2038	203	CAGAGGACUAAAUACCAUU	AAUGGUAUUUAGUCCUCUGUU	1933
R-008362686-000T	2038	203	CAGAGGACUAAAUACCAUU	B CAGAGGACUAAAUACCAUUTT B	1932
R-008362875-000L	1786	204	GAUAAAGGCUACUGUUGGA	UCCAACAGUAGCCUUUAUCUU	1935
R-008362875-000L	1786	204	GAUAAAGGCUACUGUUGGA	B GAUAAAGGCUACUGUUGGATT B	1934
R-008363025-000R	1501	205	AGAUGAUAUAAAUGUGGUC	B AGAUGAUAUAAAUGUGGUCTT B	1936
R-008363025-000R	1501	205	AGAUGAUAUAAAUGUGGUC	GACCACAUUUAUAUCAUCUUU	1937
R-008362914-000H	1834	206	AAAUCAUGCACCUUUGCGU	ACGCAAAGGUGCAUGAUUUUU	1939
R-008362914-000H	1834	206	AAAUCAUGCACCUUUGCGU	B AAAUCAUGCACCUUUGCGUTT B	1938
R-008362872-000K	1157	207	ACGACAGACUGCCUUCAAA	B ACGACAGACUGCCUUCAAATT B	1940
R-008362872-000K	1157	207	ACGACAGACUGCCUUCAAA	UUUGAAGGCAGUCUGUCGUUU	1941
R-008362974-000M	1239	208	UAGUAAAUAUAAUGAGGAC	B UAGUAAAUAUAAUGAGGACTT B	1942
R-008362974-000M	1239	208	UAGUAAAUAUAAUGAGGAC	GUCCUCAUUAUAUUUACUAUU	1943
R-008362821-000P	1248	209	UAAUGAGGACCUAUACUUA	B UAAUGAGGACCUAUACUUATT B	1944
R-008362821-000P	1248	209	UAAUGAGGACCUAUACUUA	UAAGUAUAGGUCCUCAUUAUU	1945
R-008362683-000S	660	210	UGCUGAAACAUGCAGUUGU	B UGCUGAAACAUGCAGUUGUTT B	1946
R-008362683-000S	660	210	UGCUGAAACAUGCAGUUGU	ACAACUGCAUGUUUCAGCAUU	1947
R-008363022-000P	285	211	AUUUGAUGGAGUUGGACAU	B AUUUGAUGGAGUUGGACAUTT B	1948
R-008363022-000P	285	211	AUUUGAUGGAGUUGGACAU	AUGUCCACCUCCAUCAAAUUU	1949
R-008362779-000L	1582	212	CUGCCAAGUGGGUGGUAUA	B CUGCCAAGUGGGUGGUAUATT B	1950
R-008362779-000L	1582	212	CUGCCAAGUGGGUGGUAUA	UAUACCACCCACUUGGCAGUU	1951
R-008363019-000H	1735	213	UGGACUACCAGUUGUGGUU	AACCACAACUGGUAGUCCAUU	1953
R-008363019-000H	1735	213	UGGACUACCAGUUGUGGUU	B UGGACUACCAGUUGUGGUUTT B	1952
R-008362776-000K	771	214	UUAAUAAGGCUGCAGUUAU	AUAACUGCAGCCUUAUUAAUU	1955
R-008362776-000K	771	214	UUAAUAAGGCUGCAGUUAU	B UUAAUAAGGCUGCAGUUAUTT B	1954
R-008363016-000G	1060	215	ACAUCAAGAAGGAGCUAAA	B ACAUCAAGAAGGAGCUAAATT B	1956
R-008363016-000G	1060	215	ACAUCAAGAAGGAGCUAAA	UUUAGCUCCUUCUUGAUGUUU	1957

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008362773-000J	2390	216	GGAUAUCGCCAGGAUGAUC	GAUCAUCCUGGCGAUAUCCUU	1959
R-008362773-000J	2390	216	GGAUAUCGCCAGGAUGAUC	B GGAUAUCGCCAGGAUGAUCTT B	1958
R-008362971-000L	2509	81	CUAUCCAGUUGAUGGGCUG	CAGCCCAUCAACUGGAUAGUU	1961
R-008362971-000L	2509	81	CUAUCCAGUUGAUGGGCUG	B CUAUCCAGUUGAUGGGCUGTT B	1960
R-008362722-000N	2186	217	CUGACAGAGUUACUUCACU	B CUGACAGAGUUACUUCACUTT B	1962
R-008362722-000N	2186	217	CUGACAGAGUUACUUCACU	AGUGAAGUAACUCUGUCAGUU	1963
R-008363013-000F	1632	218	GUGACAGGGAAGACAUCAC	B GUGACAGGGAAGACAUCACTT B	1964
R-008363013-000F	1632	218	GUGACAGGGAAGACAUCAC	GUGAUGUCUUCCCUGUCACUU	1965
R-008362818-000H	619	219	UCAUCCCACUAAUGUCCAG	CUGGACAUUAGUGGGAUGAUU	1967
R-008362818-000H	619	219	UCAUCCCACUAAUGUCCAG	G UCAUCCCACUAAUGUCCAGTT B	1966
R-008362968-000E	1656	220	CUGCCAUCUGUGCUCUUCG	B CUGCCAUCUGUGCUCUUCGTT B	1968
R-008362968-000E	1656	220	CUGCCAUCUGUGCUCUUCG	CGAAGAGCACAGAUGGCAGUU	1969
R-008362815-000G	1506	221	AUAUAAAUGUGGUCACCUG	B AUAUAAAUGUGGUCACCUGTT B	1970
R-008362815-000G	1506	221	AUAUAAAUGUGGUCACCUG	CAGGUGACCACAUUUAUAUUU	1971
R-008362869-000D	2501	76	GGUGCUGACUAUCCAGUUG	B GGUGCUGACUAUCCAGUUGTT B	1972
R-008362869-000D	2501	76	GGUGCUGACUAUCCAGUUG	CAACUGGAUAGUCAGCACCUU	1973
R-008362719-000G	2494	222	CCACCCUGGUGCUGACUAU	AUAGUCAGCACCAGGGUGGUU	1975
R-008362719-000G	2494	222	CCACCCUGGUGCUGACUAU	B CCACCCUGGUGCUGACUAUTT B	1974
R-008362770-000H	1666	223	UGCUCUUCGUCAUCUGACC	GGUCAGAUGACGAAGAGCAUU	1977
R-008362770-000H	1666	223	UGCUCUUCGUCAUCUGACC	B UGCUCUUCGUCAUCUGACCTT B	1976
R-008362680-000R	1635	224	ACAGGGAAGACAUCACUGA	B ACAGGGAAGACAUCACUGATT B	1978
R-008362680-000R	1635	224	ACAGGGAAGACAUCACUGA	UCAGUGAUGUCUUCCCUGUUU	1979
R-008362866-000C	294	225	AGUUGGACAUGGCCAUGGA	UCCAUGGCCAUGUCCAACUUU	1981
R-008362866-000C	294	225	AGUUGGACAUGGCCAUGGA	B AGUUGGACAUGGCCAUGGATT B	1980
R-008362863-000B	641	226	UUGGCUGAACCAUCACAGA	B UUGGCUGAACCAUCACAGATT B	1982
R-008362863-000B	641	226	UUGGCUGAACCAUCACAGA	UCUGUGAUGGUUCAGCCAAUU	1983
R-008362965-000D	576	227	UAGAUGAGGGCAUGCAGAU	AUCUGCAUGCCCUCAUCUAUU	1985
R-008362965-000D	576	227	UAGAUGAGGGCAUGCAGAU	B UAGAUGAGGGCAUGCAGAUTT B	1984
R-008362911-000G	577	228	AGAUGAGGGCAUGCAGAUC	B AGAUGAGGGCAUGCAGAUCTT B	1986
R-008362911-000G	577	228	AGAUGAGGGCAUGCAGAUC	GAUCUGCAUGCCCUCAUCUUU	1987
R-008362767-000B	1661	229	AUCUGUGCUCUUCGUCAUC	GAUGACGAAGAGCACAGAUUU	1989
R-008362767-000B	1661	229	AUCUGUGCUCUUCGUCAUC	B AUCUGUGCUCUUCGUCAUCTT B	1988
R-008362962-000C	707	230	GAACUUGCCACACGUGCAA	B GAACUUGCCACACGUGCAATT B	1990
R-008362962-000C	707	230	GAACUUGCCACACGUGCAA	UUGCACGUGUGGCAAGUUCUU	1991
R-008362677-000J	1659	231	CCAUCUGUGCUCUUCGUCA	B CCAUCUGUGCUCUUCGUCATT B	1992
R-008362677-000J	1659	231	CCAUCUGUGCUCUUCGUCA	UGACGAAGAGCACAGAUGGUU	1993

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008362674-000H	1547	88	CUCACUUGCAAUAAUUAUA	UAUAAUUAUUGCAAGUGAGUU	1995
R-008362674-000H	1547	88	CUCACUUGCAAUAAUUAUA	B CUCACUUGCAAUAAUUAUATT B	1994
R-008362959-000W	867	90	GUACCAUGCAGAAUACAAA	UUUGUAUUCUGCAUGGUACUU	1997
R-008362959-000W	867	90	GUACCAUGCAGAAUACAAA	B GUACCAUGCAGAAUACAAATT B	1996
R-008362956-000V	1185	232	AUGGCAACCAAGAAAGCAA	UUGCUUUCUUGGUUGCCAUUU	1999
R-008362956-000V	1185	232	AUGGCAACCAAGAAAGCAA	B AUGGCAACCAAGAAAGCAATT B	1998
R-008362764-000A	664	233	GAAACAUGCAGUUGUAAAC	GUUUACAACUGCAUGUUUCUU	2001
R-008362764-000A	664	233	GAAACAUGCAGUUGUAAAC	B GAAACAUGCAGUUGUAAACTT B	2000
R-008362716-000F	820	18	CAGACACGCUAUCAUGCGU	B CAGACACGCUAUCAUGCGUTT B	2002
R-008362716-000F	820	18	CAGACACGCUAUCAUGCGU	ACGCAUGAUAGCGUGUCUGUU	2003
R-008362812-000F	2266	101	GCCACAAGAUUACAAGAAA	UUUCUUGUAAUCUUGUGGCUU	2005
R-008362812-000F	2266	101	GCCACAAGAUUACAAGAAA	B GCCACAAGAUUACAAGAAATT B	2004
R-008362671-000G	1749	234	UGGUUAAGCUCUUACACCC	GGGUGUAAGAGCUUAACCAUU	2007
R-008362671-000G	1749	234	UGGUUAAGCUCUUACACCC	B UGGUUAAGCUCUUACACCCTT B	2006
R-008362953-000U	1234	235	AGCUUUAGUAAAUAUAAUG	B AGCUUUAGUAAAUAUAAUGTT B	2008
R-008362953-000U	1234	235	AGCUUUAGUAAAUAUAAUG	CAUUAUAUUUACUAAAGCUUU	2009
R-008362950-000T	691	236	CUAUCAAGAUGAUGCAGAA	B CUAUCAAGAUGAUGCAGAATT B	2010
R-008362950-000T	691	236	CUAUCAAGAUGAUGCAGAA	UUCUGCAUCAUCUUGAUAGUU	2011
R-008363010-000E	1387	237	AAGUCAACGUCUUGUUCAG	B AAGUCAACGUCUUGUUCAGTT B	2012
R-008363010-000E	1387	237	AAGUCAACGUCUUGUUCAG	CUGAACAAGACGUUGACUUUU	2013
R-008381224-000R	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2015
R-008381224-000R	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2014
R-008381211-000X	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2017
R-008381211-000X	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAAucAAuccAAcAGUsU	2016
R-008381038-000Y	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUsU	2019
R-008381038-000Y	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2018
R-008381052-000F	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAAucAAuccAAcAGUsU	2016
R-008381052-000F	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381158-000T	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAAucAAuccAAcAGUsU	2016
R-008381158-000T	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381341-000J	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAAucAAuccAAcAGUsU	2016
R-008381341-000J	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381109-000P	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381109-000P	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2023
R-008380818-000X	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008380818-000X	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2023
R-008381199-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2023

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381199-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381296-000E	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2024
R-008381296-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381042-000N	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2024
R-008381042-000N	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008380923-000F	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008380923-000F	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2024
R-008381104-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2025
R-008381104-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381098-000C	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2025
R-008381098-000C	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008380916-000P	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008380916-000P	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2025
R-008380906-000X	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008380906-000X	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUsU	2019
R-008381291-000L	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUsU	2019
R-008381291-000L	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381334-000T	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUsU	2019
R-008381334-000T	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381330-000H	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381330-000H	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2026
R-008381036-000F	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2026
R-008381036-000F	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381287-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381287-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2026
R-008381027-000X	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2027
R-008381027-000X	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2028
R-008380896-000U	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2029
R-008380896-000U	2398	151	CCAGGAUGAUCCUAGCUAU	AuAGcuAGGAucAuccuGGUsU	2030
R-008381153-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUsU	2032
R-008381153-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2031
R-008381323-000S	2398	151	CCAGGAUGAUCCUAGCUAU	AuAGcuAGGAucAuccuGGUsU	2030
R-008381323-000S	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381315-000S	2398	151	CCAGGAUGAUCCUAGCUAU	AuAGcuAGGAucAuccuGGUsU	2030
R-008381315-000S	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008380888-000U	2398	151	CCAGGAUGAUCCUAGCUAU	AuAGcuAGGAucAuccuGGUsU	2030

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008380888-000U	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381013-000V	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381013-000V	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2036
R-008381007-000M	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2036
R-008381007-000M	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008380995-000V	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008380995-000V	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2036
R-008380878-000B	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2037
R-008380878-000B	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381143-000G	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2037
R-008381143-000G	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381282-000C	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381282-000C	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2037
R-008380985-000C	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2038
R-008380985-000C	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2035
R-008381278-000M	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2038
R-008381278-000M	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381139-000S	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2038
R-008381139-000S	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008380871-000R	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUsU	2032
R-008380871-000R	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381272-000K	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAcAuccuGGUsU	2032
R-008381272-000K	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381268-000V	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUsU	2032
R-008381268-000V	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAucuAGcuAuUsU B	2035
R-008381133-000P	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2039
R-008381133-000P	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381261-000J	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2039
R-008381261-000J	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381091-000S	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381091-000S	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2039
R-008380861-000Y	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2041
R-008380861-000Y	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2040
R-008380853-000Y	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2043
R-008380853-000Y	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2042
R-008380811-000L	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2044
R-008380811-000L	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2045

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008380974-000B	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2043
R-008380974-000B	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008380966-000B	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2043
R-008380966-000B	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCCUUUsU B	2047
R-008381310-000Y	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2043
R-008381310-000Y	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381194-000C	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381194-000C	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2049
R-008380833-000N	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008380833-000N	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2049
R-008381115-000X	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2049
R-008381115-000X	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381242-000H	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2050
R-008381242-000H	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381235-000S	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008381235-000S	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2050
R-008381231-000G	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2050
R-008381231-000G	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381304-000R	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2051
R-008381304-000R	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008380828-000P	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008380828-000P	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2051
R-008380926-000G	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2051
R-008380926-000G	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381350-000T	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2045
R-008381350-000T	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381162-000H	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008381162-000H	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2045
R-008380823-000W	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2045
R-008380823-000W	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381068-000A	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2052
R-008381068-000A	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381190-000T	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2052
R-008381190-000T	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008380959-000K	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2052
R-008380959-000K	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381084-000A	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUGCUAGGAUCAUCCUsU	2054
R-008381084-000A	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2053
R-008380848-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2055
R-008380848-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAuAGcuAGGAucAuccUsU	2056
R-008380807-000W	2401	196	GGAUGAUCCUAGCUAUCGU	B *GG*AuGAuccuAGcuAucGuUsU B	2057
R-008380807-000W	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUsU	2058
R-008380843-000F	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008380843-000F	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAuAGcuAGGAucAuccUsU	2056
R-008381185-000U	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381185-000U	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAuAGcuAGGAucAuccUsU	2056
R-008380951-000R	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008380951-000R	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAuAGcuAGGAucAuccUsU	2056
R-008380804-000V	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008380804-000V	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2062
R-008381179-000L	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381179-000L	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2062
R-008381127-000G	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2062
R-008381127-000G	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008380945-000H	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008380945-000H	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2063
R-008381071-000G	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381071-000G	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2063
R-008381173-000J	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008381173-000J	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2063
R-008381122-000N	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008381122-000N	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2064
R-008380801-000J	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008380801-000J	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2064
R-008380839-000R	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008380839-000R	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUGCUAGGAUCAUCCUsU	2064
R-008380835-000F	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUsU	2058
R-008380835-000F	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008381258-000C	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUsU	2058
R-008381258-000C	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381169-000U	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUsU	2058
R-008381169-000U	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008380937-000H	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008380937-000H	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2065
R-008381251-000S	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381251-000S	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2065
R-008380933-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008380933-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2065
R-008381748-000J	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUuGGAUUGAUUCGaAAUsU B	2066
R-008381748-000J	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGaAUCAauccaACAGUsU	2067
R-008381708-000P	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUuGGaUUGaUUCGAAaUsU B	2069
R-008381708-000P	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAauCaAUCcAaCaGUsU	2068
R-008381704-000E	1797	5	CUGUUGGAUUGAUUCGAAA	uUUcgAaUCaAuCCAACAGUsU	2070
R-008381704-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUuGgaUUGAUuCGaAAUsU B	2071
R-008381746-000S	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGaaUCAAUCcAacaGUsU	2073
R-008381746-000S	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUGgaUUGaUUCgAAAUsU B	2072
R-008381728-000Z	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUGGAUUGAUuCgAAAUsU B	2074
R-008381728-000Z	1797	5	CUGUUGGAUUGAUUCGAAA	UUucGaAUCAAUCcAAcagUsU	2075
R-008381686-000B	1797	5	CUGUUGGAUUGAUUCGAAA	uuUCGAAUcaaUCCAAcAgUsU	2076
R-008381686-000B	1797	5	CUGUUGGAUUGAUUCGAAA	B CuGUUGgaUUgAuUCGAaaUsU B	2077
R-008381726-000G	1797	5	CUGUUGGAUUGAUUCGAAA	uuUcGAAUCaaUcCAACaGUsU	2078
R-008381726-000G	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUgGaUUGAUUCGaaAUsU B	2079
R-008381629-000Y	1797	5	CUGUUGGAUUGAUUCGAAA	UUucGAAuCaaUCCAacAGUsU	2081
R-008381629-000Y	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGuUUCGAuAUsU B	2080
R-008381724-000P	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUGgAUugAUUCgAAaUsU B	2083
R-008381724-000P	1797	5	CUGUUGGAUUGAUUCGAAA	uuuCgaAUCAAUCcAACagUsU	2082
R-008381670-000G	1797	5	CUGUUGGAUUGAUUCGAAA	B CugUUGGAUUGaUUcgaaaUsU B	2084
R-008381670-000G	1797	5	CUGUUGGAUUGAUUCGAAA	UuuCgAAUCAAUCcaACAGUsU	2085
R-008381666-000S	1797	5	CUGUUGGAUUGAUUCGAAA	UuuCGaauCAaUccaACAGUsU	2087
R-008381666-000S	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUgGaUugAUuCGaAAUsU B	2086
R-008381722-000X	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUgGAUUGAUUCgAAAUsU B	2088
R-008381722-000X	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgAauCAAUCcAAcagUsU	2089
R-008381700-000V	1797	5	CUGUUGGAUUGAUUCGAAA	uUuCGAAUCAaUCcaaCAGUsU	2090
R-008381700-000V	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUggAUUgaUUCGaAAUsU B	2091
R-008381650-000X	1797	5	CUGUUGGAUUGAUUCGAAA	UuUCGAAUcaaaCCaACaGUsU	2093
R-008381650-000X	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGaUUGaUUCgAAAUsU B	2092
R-008381647-000R	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGaUUgaUUCgAaaUsU B	2094
R-008381647-000R	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgAAuCAauCcaaCAgUsU	2095
R-008381624-000E	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGaAUCAauCCAaCAGUsU	2097

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381624-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B CuGuUgGAUUgaUUCGAaAUsU B	2096
R-008381682-000S	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGgAUUGAUUCGaaaUsU B	2098
R-008381682-000S	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcgaAUcAAUcCAACagUsU	2099
R-008381622-000M	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAaUcaAUCcaACAgUsU	2101
R-008381622-000M	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUggaUUgaUUCgaaaUsU B	2100
R-008381680-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	AuaGCUAggAUCAuCCuGGUsU	2103
R-008381680-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUgaUcCUaGCUAUUsU B	2102
R-008381606-000M	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGgaUGaUCCUAgCUAUUsU B	2104
R-008381606-000M	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgcuaGgaUCAuCcUGgUsU	2105
R-008381714-000X	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCUAGGaUCauccUGgUsU	2106
R-008381714-000X	2398	151	CCAGGAUGAUCCUAGCUAU	B CCagGAUgAUCCUAGCUaUUsU B	2107
R-008381642-000X	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUaUUsU B	2109
R-008381642-000X	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCuagGAUCAucCugGUsU	2108
R-008381662-000G	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcUAgGAuCauCCUggUsU	2111
R-008381662-000G	2398	151	CCAGGAUGAUCCUAGCUAU	B cCAGgAUGaUCCUagCUAUUsU B	2110
R-008381618-000X	2398	151	CCAGGAUGAUCCUAGCUAU	auAgCUaGGAuCauCCUGGUsU	2112
R-008381618-000X	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2113
R-008381698-000L	2398	151	CCAGGAUGAUCCUAGCUAU	aUaGCuaggAUcaUcCUGGUsU	2114
R-008381698-000L	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUagCUaUUsU B	2115
R-008381742-000G	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAgGAUgaUCCUaGCUAUUsU B	2117
R-008381742-000G	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCUAggAuCAuCCuGgUsU	2116
R-008381738-000S	2398	151	CCAGGAUGAUCCUAGCUAU	B CCaggaUgaUCCUagCUaUUsU B	2118
R-008381738-000S	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUaGGAUcauCCUgGUsU	2119
R-008381660-000P	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAgGAUGAUCCUAGcUAUUsU B	2121
R-008381660-000P	2398	151	CCAGGAUGAUCCUAGCUAU	aUagcUAGGAUcaUCCagGUsU	2120
R-008381696-000U	2398	151	CCAGGAUGAUCCUAGCUAU	B CCaGGaUGAUCCUAGCUAUUsU B	2123
R-008381696-000U	2398	151	CCAGGAUGAUCCUAGCUAU	auAGcUaggauCAUCCuGGUsU	2122
R-008381636-000P	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGgaUCauCcuGGUsU	2125
R-008381636-000P	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGaUGaUCCaAgCUAUUsU B	2124
R-008381634-000X	2398	151	CCAGGAUGAUCCUAGCUAU	AUaGCUagGAucAuCCUgGUsU	2127
R-008381634-000X	2398	151	CCAGGAUGAUCCUAGCUAU	B cCAGGaUGAuCCUaGCUaUUsU B	2126
R-008381632-000E	2398	151	CCAGGAUGAUCCUAGCUAU	B CCaGgAUgAuCCUAGcUAUUsU B	2129
R-008381632-000E	2398	151	CCAGGAUGAUCCUAGCUAU	aUAGCuAGGAUCAUCcUggUsU	2128
R-008381736-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	AUaGCuAGGaUcAUcCUggUsU	2131
R-008381736-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B CcaggAugaUCCUAGCUaUUsU B	2130
R-008381600-000K	2398	151	CCAGGAUGAUCCUAGCUAU	aUaGcUaggAUCAucCUGGUsU	2132
R-008381600-000K	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAgGaUGAUcCUaGCUAUUsU B	2133

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381732-000P	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCuAGGaUCAuCcUgGUsU	2134
R-008381732-000P	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAggaUGAUCCUAgCUAuUsU B	2135
R-008381656-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGgAUgAUCCUAGcuaUUsU B	2136
R-008381656-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	AuagCUAgGauCAUcCUGGUsU	2137
R-008381750-000G	1870	194	ACGACUAGUUCAGUUGCUU	aagCAaCUGaAcuAGUCgUUsU	2138
R-008381750-000G	1870	194	ACGACUAGUUCAGUUGCUU	B ACgACuAgUUcAGUUGCUUUsU B	2139
R-008381690-000S	1870	194	ACGACUAGUUCAGUUGCUU	aAGcAACUgAaCUaGUCguUsU	2140
R-008381690-000S	1870	194	ACGACUAGUUCAGUUGCUU	BaCGACUAGuUCAgUagcUUUsU B	2141
R-008381616-000E	1870	194	ACGACUAGUUCAGUUGCUU	AAGcaACuGaaCUaGuCGUUsU	2143
R-008381616-000E	1870	194	ACGACUAGUUCAGUUGCUU	B aCGACUagUUCaGUUgCUUUsU B	2142
R-008381688-000U	1870	194	ACGACUAGUUCAGUUGCUU	aAgCaAcUGAACUAgUcGUUsU	2144
R-008381688-000U	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaCuAGUuCAgUUgcUUUsU B	2145
R-008381614-000M	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaCUAguUCAGUUGCUUUsU B	2147
R-008381614-000M	1870	194	ACGACUAGUUCAGUUGCUU	aaGCAAcUgAaCuagUcGUUsU	2146
R-008381706-000X	1870	194	ACGACUAGUUCAGUUGCUU	B ACGaCUAGUUCAGUUGCuUUsU B	2148
R-008381706-000X	1870	194	ACGACUAGUUCAGUUGCUU	AAgCAAcUGaACUaGUcgUUsU	2149
R-008381672-000Z	1870	194	ACGACUAGUUCAGUUGCUU	AAgCAacugAAcUagUCGUUsU	2151
R-008381672-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B ACgACUAGUUCaGUUGcUUUsU B	2150
R-008381730-000X	1870	194	ACGACUAGUUCAGUUGCUU	AagcAaCUGAACUAGucgUUsU	2153
R-008381730-000X	1870	194	ACGACUAGUUCAGUUGCUU	B acGACUagUUCagUuGCuUUsU B	2152
R-008381612-000V	1870	194	ACGACUAGUUCAGUUGCUU	B aCGAcUAGUUCAGUUgCUUUsU B	2154
R-008381612-000V	1870	194	ACGACUAGUUCAGUUGCUU	AaGCaAcUGAacUaGUcGUUsU	2155
R-008381702-000M	1870	194	ACGACUAGUUCAGUUGCUU	AAgcaaCUGAACuaGUCGUUsU	2157
R-008381702-000M	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUaGUUCaGUUgCUUUsU B	2156
R-008381744-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B ACGaCUaGUUCAGUUGcUUUsU B	2158
R-008381744-000Z	1870	194	ACGACUAGUUCAGUUGCUU	AaGCAACUgaACUAGuCGUUsU	2159
R-008381610-000C	1870	194	ACGACUAGUUCAGUUGCUU	aAgCAACUGAacUaGuCgUUsU	2160
R-008381610-000C	1870	194	ACGACUAGUUCAGUUGCUU	B ACgACUAgUUCAgUUgCUUUsU B	2161
R-008381608-000E	1870	194	ACGACUAGUUCAGUUGCUU	B ACGaCUaGuUCagUUGCUUUsU B	2162
R-008381608-000E	1870	194	ACGACUAGUUCAGUUGCUU	AAgCAACUGaACUaGUCguUSU	2163
R-008381655-000G	1870	194	ACGACUAGUUCAGUUGCUU	aAgCAaCuGaAcuaGUCgUUsU	2164
R-008381655-000G	1870	194	ACGACUAGUUCAGUUGCUU	B ACGaCUaGUUCaguUgCUuUSU B	2165
R-008381668-000J	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2167
R-008381668-000J	1870	194	ACGACUAGUUCAGUUGCUU	aAgCAACugAACuaguCgUUsU	2166
R-008381627-000F	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaCUAGUUCaGUUGCUUUsU B	2169
R-008381627-000F	1870	194	ACGACUAGUUCAGUUGCUU	aAGCAacUgaACUaGUcGUUsU	2168

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381719-000R	1870	194	ACGACUAGUUCAGUUGCUU	B ACgAcUAgUuCAgUUGCUUsU B	2170
R-008381719-000R	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAAcUGAaCUaGUCGuUsU	2171
R-008381717-000Y	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaCUagUUCagUUgCUUUsU B	2173
R-008381717-000Y	1870	194	ACGACUAGUUCAGUUGCUU	aaGCAACuGaACUagUcGuUsU	2172
R-008381652-000P	2401	196	GGAUGAUCCUAGCUAUCGU	ACgaUAGcuAGgauCAUCcUsU	2175
R-008381652-000P	2401	196	GGAUGAUCCUAGCUAUCGU	B gGaugaUcCUaGCuAUCgUUsU B	2174
R-008381684-000J	2401	196	GGAUGAUCCUAGCUAUCGU	B GgAUGaUCCuagcUAUCgUUsU B	2177
R-008381684-000J	2401	196	GGAUGAUCCUAGCUAUCGU	aCgAUagcuaGGAUcAUCCUsU	2176
R-008381664-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	B gGAUgAUCCUAGCuaUCGUUsU B	2179
R-008381664-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	aCGauAGCuAgGaUcauCCUsU	2178
R-008381645-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	acgAUAGCUaGgAUCAuCCUsU	2180
R-008381645-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	B gGAUGAUCCUAgCUauCGUUsU B	2181
R-008381678-000B	2401	196	GGAUGAUCCUAGCUAUCGU	ACgaUAgCUaGGAuCAUCcUsU	2183
R-008381678-000B	2401	196	GGAUGAUCCUAGCUAUCGU	B ggaUgaUCCUagCUaUCgUUsU B	2182
R-008381620-000V	2401	196	GGAUGAUCCUAGCUAUCGU	aCgauAgCUAggAucaUcCUsU	2184
R-008381620-000V	2401	196	GGAUGAUCCUAGCUAUCGU	B GGaUGAUCCUAGCUaUCgUUsU B	2185
R-008381712-000E	2401	196	GGAUGAUCCUAGCUAUCGU	aCGAuaGCuAGGAuCaUCCUsU	2186
R-008381712-000E	2401	196	GGAUGAUCCUAGCUAUCGU	B GGaUGAUCCUaGCUAUCgUUsU B	2187
R-008381710-000M	2401	196	GGAUGAUCCUAGCUAUCGU	B gGaUgAUCCUaGCUAUCGUUsU B	2188
R-008381710-000M	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAgcUaGGAUCauCCUsU	2189
R-008381676-000J	2401	196	GGAUGAUCCUAGCUAUCGU	aCGAuaGCUAGgAUCaUccUsU	2190
R-008381676-000J	2401	196	GGAUGAUCCUAGCUAUCGU	B GgAUGauCCUAGCUAUCguUsU B	2191
R-008381604-000V	2401	196	GGAUGAUCCUAGCUAUCGU	B GgaUgAUCcUagCUaUCGuUsU B	2192
R-008381604-000V	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAgCUagGAuCAUCcUsU	2193
R-008381640-000E	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGaUCCUaGCUaUcgUUsU B	2194
R-008381640-000E	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAUAGCUAGgaucaUCCUsU	2195
R-008381740-000P	2401	196	GGAUGAUCCUAGCUAUCGU	acgAuaGCUagGauCAUcCUsU	2196
R-008381740-000P	2401	196	GGAUGAUCCUAGCUAUCGU	B GgAUGAUCCUagCUAUCGUUsU B	2197
R-008381674-000S	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAuCCUaGCUAUCGUUsU B	2199
R-008381674-000S	2401	196	GGAUGAUCCUAGCUAUCGU	aCgAUagcUAGGAuCAuCCUsU	2198
R-008381694-000B	2401	196	GGAUGAUCCUAGCUAUCGU	B GgaUGaUCCUAgCUAUCGUUsU B	2201
R-008381694-000B	2401	196	GGAUGAUCCUAGCUAUCGU	aCGAUaGCuAGGauCauCCUsU	2200
R-008381638-000G	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUgAUCCUAgcUAUCgUUsU B	2203
R-008381638-000G	2401	196	GGAUGAUCCUAGCUAUCGU	aCGaUagcUAgGAUcAuCcUsU	2202
R-008381602-000C	2401	196	GGAUGAUCCUAGCUAUCGU	B GGaUgaUCCaAGCuAUCGUUsU B	2204
R-008381602-000C	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAUaGCUaGGauCAUccUsU	2205
R-008381692-000J	2401	196	GGAUGAUCCUAGCUAUCGU	AcgaUagCUAGGAUcAucCUsU	2207

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381692-000J	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGA*UCCU*agCUAuC*GU*UsU B	2206
R-008381658-000S	2401	196	GGAUGAUCCUAGCUAUCGU	B g*GAU*gaU*CCUAGC*Ua*UCGU*UsU B	2208
R-008381658-000S	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUAGcuaggAuCAUcCUsU	2209
R-008381178-000C	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381178-000C	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGaAUCAauccaACAGUsU	2067
R-008380929-000H	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAuuCaAUCcAaCaGUsU	2068
R-008380929-000H	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381029-000X	1797	5	CUGUUGGAUUGAUUCGAAA	uUUcgAaUCaAuCCAACAGUsU	2070
R-008381029-000X	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381256-000K	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381256-000K	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGaaUCAAUCcAacaGUsU	2073
R-008381552-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381552-000E	1797	5	CUGUUGGAUUGAUUCGAAA	UUucGaAUCAAUCcAAcagUsU	2075
R-008381002-000U	1797	5	CUGUUGGAUUGAUUCGAAA	uuUCGAAUcaaUCCAAcAgUsU	2076
R-008381002-000U	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381394-000X	1797	5	CUGUUGGAUUGAUUCGAAA	uuUcGAAUCaaUcCAACuGUsU	2078
R-008381394-000X	1797	5	CUGUUGGAUUGAUUCGAAA	G CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381383-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UUucGAAuCaaUCCAacAGUsU	2081
R-008381383-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381093-000J	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381093-000J	1797	5	CUGUUGGAUUGAUUCGAAA	uuuCgaAUCAAUCcAACagUsU	2082
R-008381375-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UuuCgAAUCAAUCcaACAGUsU	2085
R-008381375-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381543-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UuuCGaauCAaUccaACAGUsU	2087
R-008381543-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381535-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgAauCAAUCcAAcagUsU	2087
R-008381535-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381528-000E	1797	5	CUGUUGGAUUGAUUCGAAA	uUuCGAAUCAaUCcaaCAGUsU	2090
R-008381528-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008381365-000D	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381365-000D	1797	5	CUGUUGGAUUGAUUCGAAA	UuUCGAAUcaauCCaACaGUsU	2093
R-008381520-000K	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgAAuCAauCcaaCAgUsU	2095
R-008381520-000K	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008380915-000F	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2020
R-008380915-000F	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGaAUCAauCCAaCAGUsU	2097
R-008381359-000W	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcgaAUcAAUcCAACagUsU	2099

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381359-000W	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUsU B	2021
R-008381249-000U	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAAUsU B	2022
R-008381249-000U	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAaUcaAUCcaACAgUsU	2101
R-008381082-000H	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381082-000H	2398	151	CCAGGAUGAUCCUAGCUAU	AuaGCUAggAUCAuCCuGGUsU	2103
R-008381240-000R	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381240-000R	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgcuaGgaUCAuCcUGgUsU	2105
R-008380907-000F	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008380907-000F	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCUAGGaUCauccUGgUsU	2106
R-008381164-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381164-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCuagGAUCAucCugGUsU	2108
R-008381072-000R	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381072-000R	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcUAgGAuCauCCUggUsU	2111
R-008381450-000C	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381450-000C	2398	151	CCAGGAUGAUCCUAGCUAU	auAgCUaGGAuCauCCUGGUsU	2112
R-008381059-000S	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381059-000S	2398	151	CCAGGAUGAUCCUAGCUAU	aUaGCuaggAUcaUcCUGGUsU	2114
R-008381154-000H	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCUAggAuCAuCCuGgUsU	2116
R-008381154-000H	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381443-000L	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUaGGAUcauCCUgGUsU	2119
R-008381443-000L	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381049-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381049-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	aUagcUAGGAUcaUCCagGUsU	2120
R-008381292-000V	2398	151	CCAGGAUGAUCCUAGCUAU	auAGcUaggauCAUCCuGGUsU	2122
R-008381292-000V	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381010-000U	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGgAUCauCcuGGUsU	2125
R-008381010-000U	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381284-000V	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381284-000V	2398	151	CCAGGAUGAUCCUAGCUAU	AUaGCUagGAucAuCCUgGUsU	2127
R-008381417-000U	2398	151	CCAGGAUGAUCCUAGCUAU	aUAGCuAGGAUCAUCcUggUsU	2128
R-008381417-000U	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034
R-008381265-000U	2398	151	CCAGGAUGAUCCUAGCUAU	AUaGCuAGGaUcAUcCUggUsU	2131
R-008381265-000U	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381464-000E	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2033
R-008381464-000E	2398	151	CCAGGAUGAUCCUAGCUAU	aUaGcUaggAUCAucCUGGUsU	2132
R-008381170-000H	2398	151	CCAGGAUGAUCCUAGCUAU	aUagCuAGGaUCAuCcUgGUsU	2134
R-008381170-000H	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAGGAUGAUCCUAGCUAUUsU B	2034

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381408-000K	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuUsU B	2035
R-008381408-000K	2398	151	CCAGGAUGAUCCUAGCUAU	AuagCUAgGauCAUcCUGGUsU	2137
R-008381110-000D	1870	194	ACGACUAGUUCAGUUGCUU	aagCAaCUGaAcuAGUCgUUsU	2138
R-008381110-000D	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381558-000G	1870	194	ACGACUAGUUCAGUUGCUU	aAGcAACUgAaCUaGUCguUsU	2140
R-008381558-000G	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008381456-000E	1870	194	ACGACUAGUUCAGUUGCUU	AAGcaACuGaaCUaGuCGUUsU	2143
R-008381456-000E	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381401-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381401-000Z	1870	194	ACGACUAGUUCAGUUGCUU	aAgCaAcUGAACUAgUcGUUsU	2144
R-008380922-000X	1870	194	ACGACUAGUUCAGUUGCUU	aaGCAAcUgAaCuagUcGUUsU	2146
R-008380922-000X	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008381101-000V	1870	194	ACGACUAGUUCAGUUGCUU	AAgCAAcUGaACUaGUcgUUsU	2149
R-008381101-000V	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381556-000P	1870	194	ACGACUAGUUCAGUUGCUU	AAgCAacugAAcUagUCGUUsU	2151
R-008381556-000P	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381426-000C	1870	194	ACGACUAGUUCAGUUGCUU	AagcAaCUgaaCUAGucgUUsU	2153
R-008381426-000C	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008380979-000V	1870	194	ACGACUAGUUCAGUUGCUU	AaGCaAcUGAacUaGUcGUUsU	2155
R-008380979-000V	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008380882-000S	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008380882-000S	1870	194	ACGACUAGUUCAGUUGCUU	AAgcaaCUGAACuaGUCGUUsU	2157
R-008381204-000F	1870	194	ACGACUAGUUCAGUUGCUU	AaGCAACUgaACUAGuCGUUsU	2159
R-008381204-000F	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008381471-000W	1870	194	ACGACUAGUUCAGUUGCUU	aAgCAACUGAacUaGuCgUUsU	2160
R-008381471-000W	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381197-000D	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008381197-000D	1870	194	ACGACUAGUUCAGUUGCUU	AAgCAACUGaACUaGUCguUsU	2163
R-008380970-000S	1870	194	ACGACUAGUUCAGUUGCUU	aAgCAaCuGaAcuaGUCgUUsU	2164
R-008380970-000S	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047
R-008381511-000B	1870	194	ACGACUAGUUCAGUUGCUU	aAgCAACugAACuaguCgUUsU	2166
R-008381511-000B	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008380992-000U	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2046
R-008380992-000U	1870	194	ACGACUAGUUCAGUUGCUU	aAGCAacUgaACUaGUcGUUsU	2168
R-008381233-000Z	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAAcUGAaCUaGUCGuUsU	2171
R-008381233-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B ACGACUAGUUCAGUUGCUUUsU B	2047

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381352-000K	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuUsU B	2048
R-008381352-000K	1870	194	ACGACUAGUUCAGUUGCUU	aaGCAACuGaACUagUcGuUSU	2172
R-008380987-000V	2401	196	GGAUGAUCCUAGCUAUCGU	ACgaUAGcuAGgauCAUCcUsU	2175
R-008380987-000V	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008381345-000U	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381345-000U	2401	196	GGAUGAUCCUAGCUAUCGU	aCgAUagcuaGGAUcAUCCUsU	2176
R-008381146-000H	2401	196	GGAUGAUCCUAGCUAUCGU	aCGauAGCuAgGaUcauCCUsU	2178
R-008381146-000H	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008381503-000B	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008381503-000B	2401	196	GGAUGAUCCUAGCUAUCGU	acgAUAGCUaGgAUCAuCCUsU	2180
R-008381137-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381137-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	ACgaUAgCUaGGAuCAUCcUsU	2183
R-008381337-000U	2401	196	GGAUGAUCCUAGCUAUCGU	aCgauAgCUAggAucaUcCUsU	2184
R-008381337-000U	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008380900-000V	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008380900-000V	2401	196	GGAUGAUCCUAGCUAUCGU	aCGAuaGCuAGGAuCaUCCUsU	2186
R-008381328-000K	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381328-000K	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAgcUaGGAUCauCCUsU	2189
R-003831222-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-003831222-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	aCGAuaGCUAGgAUCaUccUsU	2190
R-008381494-000G	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAgCUagGAuCAUCcUsU	2193
R-008381494-000G	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008381212-000F	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381212-000F	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAUAGCUAGgaucaUCCUsU	2195
R-008381434-000C	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008381434-000C	2401	196	GGAUGAUCCUAGCUAUCGU	acgAuaGCUagGauCAUcCUsU	2196
R-008380895-000K	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008380895-000K	2401	196	GGAUGAUCCUAGCUAUCGU	aCgAUagcUAGGAuCAuCCUsU	2198
R-008381488-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008381488-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	aCGAUaGCuAGGauCauCCUsU	2200
R-008381126-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	aCGaUagcUAgGAUcAuCcUsU	2202
R-008381126-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061
R-008381479-000R	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2059
R-008381479-000R	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAUaGCUaGGauCAUccUsU	2205
R-008381319-000B	2401	196	GGAUGAUCCUAGCUAUCGU	AcgaUagCUAGGAUcAucCUsU	2207
R-008381319-000B	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGAUCCUAGCUAUCGUUsU B	2060
R-008380889-000C	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuUsU B	2061

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008380889-000C	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUAGcuaggAuCAUcCUsU	2209
R-008381831-000R	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUuGGAUUGAUUCGaAAUsU B	2066
R-008381831-000R	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAAucAAuccAAcAGUsU	2016
R-008381842-000S	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUuGGaUUGaUUCGAAaUsU B	2069
R-008381842-000S	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAAucAAuccAAcAGUsU	2016
R-008381850-000S	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUuGgaUUGAUuCGaAAUsU B	2071
R-008381850-000S	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAAucAAuccAAcAGUsU	2016
R-008381815-000R	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2023
R-008381815-000R	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUGgaUUGaUUCgAAAUsU B	2072
R-008381783-000K	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUGGAUUGAUuCgAAAUsU B	2074
R-008381783-000K	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2023
R-008381799-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B CuGUUGgaUUgAuUCGAaaUsU B	2077
R-008381799-000E	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2023
R-008381814-000G	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUgGaUUGAUUCGaaAUsU B	2079
R-008381814-000G	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2024
R-008381780-000J	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2024
R-008381780-000J	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGaUUCGAaAUsU B	2080
R-008381841-000H	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUGgAUugAUUCgAAaUsU B	2083
R-008381841-000H	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2024
R-008381791-000K	1797	5	CUGUUGGAUUGAUUCGAAA	B CugUUGGAUUGaUUcgaaaUsU B	2084
R-008381791-000K	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2025
R-008381839-000K	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2025
R-008381839-000K	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUgGaUugAUuCGaAAUsU B	2086
R-008381796-000D	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUgGAUUGAUUCgAAAUsU B	2088
R-008381796-000D	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCGAAUCAAUCCAACAGUsU	2025
R-008381838-000B	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUsU	2019
R-008381838-000B	1797	5	CUGUUGGAUUGAUUCGAAA	B CUgUUggAUUgaUUCGaAAUsU B	2091
R-008381790-000B	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGaUUGaUUCgAAAUsU B	2092
R-008381790-000B	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUsU	2019
R-008381825-000H	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGuUUgaUUCgAaaUsU B	2094
R-008381825-000H	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUsU	2019
R-008381789-000M	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2026
R-008381789-000M	1797	5	CUGUUGGAUUGAUUCGAAA	B CuGuUgGAUUgaUUCGAaAUsU B	2096
R-008381805-000Y	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2026
R-008381805-000Y	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGgAUUGAUUCGauaUsU B	2098
R-008381788-000D	1797	5	CUGUUGGAUUGAUUCGAAA	UUUCgaaUCaaUCCaaCagUsU	2026

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381788-000D	1797	5	CUGUUGGAUUGAUUCGAAA	B *CUgUU*ggaUUga*UUC*gaaaUsU B	2100
R-008381847-000K	2398	151	CCAGGAUGAUCCUAGCUAU	B CCA*GGA*UGa*UcCU*aGCUAUUsU B	2102
R-008381847-000K	2398	151	CCAGGAUGAUCCUAGCUAU	AuAGcUAGGAucAuccuGGUsU	2030
R-008381837-000T	2398	151	CCAGGAUGAUCCUAGCUAU	AuAGcuAGGAucAuccuGGUsU	2030
R-008381837-000T	2398	151	CCAGGAUGAUCCUAGCUAU	B *CCAG*gaU*GaUCCU*Ag*CUA*UUsU B	2104
R-008381824-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B *CC*agGA*UgAUCCUAGC*UaUUsU B	2107
R-008381824-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	AuAGcuAGGAucAuccuGGUsU	2030
R-008381810-000X	2398	151	CCAGGAUGAUCCUAGCUAU	B *CCAGGAUGAUCCUAGC*UaUUsU B	2109
R-008381810-000X	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2036
R-008381802-000X	2398	151	CCAGGAUGAUCCUAGCUAU	B cCA*GgAUGa*UCCUagCUAUUsU B	2110
R-008381802-000X	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2036
R-008381820-000P	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2036
R-008381820-000P	2398	151	CCAGGAUGAUCCUAGCUAU	B CCA*GGAUGAUCCUAGCU*AUUsU B	2113
R-008381819-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2037
R-008381819-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B *CCAGGAUGAUCC*UagC*U*aUUsU B	2115
R-008381787-000V	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2037
R-008381787-000V	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAg*GA*UGa*UCCUaGCUA*UUsU B	2117
R-008381835-000A	2398	151	CCAGGAUGAUCCUAGCUAU	B *CC*aggaU*g*a*UCCU*ag*CUa*UUsU B	2118
R-008381835-000A	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2037
R-008381844-000J	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2038
R-008381844-000J	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAgGAUGA*UCCUAGcUA*UUsU B	2121
R-008381853-000T	2398	151	CCAGGAUGAUCCUAGCUAU	B CCa*GGaUGAUCCUAGCUA*UUsU B	2123
R-008381853-000T	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2038
R-008381833-000H	2398	151	CCAGGAUGAUCCUAGCUAU	B CCA*GGaUG*aUCCuAgCUAUUsU B	2124
R-008381833-000H	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGCUAGGAUCAUCCUGGUsU	2038
R-008381817-000H	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUsU	2032
R-008381817-000H	2398	151	CCAGGAUGAUCCUAGCUAU	B cCAGGaUGAuCCUa*GCUaUU*sU B	2126
R-008381786-000L	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUsU	2032
R-008381786-000L	2398	151	CCAGGAUGAUCCUAGCUAU	B CCaGg*AUg*AuC*CUA*GcUAUUsU B	2129
R-008381851-000A	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUsU	2032
R-008381851-000A	2398	151	CCAGGAUGAUCCUAGCUAU	B *Cc*aggAuga*UCCUAGC*UaUUsU B	2130
R-008381809-000H	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2039
R-008381809-000H	2398	151	CCAGGAUGAUCCUAGCUAU	B CCAg*GaUGAUc*C*UaGCUA*UUsU B	2133
R-008381808-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	B *CC*AggaU*GAUCC*UAgCUAuUsU B	2135
R-008381808-000Z	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2039
R-008381784-000U	2398	151	CCAGGAUGAUCCUAGCUAU	AUAgCUaggaUCaUCCUggUsU	2039
R-008381784-000U	2398	151	CCAGGAUGAUCCUAGCUAU	B CCA*GgAUgAUCCUAGcua*UUsU B	2136

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381793-000C	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2043
R-008381793-000C	1870	194	ACGACUAGUUCAGUUGCUU	B ACgACuAg*UUcAGUUGCUUU*sU B	2139
R-008381807-000R	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2043
R-008381807-000R	1870	194	ACGACUAGUUCAGUUGCUU	B aCGA*CUAGuUCAg*UugcUUUsU B	2141
R-008381816-000Z	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2043
R-008381816-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B aCGACUag*UUCaGUUgCUUU*sU B	2142
R-008381830-000G	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2049
R-008381830-000G	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaCuA*GUuCAgUUgcUUU*sU B	2145
R-008381782-000B	1870	194	ACGACUAGUUCAGUUGCUU	B aCga*CUAguUCAGUUGCUUU*sU B	2147
R-008381782-000B	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2049
R-008381849-000C	1870	194	ACGACUAGUUCAGUUGCUU	B A*CGaCUAGUUCAGUUGCuUUsU* B	2148
R-008381849-000C	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2049
R-008381781-000T	1870	194	ACGACUAGUUCAGUUGCUU	B A*CgACUAGUUCaGUUGcUUUsU* B	2150
R-008381781-000T	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2050
R-008381829-000T	1870	194	ACGACUAGUUCAGUUGCUU	B acGACUag*UUCagUuGCuUUsU* B	2152
R-008381829-000T	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2050
R-008381792-000U	1870	194	ACGACUAGUUCAGUUGCUU	B a*CGAcUAGUUCAGUUgCUUUsU* B	2154
R-008381792-000U	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2050
R-008381798-000W	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2051
R-008381798-000W	1870	194	ACGACUAGUUCAGUUGCUU	B A*CGACUaGUUCaGUUgCUUUsU* B	2156
R-008381828-000J	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2051
R-008381828-000J	1870	194	ACGACUAGUUCAGUUGCUU	B ACGaCUa*GUUCAGUUGcUUUsU* B	2158
R-008381840-000Z	1870	194	ACGACUAGUUCAGUUGCUU	AAGCAACUGAACUAGUCGUUsU	2051
R-008381840-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B A*CgACUAgUUCAgUUgCUUUsU* B	2161
R-008381797-000M	1870	194	ACGACUAGUUCAGUUGCUU	B A*CGaCUaGuUCagUUGCUUUsU* B	2162
R-008381797-000M	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2045
R-008381813-000Y	1870	194	ACGACUAGUUCAGUUGCUU	B A*CGaCUaGUUCaguUgCUuUsU* B	2165
R-008381813-000Y	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2045
R-008381827-000A	1870	194	ACGACUAGUUCAGUUGCUU	B A*CGACUAGUUCAGUUGCUUUsU* B	2167
R-008381827-000A	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUsU	2045
R-008381812-000P	1870	194	ACGACUAGUUCAGUUGCUU	B aCga*CUAGUUCaGUUGCUUUsU* B	2169
R-008381812-000P	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2052
R-008381848-000U	1870	194	ACGACUAGUUCAGUUGCUU	B ACgAcUAgUuCAg*UUGCUUUsU* B	2170
R-008381848-000U	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2052
R-008381779-000V	1870	194	ACGACUAGUUCAGUUGCUU	B aCga*CUag UUCagUUgCUUUsU* B	2173
R-008381779-000V	1870	194	ACGACUAGUUCAGUUGCUU	AAGCaaCUgaaCUagUCgUUsU	2052

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008381846-000B	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAuagCUAGGAucAuccUsU	2056
R-008381846-000B	2401	196	GGAUGAUCCUAGCUAUCGU	B g*G*augaUcCUaGCuAUCg*UU*sU B	2174
R-008381811-000F	2401	196	GGAUGAUCCUAGCUAUCGU	B G*g*AU*G*aUCCuagcUA*U*CgUUsU B	2177
R-008381811-000F	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAuAGcuAGGAucAuccUsU	2056
R-008381845-000T	2401	196	GGAUGAUCCUAGCUAUCGU	B g*GA*UgAUCC*U*AGCua*UC*GUUsU B	2179
R-008381845-000T	2401	196	GGAUGAUCCUAGCUAUCGU	AcGAuAGcaAGGAucAuccUsU	2056
R-008381795-000V	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2062
R-008381795-000V	2401	196	GGAUGAUCCUAGCUAUCGU	B g*GAUGA*UCCU*A*g*CU*au*CGUU*sU B	2181
R-008381823-000R	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2062
R-008381823-000R	2401	196	GGAUGAUCCUAGCUAUCGU	B gca*U*ga*UCCU*ag*CU*a*UC*g*UU*sU B	2182
R-008381803-000F	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2062
R-008381803-000F	2401	196	GGAUGAUCCUAGCUAUCGU	B *GGa*U*GAUCCUAG*CUaUCg*UU*sU B	2185
R-008381822-000G	2401	196	GGAUGAUCCUAGCUAUCGU	B *GGa*U*GAUCCUa*G*CU*AUCgUUsU B	2187
R-008381822-000G	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2063
R-008381836-000J	2401	196	GGAUGAUCCUAGCUAUCGU	B g*GaUgA*U*CCU*a*GCUA*UCG*UU*sU B	2188
R-008381836-000J	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2063
R-008381854-000B	2401	196	GGAUGAUCCUAGCUAUCGU	B Gg*AUG*auCCUAGCUAUCguUsU B	2191
R-008381854-000B	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2063
R-008381801-000N	2401	196	GGAUGAUCCUAGCUAUCGU	B GgaUgA*U*CcUagC*U*aUCGuUsU B	2192
R-008381801-000N	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUGCUAGGAUCAUCCUsU	2064
R-008381800-000E	2401	196	GGAUGAUCCUAGCUAUCGU	B *GGAUGa*U*CCU*aGCUaUcg*UU*sU B	2194
R-008381800-000E	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2064
R-008381834-000S	2401	196	GGAUGAUCCUAGCUAUCGU	B G*gAUGA*UCCUag*CU*A*UC*G*UU*sU B	2197
R-008381834-000S	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAUAGCUAGGAUCAUCCUsU	2064
R-008381852-000J	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUsU	2058
R-008381852-000J	2401	196	GGAUGAUCCUAGCUAUCGU	B *GGAUG*AuC*CU*aG*CUAUCGUU*sU B	2199
R-008381843-000A	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUsU	2059
R-008381843-000A	2401	196	GGAUGAUCCUAGCUAUCGU	B *Gga*U*GaUCCU*Ag*CUAUCGUU*sU B	2201
R-008381832-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUsU	2058
R-008381832-000Z	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUgA*UCCU*Agc*UAUC*gUUsU B	2203
R-008381818-000S	2401	196	GGAUGAUCCUAGCUAUCGU	B GGaUga*UCC*uAG*C*uA*UCGUU*sU B	2204
R-008381818-000S	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2065
R-008381785-000C	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAUGA*UCCU*agCUAu*C*G*UU*sU B	2206
R-008381785-000C	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2065
R-008381794-000L	2401	196	GGAUGAUCCUAGCUAUCGU	ACGaUagCUaggaUCaUCCUsU	2065
R-008381794-000L	2401	196	GGAUGAUCCUAGCUAUCGU	B g*GAU*gaUCCUAGCUaU*C*G*UU*sU B	2208
R-008395187-000D	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAA*TT* B	2210

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008395187-000D	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAucAAuccAAcAGUU	1463
R-008395244-000T	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395244-000T	1797	5	CUGUUGGAUUGAUUCGAAA	IUUcGAAucAAuccAAcAGUU	2211
R-008395198-000E	1797	5	CUGUUGGAUUGAUUCGAAA	UIUcGAAucAAuccAAcAGUU	2212
R-008395198-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395222-000R	1797	5	CUGUUGGAUUGAUUCGAAA	UUIcGAAucAAuccAAcAGUU	2213
R-008395222-000R	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395155-000J	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395155-000J	1797	5	CUGUUGGAUUGAUUCGAAA	UUUIGAAucAAuccAAcAGUU	2214
R-008395242-000A	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395242-000A	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcIAAucAAuccAAcAGUU	2215
R-008395267-000D	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395267-000D	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGIAucAAuccAAcAGUU	2216
R-008395153-000S	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395153-000S	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAIucAAuccAAcAGUU	2217
R-008395286-000E	1797	5	CUGUUGGAUUGAUUCGAAA	B cuGuuGGAuuGAuucGAAATT B	2210
R-008395286-000E	1797	5	CUGUUGGAUUGAUUCGAAA	UUUcGAAIcAAuccAAcAGUU	2218
R-008395196-000M	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395196-000M	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcuGAAcuAGucGuUU	1841
R-008395168-000C	1870	194	ACGACUAGUUCAGUUGCUU	IAGcAAcuGAAcuAGucGuUU	2220
R-008395168-000C	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395265-000L	1870	194	ACGACUAGUUCAGUUGCUU	AIGcAAcuGAAcuAGucGuUU	2221
R-008395265-000L	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395150-000R	1870	194	ACGACUAGUUCAGUUGCUU	AAIcAAcuGAAcuAGucGuUU	2222
R-008395150-000R	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395263-000U	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395263-000U	1870	194	ACGACUAGUUCAGUUGCUU	AAGIAAcuGAAcuAGucGuUU	2223
R-008395172-000T	1870	194	ACGACUAGUUCAGUUGCUU	AAGcIAcuGAAcuAGucGuUU	2224
R-008395172-000T	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395170-000A	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395170-000A	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAIcuGAAcuAGucGuUU	2225
R-008395226-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395226-000Z	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAIuGAAcuAGucGuUU	2226
R-008395207-000Z	1870	194	ACGACUAGUUCAGUUGCUU	AAGcAAcIGAAcuAGucGuUU	2227
R-008395207-000Z	1870	194	ACGACUAGUUCAGUUGCUU	B AcGAcuAGuucAGuuGcuuTT B	2219
R-008395205-000G	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAGGAucAuccuGGUU	1755

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008395205-000G	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuTT B	2228
R-008395250-000A	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAaGAuccuAGcuAuTT B	2228
R-008395250-000A	2398	151	CCAGGAUGAUCCUAGCUAU	IUAGcuAGGAucAuccuGGUU	2229
R-008395248-000C	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuTT B	2228
R-008395248-000C	2398	151	CCAGGAUGAUCCUAGCUAU	AIAGcuAGGAucAuccuGGUU	2230
R-008395275-000D	2398	151	CCAGGAUGAUCCUAGCUAU	AUIGcuAGGAucAuccuGGUU	2231
R-008395275-000D	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuTT B	2228
R-008395163-000J	2398	151	CCAGGAUGAUCCUAGCUAU	AUAIcuAGGAucAuccuGGUU	2232
R-008395163-000J	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccUAGcuAuTT B	2228
R-008395224-000H	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuTT B	2228
R-008395224-000H	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGIuAGGAucAuccuGGUU	2233
R-008395161-000S	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcIAGGAucAuccuGGUU	2234
R-008395161-000S	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuTT B	2228
R-008395290-000V	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccuAGcuAuTT B	2228
R-008395290-000V	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuIGGAucAuccuGGUU	2235
R-008395273-000L	2398	151	CCAGGAUGAUCCUAGCUAU	B ccAGGAuGAuccUAGcuAuTT B	2228
R-008395273-000L	2398	151	CCAGGAUGAUCCUAGCUAU	AUAGcuAIGAucAuccuGGUU	2236
R-008395188-000M	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGcuAGGAucAuccUU	1845
R-008395188-000M	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccUAGcuAucGuTT B	2237
R-008395204-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	ICGAuAGcuAGGAucAuccUU	2238
R-008395204-000Y	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-003295202-000F	2401	196	GGAUGAUCCUAGCUAUCGU	AIGAuAGcuAGGAucAuccUU	2239
R-003295202-000F	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-008395158-000K	2401	196	GGAUGAUCCUAGCUAUCGU	ACIAuAGcuAGGAucAccUU	2240
R-008395158-000K	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-008395246-000K	2401	196	GGAUGAUCCUAGCUAUCGU	ACGIuAGcuAGGAucAuccUU	2241
R-008395246-000K	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-008395271-000U	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-008395271-000U	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAIAGcuAGGAucAuccUU	2242
R-008395200-000N	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAutGcuAGGAucAuccUU	2243
R-008395200-000N	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-008395288-000X	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-008395288-000X	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAIcuAGGAucAuccUU	2244
R-008395269-000W	2401	196	GGAUGAUCCUAGCUAUCGU	ACGAuAGIuAGGAucAuccUU	2245
R-008395269-000W	2401	196	GGAUGAUCCUAGCUAUCGU	B GGAuGAuccuAGcuAucGuTT B	2237
R-008397891-000B	1382	238	GAUCCAAGUCAACGUCUUG	B GAUCCAAGUCAACGUCUUGTT B	2246
R-008397891-000B	1382	238	GAUCCAAGUCAACGUCUUG	CAAGACGUUGACUUGGAUCUU	2247

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397894-000C	828	239	CUAUCAUGCGUUCUCCUCA	B CUAUCAUGCGUUCUCCUCATT B	2248
R-008397894-000C	828	239	CUAUCAUGCGUUCUCCUCA	UGAGGAGAACGCAUGAUAGUU	2249
R-008396925-000E	1244	240	AAUAUAAUGAGGACCUAUA	B AAUAUAAUGAGGACCUAUATT B	2250
R-008396925-000E	1244	240	AAUAUAAUGAGGACCUAUA	UAUAGGUCCUCAUUAUAUUUU	2251
R-008395941-000K	1304	241	GUGCUAUCUGUCUGCUCUA	B GUGCUAUCUGUCUGCUCUATT B	2252
R-008395941-000K	1304	241	GUGCUAUCUGUCUGCUCUA	UAGAGCAGACAGAUAGCACUU	2253
R-008395944-000L	812	242	GAAGCUUCCAGACACGCUA	B GAAGCUUCCAGACACGCUATT B	2254
R-008395944-000L	812	242	GAAGCUUCCAGACACGCUA	UAGCGUGUCUGGAAGCUUCUU	2255
R-008397498-000Y	1558	243	UAAUUAUAAGAACAAGAUG	B UAAUUAUAAGAACAAGAUGTT B	2256
R-008397498-000Y	1558	243	UAAUUAUAAGAACAAGAUG	CAUCUUGUUCUUAUAAUUAUU	2257
R-008397501-000R	879	244	AUACAAAUGAUGUAGAAAC	B AUACAAAUGAUGUAGAAACTT B	2258
R-008397501-000R	879	244	AUACAAAUGAUGUAGAAAC	GUUUCUACAUCAUUUGUAUUU	2259
R-008396451-000Y	1311	245	CUGUCUGCUCUAGUAAUAA	UUAUUACUAGAGCAGACAGUU	2261
R-008396451-000Y	1311	245	CUGUCUGCUCUAGUAAUAA	B CUGUCUGCUCUAGUAAUAATT B	2260
R-008397504-000S	856	246	UGCUAUUGUACGUACCAUG	B UGCUAUUGUACGUACCAUGTT B	2262
R-008397504-000S	856	246	UGCUAUUGUACGUACCAUG	CAUGGUACGUACAAUAGCAUU	2263
R-008396961-000P	1296	247	UGCUGAAGGUGCUAUCUGU	B UGCUGAAGGUGCUAUCUGUTT B	2264
R-008396961-000P	1296	247	UGCUGAAGGUGCUAUCUGU	ACAGAUAGCACCUUCAGCAUU	2265
R-008396967-000S	1235	39	GCUUUAGUAAAUAUAAUGA	B GCUUUAGUAAAUAUAAUGATT B	2266
R-008396967-000S	1235	39	GCUUUAGUAAAUAUAAUGA	UCAUUAUAUUUACUAAAGCUU	2267
R-008396463-000H	960	248	UCUUUAAGUCUGGAGGCAU	AUGCCUCCAGACUUAAAGAUU	2269
R-008396463-000H	960	248	UCUUUAAGUCUGGAGGCAU	B UCUUUAAGUCUGGAGGCAUTT B	2268
R-008398998-000S	2049	249	AUACCAUUCCAUUGUUUGU	BAUAUCCAUUCCAUUGUUUGUTT B	2270
R-008398998-000S	2049	249	AUACCAUUCCAUUGUUUGU	ACAAACAAUGGAAUGGUAUUU	2271
R-008398515-000M	1791	250	AGGCUACUGUUGGAUUGAU	AUCAAUCCAACAGUAGCCUUU	2273
R-008398515-000M	1791	250	AGGCUACUGUUGGAUUGAU	B AGGCUACUGUUGGAUUGAUTT B	2272
R-008395947-000M	783	251	CAGUUAUGGUCCAUCAGCU	B CAGUUAUGGUCCAUCAGCUTT B	2274
R-008395947-000M	783	251	CAGUUAUGGUCCAUCAGCU	AGCUGAUGGACCAUAACUGUU	2275
R-008396466-000J	159	252	ACAAGAUGAUGGUCUGCCA	B ACAAGAUGAUGGUCUGCCATT B	2276
R-008396466-000J	159	252	ACAAGAUGAUGGUCUGCCA	UGGCAGACCAUCAUCUUGUUU	2277
R-008396970-000Y	2224	253	GACAUAUGCAGCUGCUGUU	AACAGCAGCUGCAUAUGUCUU	2279
R-008396970-000Y	2224	253	GACAUAUGCAGCUGCUGUU	B GACAUAUGCAGCUGCUGUUTT B	2278
R-008395989-000Z	1882	123	GUUGCUUGUUCGUGCACAU	B GUUGCUUGUUCGUGCACAUTT B	2280
R-008395989-000Z	1882	123	GUUGCUUGUUCGUGCACAU	AUGUGCACGAACAAGCAACUU	2281
R-008398626-000Y	934	254	CCAUCAUCGUGAGGGCUUA	B CCAUCAUCGUGAGGGCUUATT B	2282
R-008398626-000Y	934	254	CCAUCAUCGUGAGGGCUUA	UAAGCCCUCACGAUGAUGGUU	2283

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396121-000S	1378	255	GACAGAUCCAAGUCAACGU	B GACAGAUCCAAGUCAACGU*TT* B	2284
R-008396121-000S	1378	255	GACAGAUCCAAGUCAACGU	ACGUUGACUUGGAUCUGUCUU	2285
R-008396001-000X	659	256	GAGACAUUAGAUGAGGGCA	UGCCCUCAUCUAAUGUCUCUU	2287
R-008396001-000X	659	256	GAGACAUUAGAUGAGGGCA	B GAGACAUUAGAUGAGGGCA*TT* B	2286
R-008396007-000Z	1722	257	UUCGCCUUCACUAUGGACU	B UUCGCCUUCACUAUGGACU*TT* B	2288
R-008396007-000Z	1722	257	UUCGCCUUCACUAUGGACU	AGUCCAUAGUGAAGGCGAAUU	2289
R-008396457-000T	1483	258	UGUUCAGCUUCUGGGUUCA	B UGUUCAGCUUCUGGGUUCA*TT* B	2290
R-008396457-000T	1483	258	UGUUCAGCUUCUGGGUUCA	UGAACCCAGAAGCUGAACAUU	2291
R-008399088-000F	2352	259	AUCUUGGACUUGAUAUUGG	CCAAUAUCAAGUCCAAGAUUU	2293
R-008399088-000F	2352	259	AUCUUGGACUUGAUAUUGG	B AUCUUGGACUUGAUAUUGG*TT* B	2292
R-008398596-000K	719	260	CGUGCAAUCCCUGAACUGA	B CGUGCAAUCCCUGAACUGA*TT* B	2294
R-008398596-000K	719	260	CGUGCAAUCCCUGAACUGA	UCAGUUCAGGGAUUGCACGUU	2295
R-008399094-000N	762	261	AGGUGGUGGUUAAUAAGGC	B AGGUGGUGGUUAAUAAGGC*TT* B	2296
R-008399094-000N	762	261	AGGUGGUGGUUAAUAAGGC	GCCUUAUUAACCACCACCUUU	2297
R-008397585-000P	599	262	UCUACACAGUUUGAUGCUG	B UCUACACAGUUUGAUGCUG*TT* B	2298
R-008397585-000P	599	262	UCUACACAGUUUGAUGCUG	CAGCAUCAAACUGUGUAGAUU	2299
R-008396073-000L	1704	263	AGAUGGCCCAGAAUGCAGU	B AGAUGGCCCAGAAUGCAGU*TT* B	2300
R-008396073-000L	1704	263	AGAUGGCCCAGAAUGCAGU	ACUGCAUUCUGGGCCAUCUUU	2301
R-008398599-000L	2270	264	CAAGAUUACAAGAAACGGC	GCCGUUUCUUGUAAUCUUGUU	2303
R-008398599-000L	2270	264	CAAGAUUACAAGAAACGGC	B CAAGAUUACAAGAAACGGC*TT* B	2302
R-008399532-000R	1810	103	UCGAAAUCUUGCCCUUUGU	ACAAAGGGCAAGAUUUCGAUU	2305
R-008399532-000R	1810	103	UCGAAAUCUUGCCCUUUGU	B UCGAAAUCUUGCCCUUUGU*TT* B	2304
R-008398602-000D	662	265	CUGAAACAUGCAGUUGUAA	B CUGAAACAUGCAGUUGUAA*TT* B	2306
R-008398602-000D	662	265	CUGAAACAUGCAGUUGUAA	UUACAACUGCAUGUUUCAGUU	2307
R-008399106-000J	396	266	CUCCUUCUCUGAGUGGUAA	UUACCACUCAGAGAAGGAGUU	2309
R-008399106-000J	396	266	CUCCUUCUCUGAGUGGUAA	B CUCCUUCUCUGAGUGGUAA*TT* B	2308
R-008398053-000R	1199	267	AGCAAGCUCAUCAUACUGG	CCAGUAUGAUGAGCUUGCUUU	2311
R-008398053-000R	1199	267	AGCAAGCUCAUCAUACUGG	B AGCAAGCUCAUCAUACUGG*TT* B	2310
R-008396583-000C	1560	268	AUUAUAAGAACAAGAUGAU	B AUUAUAAGAACAAGAUGAU*TT* B	2312
R-008396583-000C	1560	268	AUUAUAAGAACAAGAUGAU	AUCAUCUUGUUCUUAUAAUUU	2312
R-008399028-000B	593	92	AUCCCAUCUACACAGUUUG	CAAACUGUGUAGAUGGGAUUU	2315
R-008399028-000B	593	92	AUCCCAUCUACACAGUUUG	B AUCCCAUCUACACAGUUUG*TT* B	2314
R-008398104-000X	1310	269	UCUGUCUGCUCUAGUAAUA	B UCUGUCUGCUCUAGUAAUA*TT* B	2316
R-008398104-000X	1310	269	UCUGUCUGCUCUAGUAAUA	UAUUACUAGAGCAGACAGAUU	2317
R-008398113-000F	1233	270	AAGCUUUAGUAAAUAUAAU	B AAGCUUUAGUAAAUAUAAU*TT* B	2318
R-008398113-000F	1233	270	AAGCUUUAGUAAAUAUAAU	AUUAUAUUUACUAAAGCUUUU	2319
R-008399622-000H	1330	271	GCCGGCUAUUGUAGAAGCU	B GCCGGCUAUUGUAGAAGCU*TT* B	2320

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399622-000H	1330	271	GCCGGCUAUUGUAGAAGCU	AGCUUCUACAAUAGCCGGCUU	2321
R-008399151-000C	1312	272	UGUCUGCUCUAGUAAUAAG	B UGUCUGCUCUAGUAAUAAGTT B	2322
R-008399151-000C	1312	272	UGUCUGCUCUAGUAAUAAG	CUUAUUACUAGAGCAGACAUU	2323
R-008396127-000U	1556	273	AAUAAUUAUAAGAACAAGA	UCUUGUUCUUAUAAUUAUUUU	2325
R-008396127-000U	1556	273	AAUAAUUAUAAGAACAAGA	B AAUAAUUAUAAGAACAAGATT B	2324
R-008395707-000Y	2438	274	UAUGGCCAGGAUGCCUUGG	B UAUGGCCAGGAUGCCUUGGTT B	2326
R-008395707-000Y	2438	274	UAUGGCCAGGAUGCCUUGG	CCAAGGCAUCCUGGCCAUAUU	2327
R-008395710-000E	1826	275	UGUCCCGCAAAUCAUGCAC	GUGCAUGAUUUGCGGGACAUU	2329
R-008395710-000E	1826	275	UGUCCCGCAAAUCAUGCAC	B UGUCCCGCAAAUCAUGCACTT B	2328
R-008395713-000F	1397	276	CUUGUUCAGAACUGUCUUU	B CUUGUUCAGAACUGUCUUUTT B	2330
R-008395713-000F	1397	276	CUUGUUCAGAACUGUCUUU	AAAGACAGUUCUGAACAAGUU	2331
R-008395716-000G	3181	277	GCUGUGAUACGAUGCUUCA	UGAAGCAUCGUAUCACAGCUU	2333
R-008395716-000G	3181	277	GCUGUGAUACGAUGCUUCA	B GCUGUGAUACGAUGCUUCATT B	2332
R-008395719-000H	1912	278	GCGCCGUACGUCCAUGGGU	B GCGCCGUACGUCCAUGGGUTT B	2334
R-008395719-000H	1912	278	GCGCCGUACGUCCAUGGGU	ACCCAUGGACGUACGGCGCUU	2335
R-008395722-000P	846	279	AGAUGGUGUCUGCUAUUGU	B AGAUGGUGUCUGCUAUUGUTT B	2336
R-008395722-000P	846	279	AGAUGGUGUCUGCUAUUGU	ACAAUAGCAGACACCAUCUUU	2337
R-008395725-000R	1404	280	AGAACUGUCUUUGGACUCU	B AGAACUGUCUUUGGACUCUTT B	2338
R-008395725-000R	1404	280	AGAACUGUCUUUGGACUCU	AGAGUCCAAAGACAGUUCUUU	2339
R-008395728-000S	586	281	CAUGCAGAUCCCAUCUACA	UGUAGAUGGGAUCUGCAUGUU	2341
R-008395728-000S	586	281	CAUGCAGAUCCCAUCUACA	B CAUGCAGAUCCCAUCUACATT B	2340
R-008395731-000Y	1469	282	CUCCUUGGGACUCUUGUUC	GAACAAGAGUCCCAAGGAGUU	2343
R-008395731-000Y	1469	282	CUCCUUGGGACUCUUGUUC	B CUCCUUGGGACUCUUGUUCTT B	2342
R-008395734-000Z	380	283	GGUGCCACUACCACAGCUC	B GGUGCCACUACCACAGCUCTT B	2344
R-008395734-000Z	380	283	GGUGCCACUACCACAGCUC	GAGCUGUGGUAGUGGCACCUU	2345
R-008395737-000A	1345	284	AGCUGGUGGAAUGCAAGCU	B AGCUGGUGGAAUGCAAGCUTT B	2346
R-008395737-000A	1345	284	AGCUGGUGGAAUGCAAGCU	AGCUUGCAUUCCACCAGCUUU	2347
R-008395740-000G	1863	285	CCAUUCCACGACUAGUUCA	B CCAUUCCACGACUAGUUCATT B	2348
R-008395740-000G	1863	285	CCAUUCCACGACUAGUUCA	UGAACUAGUCGUGGAAUGGUU	2349
R-008395743-000H	635	286	CAGCGUUUGGCUGAACCAU	AUGGUUCAGCCAAACGCUGUU	2351
R-008395743-000H	635	286	CAGCGUUUGGCUGAACCAU	B CAGCGUUUGGCUGAACCAUTT B	2350
R-008395746-000J	959	287	AUCUUUAAGUCUGGAGGCA	UGCCUCCAGACUUAAAGAUUU	2353
R-008395746-000J	959	287	AUCUUUAAGUCUGGAGGCA	B AUCUUUAAGUCUGGAGGCATT B	2352
R-008395749-000K	2440	288	UGGCCAGGAUGCCUUGGGU	B UGGCCAGGAUGCCUUGGGUTT B	2354
R-008395749-000K	2440	288	UGGCCAGGAUGCCUUGGGU	ACCCAAGGCAUCCUGGCCAUU	2355
R-008395752-000S	877	289	GAAUACAAAUGAUGUAGAA	UUCUACAUCAUUUGUAUUCUU	2357

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008395752-000S	877	289	GAAUACAAAUGAUGUAGAA	B GAAUACAAAUGAUGUAGAA*TT* B	2356
R-008395755-000T	2556	290	UGGAUGGGCUGCCUCCAGG	CCUGGAGGCAGCCCAUCCA<u>UU</u>	2359
R-008395755-000T	2556	290	UGGAUGGGCUGCCUCCAGG	B UGGAUGGGCUGCCUCCAG*TT* B	2358
R-008395758-000U	1916	291	CGUACGUCCAUGGGUGGGA	B CGUACGUCCAUGGGUGGGA*TT* B	2360
R-008395758-000U	1916	291	CGUACGUCCAUGGGUGGGA	UCCCACCCAUGGACGUACG<u>UU</u>	2361
R-008395761-000A	850	292	GGUGUCUGCUAUUGUACGU	B GGUGUCUGCUAUUGUACG*TT* B	2362
R-008395761-000A	850	292	GGUGUCUGCUAUUGUACGU	ACGUACAAUAGCAGACACC<u>UU</u>	2363
R-008395764-000B	1303	293	GGUGCUAUCUGUCUGCUCU	B GGUGCUAUCUGUCUGCUC*TT* B	2364
R-008395764-000B	1303	293	GGUGCUAUCUGUCUGCUCU	AGAGCAGACAGAUAGCACC<u>UU</u>	2365
R-008395767-000C	1726	294	CCUUCACUAUGGACUACCA	UGGUAGUCCAUAGUGAAGG<u>UU</u>	2367
R-008395767-000C	1726	294	CCUUCACUAUGGACUACCA	B CCUUCACAUAUGGACUACCA*TT* B	2366
R-008395770-000J	1477	295	GACUCUUGUUCAGCUUCUG	CAGAAGCUGAACAAGAGUC<u>UU</u>	2369
R-008395770-000J	1477	295	GACUCUUGUUCAGCUUCUG	B GACUCUUGUUCAGCUUCUG*TT* B	2368
R-008395773-000K	598	296	AUCUACACAGUUUGAUGCU	B AUCUACACAGUUUGAUGCU*TT* B	2370
R-008395773-000K	598	296	AUCUACACAGUUUGAUGCU	AGCAUCAAACUGUGUAGAU<u>UU</u>	2371
R-008395776-000L	2062	297	GUUUGUGCAGCUGCUUUAU	B GUUUGUGCAGCUGCUUUAU*TT* B	2372
R-008395776-000L	2062	297	GUUUGUGCAGCUGCUUUAU	AUAAAGCAGCUGCACAAAC<u>UU</u>	2373
R-008395779-000M	2278	298	CAAGAAACGGCUUUCAGUU	B CAAGAAACGGCUUUCAGU*TT* B	2374
R-008395779-000M	2278	298	CAAGAAACGGCUUUCAGUU	AACUGAAAGCCGUUUCUUG<u>UU</u>	2375
R-008395782-000U	1877	299	GUUCAGUUGCUUGUUCGUG	CACGAACAAGCAACUGAAC<u>UU</u>	2377
R-008395782-000U	1877	299	GUUCAGUUGCUUGUUCGUG	B GUUCAGUUGCUUGUUCGUG*TT* B	2376
R-008395785-000V	1499	300	UCAGAUGAUAUAAAUGUGG	B UCAGAUGAUAUAAAUGUGG*TT* B	2378
R-008395785-000V	1499	300	UCAGAUGAUAUAAAUGUGG	CCACAUUUAUAUCAUCUGA<u>UU</u>	2379
R-008395788-000W	1136	301	AAUGUUAAAUUCUUGGCUA	B AAUGUUAAAUUCUUGGCUA*TT* B	2380
R-008395788-000W	1136	301	AAUGUUAAAUUCUUGGCUA	UAGCCAAGAAUUUAACAUU<u>UU</u>	2381
R-008395791-000C	1494	302	UGGGUUCAGAUGAUAUAAA	UUUAUAUCAUCUGAACCCA<u>UU</u>	2383
R-008395791-000C	1494	302	UGGGUUCAGAUGAUAUAAA	B UGGGUUCAGAUGAUAUAAA*TT* B	2382
R-008395794-000D	1972	303	AAUAGUUGAAGGUUGUACC	B AAUAGUUGAAGGUUGUACC*TT* B	2384
R-008395794-000D	1972	303	AAUAGUUGAAGGUUGUACC	GGUACAACCUUCAACUAUU<u>UU</u>	2384
R-008395797-000E	668	304	CAUGCAGUUGUAAACUUGA	UCAAGUUUACAACUGCAUG<u>UU</u>	2387
R-008395797-000E	668	304	CAUGCAGUUGUAAACUUGA	B CAUGCAGUUGUAAACUUGA*TT* B	2386
R-008395800-000X	2945	305	AAUCUGAAUAAAGUGUAAC	GUUACACUUUAUUCAGAUU<u>UU</u>	2389
R-008395800-000X	2945	305	AAUCUGAAUAAAGUGUAAC	B AAUCUGAAUAAAGUGUAAC*TT* B	2388
R-008395803-000Y	2492	306	CACCACCCUGGUGCUGACU	B CACCACCCUGGUGCUGACU*TT* B	2390
R-008395803-000Y	2492	306	CACCACCCUGGUGCUGACU	AGUCAGCACCAGGGUGGUG<u>UU</u>	2391
R-00839580600000Z	293	307	GAGUUGGACAUGGCCAUGG	B GAGUUGGACAUGGCCAUGG*TT* B	2392
R-00839580600000Z	293	307	GAGUUGGACAUGGCCAUGG	CCAUGGCCAUGUCCAACUC<u>UU</u>	2393

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008395809-000A	1905	308	AUACCCAGCGCCGUACGUC	B AUACCCAGCGCCGUACGUCTT B	2394
R-008395809-000A	1905	308	AUACCCAGCGCCGUACGUC	GACGUACGGCGCUGGGUAUUU	2395
R-008395812-000G	944	309	GAGGGCUUACUGGCCAUCU	AGAUGGCCAGUAAGCCCUCUU	2397
R-008395812-000G	944	309	GAGGGCUUACUGGCCAUCU	B GAGGGCUUACUGGCCAUCUTT B	2396
R-008395815-000H	581	310	GAGGGCAUGCAGAUCCCAU	B GAGGGCAUGCAGAUCCCAUTT B	2398
R-008395815-000H	581	310	GAGGGCAUGCAGAUCCCAU	AUGGGAUCUGCAUGCCCUCUU	2399
R-008395818-000J	1454	311	GAAGGGAUGGAAGGUCUCC	B GAAGGGAUGGAAGGUCUCCTT B	2400
R-008395818-000J	1454	311	GAAGGGAUGGAAGGUCUCC	GGAGACCUUCCAUCCCUUCUU	2401
R-008395821-000R	2254	312	GUCUGAGGACAAGCCACAA	B GUCUGAGGACAAGCCACAATT B	2402
R-008395821-000R	2254	312	GUCUGAGGACAAGCCACAA	UUGUGGCUUGUCCUCAGACUU	2403
R-008395824-000S	1837	313	UCAUGCACCUUUGCGUGAG	CUCACGCAAAGGUGCAUGAUU	2405
R-008395824-000S	1837	313	UCAUGCACCUUUGCGUGAG	B UCAUGCACCUUUGCGUGAGTT B	2404
R-008395827-000T	1425	314	GGAAUCUUUCAGAUGCUGC	B GGAAUCUUUCAGAUGCUGCTT B	2406
R-008395827-000T	1425	314	GGAAUCUUUCAGAUGCUGC	GCAGCAUCUGAAAGAUUCCUU	2407
R-008395830-000Z	1372	315	UCACCUGACAGAUCCAAGU	ACUUGGAUCUGUCAGGUGAUU	2409
R-008395830-000Z	1372	315	UCACCUGACAGAUCCAAGU	B UCACCUGACAGAUCCAAGUTT B	2408
R-008395833-000A	1298	316	CUGAAGGUGCUAUCUGUCU	B CUGAAGGUGCUAUCUGUCUTT B	2410
R-008395833-000A	1298	316	CUGAAGGUGCUAUCUGUCU	AGACAGAUAGCACCUUCAGUU	2411
R-008395836-000B	1674	317	GUCAUCUGACCAGCCGACA	B GUCAUCUGACCAGCCGACATT B	2412
R-008395836-000B	1674	317	GUCAUCUGACCAGCCGACA	UGUCGGCUGGUCAGAUGACUU	2413
R-008395839-000C	1864	318	CAUUCCACGACUAGUUCAG	CUGAACUAGUCGUGGAAUGUU	2415
R-008395839-000C	1864	318	CAUUCCACGACUAGUUCAG	B CAUUCCACGACUAGUUCAGTT B	2414
R-008395842-000J	2404	319	UGAUCCUAGCUAUCGUUCU	AGAACGAUAGCUAGGAUCAUU	2417
R-008395842-000J	2404	319	UGAUCCUAGCUAUCGUUCU	B UGAUCCUAGCUAUCGUUCUTT B	2416
R-008395845-000K	1992	320	GAGCCCUUCACAUCCUAGC	GCUAGGAUGUGAAGGGCUCUU	2419
R-008395845-000K	1992	320	GAGCCCUUCACAUCCUAGC	B GAGCCCUUCACAUCCUAGCTT B	2418
R-008395848-000L	2124	73	GUGAACUUGCUCAGGACAA	UUGUCCUGAGCAAGUUCACUU	2421
R-008395848-000L	2124	73	GUGAACUUGCUCAGGACAA	B GUGAACUUGCUCAGGACAATT B	2420
R-008395851-000T	578	321	GAUGAGGGCAUGCAGAUCC	GGAUCUGCAUGCCCUCAUCUU	2423
R-008395851-000T	578	321	GAUGAGGGCAUGCAGAUCC	B GAUGAGGGCAUGCAGAUCCTT B	2422
R-008395854-000U	3091	322	AUGGGUAGGGUAAAUCAGU	B AUGGGUAGGGUAAAUCAGUTT B	2424
R-008395854-000U	3091	322	AUGGGUAGGGUAAAUCAGU	ACUGAUUUACCCUACCCAUUU	2425
R-008395857-000V	720	323	GUGCAAUCCCUGAACUGAC	B GUGCAAUCCCUGAACUGACTT B	2426
R-008395857-000V	720	323	GUGCAAUCCCUGAACUGAC	GUCAGUUCAGGGAUUGCACUU	2427
R-008395860-000B	2054	324	AUUCCAUUGUUUGUGCAGC	B AUUCCAUUGUUUGUGCAGCTT B	2428
R-008395860-000B	2054	324	AUUCCAUUGUUUGUGCAGC	GCUGCACAAACAAUGGAAUUU	2429

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008395863-000C	1237	42	UUUAGUAAAUAUAAUGAGG	CCUCAUUAUAUUUACUAAAUU	2431
R-008395863-000C	1237	42	UUUAGUAAAUAUAAUGAGG	B UUUAGUAAAUAUAAUGAGGTT B	2430
R-008395866-000D	374	325	CAUUCUGGUGCCACUACCA	UGGUAGUGGCACCAGAAUGUU	2433
R-008395866-000D	374	325	CAUUCUGGUGCCACUACCA	B CAUUCUGGUGCCACUACCATT B	2432
R-008395869-000E	868	326	UACCAUGCAGAAUACAAAU	AUUUGUAUUCUGCAUGGUAUU	2435
R-008395869-000E	868	326	UACCAUGCAGAAUACAAAU	B UACCAUGCAGAAUACAAAUTT B	2434
R-008395872-000L	626	23	ACUAAUGUCCAGCGUUUGG	CCAAACGCUGGACAUUAGUUU	2437
R-008395872-000L	626	23	ACUAAUGUCCAGCGUUUGG	B ACUAAUGUCCAGCGUUUGGTT B	2436
R-008395875-000M	1716	327	AUGCAGUUCGCCUUCACUA	B AUGCAGUUCGCCUUCACUATT B	2438
R-008395875-000M	1716	327	AUGCAGUUCGCCUUCACUA	UAGUGAAGGCGAACUGCAUUU	2439
R-008395878-000N	950	328	UUACUGGCCAUCUUUAAGU	B UUACUGGCCAUCUUUAAGUTT B	2440
R-008395878-000N	950	328	UUACUGGCCAUCUUUAAGU	ACUUAAAGAUGGCCAGUAAUU	2441
R-008395881-000V	1489	329	GCUUCUGGGUUCAGAUGAU	B GCUUCUGGGUUUCAGAUGAUTT B	2442
R-008395881-000V	1489	329	GCUUCUGGGUUCAGAUGAU	AUCAUCUGAACCCAGAAGCUU	2443
R-008395884-000W	1451	330	CAGGAAGGGAUGGAAGGUC	B CAGGAAGGGAUGGAAGGUCTT B	2444
R-008395884-000W	1451	330	CAGGAAGGGAUGGAAGGUC	GACCUUCCAUCCCUUCCUGUU	2445
R-008395887-000X	438	159	UGGAUACCUCCCAAGUCCU	AGGACUUGGGAGGUAUCCAUU	2447
R-008395887-000X	438	159	UGGAUACCUCCCAAGUCCU	B UGGAUACCUCCCAAGUCCUTT B	2446
R-008395890-000D	1181	331	GCUUAUGGCAACCAAGAAA	UUUCUUGGUUGCCAUAAGCUU	2449
R-008395890-000D	1181	331	GCUUAUGGCAACCAAGAAA	B GCUUAUGGCAACCAAGAAATT B	2448
R-008395893-0003	1633	332	UGACAGGGAAGACAUCACU	AGUGAUGUCUUCCCUGUCAUU	2451
R-008395893-0003	1633	332	UGACAGGGAAGACAUCACU	B UGACAGGGAAGACAUCACUTT B	2450
R-008395896-000F	2394	333	AUCGCCAGGAUGAUCCUAG	CUAGGAUCAUCCUGGCGAUUU	2453
R-008395896-000F	2394	333	AUCGCCAGGAUGAUCCUAG	B AUCGCCAGGAUGAUCCAUGTT B	2452
R-008395899-000G	1322	334	AGUAAUAAGCCGGCUAUUG	B AGUAAUAAGCCGGCUAUUGTT B	2454
R-008395899-000G	1322	334	AGUAAUAAGCCGGCUAUUG	CAAUAGCCGGCUUAUUACUUU	2455
R-008395902-000Z	884	335	AAUGAUGUAGAAACAGCUC	GAGCUGUUUCUACAUCAUUUU	2457
R-008395902-000Z	884	335	AAUGAUGUAGAAACAGCUC	B AAUGAUGUAGAAACAGCUCTT B	2456
R-008395905-000A	2255	336	UCUGAGGACAAGCCACAAG	B UCUGAGGACAAGCCACAAGTT B	2458
R-008395905-000A	2255	336	UCUGAGGACAAGCCACAAG	CUUGUGGCUUGUCCUCAGAUU	2459
R-008395908-000B	1466	337	GGUCUCCUUGGGACUCUUG	CAAGAGUCCCAAGGAGACCUU	2461
R-008395908-000B	1466	337	GGUCUCCUUGGGACUCUUG	B GGUCUCCUUGGGACUCUUGTT B	2460
R-008395911-000H	1399	338	UGUUCAGAACUGUCUUUGG	CCAAAGACAGUUCUGAACAUU	2463
R-008395911-000H	1399	338	UGUUCAGAACUGUCUUUGG	B UGUUCAGAACUGUCUUUGGTT B	2462
R-008395914-000J	378	339	CUGGUGCCACUACCACAGC	B CUGGUGCCACUACCACAGCTT B	2464
R-008395914-000J	378	339	CUGGUGCCACUACCACAGC	GCUGUGGUAGUGGCACCAGUU	2465
R-008395917-000K	1921	340	GUCCAUGGGUGGGACACAG	CUGUGUCCCACCCAUGGACUU	2467

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008395917-000K	1921	340	GUCCAUGGGUGGGACACAG	B GUCCAUGGGUGGGACACAGTT B	2466
R-008395920-000S	1085	341	GUGCGUUUAGCUGGUGGGC	B GUGCGUUUAGCUGGUGGGCTT B	2468
R-008395920-000S	1085	341	GUGCGUUUAGCUGGUGGGC	GCCCACCAGCUAAACGCACUU	2469
R-008395923-000T	865	342	ACGUACCAUGCAGAAUACA	B ACGUACCAUGCAGAAUACATT B	2470
R-008395923-000T	865	342	ACGUACCAUGCAGAAUACA	UGUAUUCUGCAUGGUACGUUU	2471
R-008395926-000U	2015	343	GAUGUUCACAACCGAAUUG	B GAUGUUCACAACCGAAUUGTT B	2472
R-008395926-000U	2015	343	GAUGUUCACAACCGAAUUG	CAAUUCGGUUGUGAACAUCUU	2473
R-008395929-000V	1195	344	AGAAAGCAAGCUCAUCAUA	B AGAAAGCAAGCUCAUCAUATT B	2474
R-008395929-000V	1195	344	AGAAAGCAAGCUCAUCAUA	UAUGAUGAGCUUGCUUUCUUU	2475
R-008395932-000B	1484	345	GUUCAGCUUCUGGGUUCAG	CUGAACCCAGAAGCUGAACUU	2477
R-008395932-000B	1484	345	GUUCAGCUUCUGGGUUCAG	B GUUCAGCUUCUGGGUUCAGTT B	2476
R-008395935-000C	1855	346	GCAGGGUGCCAUUCCACGA	B GCAGGGUGCCAUUCCACGATT B	2478
R-008395935-000C	1855	346	GCAGGGUGCCAUUCCACGA	UCGUGGAAUGGCACCCUGCUU	2479
R-008395938-000D	1341	347	UAGAAGCUGGUGGAAUGCA	B UAGAAGCUGGUGGAAUGCATT B	2480
R-008395938-000D	1341	347	UAGAAGCUGGUGGAAUGCA	UGCAUUCCACCAGCUUCUAUU	2481
R-008395950-000U	1963	348	CAUGGAAGAAAUAGUUGAA	UUCAACUAUUUCUUCCAUGUU	2483
R-008395950-000U	1963	348	CAUGGAAGAAAUAGUUGAA	B CAUGGAAGAAAUAGUUGAATT B	2482
R-008395953-000V	2362	349	UGAUAUUGGUGCCCAGGGA	B UGAUAUUGGUGCCCAGGGATT B	2484
R-008395953-000V	2362	349	UGAUAUUGGUGCCCAGGGA	UCCCUGGGCACCAAUAUCAUU	2485
R-008395956-000W	584	350	GGCAUGCAGAUCCCAUCUA	B GGCAUGCAGAUCCCAUCUATT B	2486
R-008395956-000W	584	350	GGCAUGCAGAUCCCAUCUA	UAGAUGGGAUCUGCAUGCCUU	2487
R-008395959-000X	1613	351	CGUACUGUCCUUCGGGCUG	B CGUACUGUCCUUCGGGCUGTT B	2488
R-008395959-000X	1613	351	CGUACUGUCCUUCGGGCUG	CAGCCCGAAGGACAGUACGUU	2489
R-008395962-000D	1155	352	UUACGACAGACUGCCUUCA	UGAAGGCAGUCUGUCGUAAUU	2491
R-008395962-000D	1155	352	UUACGACAGACUGCCUUCA	B UUACGACAGACUGCCUUCATT B	2490
R-008395965-000E	334	353	UAGUCACUGGCAGCAACAG	B UAGUCACUGGCAGCAACAGTT B	2492
R-008395965-000E	334	353	UAGUCACUGGCAGCAACAG	CUGUUGCUGCCAGUGACUAUU	2493
R-008395968-000F	1031	354	GCCAUUACAACUCUCCACA	B GCCAUUACAACUCUCCACATT B	2494
R-008395968-000F	1031	354	GCCAUUACAACUCUCCACA	UGUGGAGAGUUGUAAUGGCUU	2495
R-008395971-000M	1725	355	GCCUUCACUAUGGACUACC	B GCCUUCACUAUGGACUACCTT B	2496
R-008395971-000M	1725	355	GCCUUCACUAUGGACUACC	GGUAGUCCAUAGUGAAGGCUU	2497
R-008395974-000N	2018	356	GUUCACAACCGAAUUGUUA	B GUUCACAACCGAAUUGUUATT B	2498
R-008395974-000N	2018	356	GUUCACAACCGAAUUGUUA	UAACAAUUCGGUUGUGAACUU	2499
R-008395977-000P	914	357	GGGACCUUGCAUAACCUUU	AAAGGUUAUGCAAGGUCCCUU	2501
R-008395977-000P	914	357	GGGACCUUGCAUAACCUUU	B GGGACCUUGCAUAACCUUUTT B	2500
R-008395980-000W	2264	358	AAGCCACAAGAUUACAAGA	B AAGCCACAAGAUUACAAGATT B	2502

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008395980-000W	2264	358	AAGCCACAAGAUUACAAGA	UCUUGUAAUCUUGUGGCUUUU	2503
R-008395983-000X	343	359	GCAGCAACAGUCUUACCUG	CAGGUAAGACUGUUGCUGCUU	2505
R-008395983-000X	343	359	GCAGCAACAGUCUUACCUG	B GCAGCAACAGUCUUACCUGTT B	2504
R-008395986-000Y	1056	360	UAUUACAUCAAGAAGGAGC	B UAUUACAUCAAGAAGGAGCTT B	2506
R-008395986-000Y	1056	360	UAUUACAUCAAGAAGGAGC	GCUCCUUCUUGAUGUAAUAUU	2507
R-008395992-000F	772	361	UAAUAAGGCUGCAGUUAUG	B UAAUAAGGCUGCAGUUAUGTT B	2508
R-008395992-000F	772	361	UAAUAAGGCUGCAGUUAUG	CAUAACUGCAGCCUUAUUAUU	2509
R-008395995-000G	1390	91	UCAACGUCUUGUUCAGAAC	GUUCUGAACAAGACGUUGAUU	2511
R-008395995-000G	1390	91	UCAACGUCUUGUUCAGAAC	B UCAACGUCUUGUUCAGAACTT B	2510
R-008395998-000H	1959	183	UCCGCAUGGAAGAAAUAGU	ACUAUUUCUUCCAUGCGGAUU	2513
R-008395998-000H	1959	183	UCCGCAUGGAAGAAAUAGU	B UCCGCAUGGAAGAAAUAGUTT B	2512
R-008396004-000Y	763	362	GGUGGUGGUUAAUAAGGCU	B GGUGGUGGUUAAUAAGGCUTT B	2514
R-008396004-000Y	763	362	GGUGGUGGUUAAUAAGGCU	AGCCUUAUUAACCACCACCUU	2515
R-008396010-000F	628	363	UAAUGUCCAGCGUUUGGCU	B UAAUGUCCAGCGUUUGGCUTT B	2516
R-008396010-000F	628	363	UAAUGUCCAGCGUUUGGCU	AGCCAAACGCUGGACAUUAUU	2517
R-008396013-000G	399	364	CUUCUCUGAGUGGUAAAGG	G CUUCUCUGAGUGGUAAAGGTT B	2518
R-008396013-000G	399	364	CUUCUCUGAGUGGUAAAGG	CCUUUACCACUCAGAGAAGUU	2519
R-008396016-000H	1682	365	ACCAGCCGACACCAAGAAG	CUUCUUGGUGUCGGCUGGUUU	2521
R-008396016-000H	1682	365	ACCAGCCGACACCAAGAAG	B ACCAGCCGACACCAAGAAGTT B	2520
R-008396019-000J	441	366	AUACCUCCCAAGUCCUGUA	B AUACCUCCCAAGUCCUGUATT B	2522
R-008396019-000J	441	366	AUACCUCCCAAGUCCUGUA	UACAGGACUUGGGAGGUAUUU	2523
R-008396022-000R	1729	367	UCACUAUGGACUACCAGUU	B UCACUAUGGACUACCAGUUTT B	2524
R-008396022-000R	1729	367	UCACUAUGGACUACCAGUU	AACUGGUAGUCCAUAGUGAUU	2525
R-008396025-000S	1902	368	AGGAUACCCAGCGCCGUAC	GUACGGCGCUGGGUAUCCUUU	2527
R-008396025-000S	1902	368	AGGAUACCCAGCGCCGUAC	B AGGAUACCCAGCGCCGUACTT B	2526
R-008396028-000T	1637	369	AGGGAAGACAUCACUGAGC	B AGGGAAGACAUCACUGAGCTT B	2528
R-008396028-000T	1637	369	AGGGAAGACAUCACUGAGC	GCUCAGUGAUGUCUUCCCUUU	2529
R-008396031-000Z	2391	370	GAUAUCGCCAGGAUGAUCC	B GAUAUCGCCAGGAUGAUCCTT B	2530
R-008396031-000Z	2391	370	GAUAUCGCCAGGAUGAUCC	GGAUCAUCCUGGCGAUAUCUU	2531
R-008396034-000A	501	371	AAGUAGCUGAUAUUGAUGG	B AAGUAGCUGAUAUUGAUGGTT B	2532
R-008396034-000A	501	371	AAGUAGCUGAUAUUGAUGG	CCAUCAAUAUCAGCUACUUUU	2533
R-008396037-000B	1358	372	CAAGCUUUAGGACUUCACC	B CAAGCUUUAGGACUUCACCTT B	2534
R-008396037-000B	1358	372	CAAGCUUUAGGACUUCACC	GGUGAAGUCCUAAAGCUUGUU	2535
R-008396040-000H	1821	373	CCCUUUGUCCCGCAAAUCA	B CCCUUUGUCCCGCAAAUCATT B	2536
R-008396040-000H	1821	373	CCCUUUGUCCCGCAAAUCA	UGAUUUGCGGGACAAAGGGUU	2537
R-008396043-000J	575	374	UUAGAUGAGGGCAUGCAGA	B UUAGAUGAGGGCAUGCAGATT B	2538
R-008396043-000J	575	374	UUAGAUGAGGGCAUGCAGA	UCUGCAUGCCCUCAUCUAAUU	2539

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396046-000K	528	375	CAAUGACUCGAGCUCAGAG	B CAAUGACUCGAGCUCAGAGTT B	2540
R-008396046-000K	528	375	CAAUGACUCGAGCUCAGAG	CUCUGAGCUCGAGUCAUUGUU	2541
R-008396049-000L	2433	376	GUGGAUAUGGCCAGGAUGC	B GUGGAUAUGGCCAGGAUGCTT B	2542
R-008396049-000L	2433	376	GUGGAUAUGGCCAGGAUGC	GCAUCCUGGCCAUAUCCACUU	2543
R-008396052-000T	1497	377	GUUCAGAUGAUAUAAAUGU	ACAUUUAUAUCAUCUGAACUU	2545
R-008396052-000T	1497	377	GUUCAGAUGAUAUAAAUGU	B GUUCAGAUGAUAUAAAUGUTT B	2544
R-008396055-000U	2134	378	UCAGGACAAGGAAGCUGCA	B UCAGGACAAGGAAGCUGCATT B	2546
R-008396055-000U	2134	378	UCAGGACAAGGAAGCUGCA	UGCAGCUUCCUUGUCCUGAUU	2547
R-008396058-000V	2160	379	UUGAAGCUGAGGGAGCCAC	GUGGCUCCCUCAGCUUCAAUU	2549
R-008396058-000V	2160	379	UUGAAGCUGAGGGAGCCAC	B UUGAAGCUGAGGGAGCCACTT B	2548
R-008396061-000B	291	380	UGGAGUUGGACAUGGCCAU	AUGGCCAUGUCCAACUCCAUU	2551
R-008396061-000B	291	380	UGGAGUUGGACAUGGCCAU	B UGGAGUUGGACAUGGCCAUTT B	2550
R-008396064-000C	657	381	AGAUGCUGAAACAUGCAGU	B AGAUGCUGAAACAUGCAGUTT B	2552
R-008396064-000C	657	381	AGAUGCUGAAACAUGCAGU	ACUGCAUGUUUCAGCAUCUUU	2553
R-008396067-000D	1575	382	UGAUGGUCUGCCAAGUGGG	B UGAUGGUCUGCCAAGUGGGTT B	2554
R-008396067-000D	1575	382	UGAUGGUCUGCCAAGUGGG	CCCACUUGGCAGACCAUCAUU	2555
R-008396070-000K	667	383	ACAUGCAGUUGUAAACUUG	CAAGUUUACAACUGCAUGUUU	2557
R-008396070-000K	667	383	ACAUGCAGUUGUAAACUUG	B ACAUGCAGUUGUAAACUUGTT B	2556
R-008396076-000M	2190	384	CAGAGUUACUUCACUCUAG	B CAGAGUUACUUCACUCUAGTT B	2558
R-008396076-000M	2190	384	CAGAGUUACUUCACUCUAG	CUAGAGUGAAGUAACUCUGUU	2559
R-008396079-000N	532	385	GACUCGAGCUCAGAGGGUA	UACCCUCUGAGCUCGAGUCUU	2561
R-008396079-000N	532	385	GACUCGAGCUCAGAGGGUA	B GACUCGAGCUCAGAGGGUATT B	2560
R-008396082-000V	953	386	CUGGCCAUCUUUAAGUCUG	CAGACUUAAAGAUGGCCAGUU	2563
R-008396082-000V	953	386	CUGGCCAUCUUUAAGUCUG	B CUGGCCAUCUUUAAGUCUGTT B	2562
R-008396085-000W	3188	387	UACGAUGCUUCAAGAGAAA	UUUCUCUUGAAGCAUCGUAUU	2565
R-008396085-000W	3188	387	UACGAUGCUUCAAGAGAAA	B UACGAUGCUUCAAGAGAAATT B	2564
R-008396088-000X	2301	388	UGACCAGCUCUCUCUUCAG	B UGACCAGCUCUCUCUUCAGTT B	2566
R-008396088-000X	2301	388	UGACCAGCUCUCUCUUCAG	CUGAAGAGAGAGCUGGUCAUU	2567
R-008396091-000D	2310	389	CUCUCUUCAGAACAGAGCC	B CUCUCUUCAGAACAGAGCCTT B	2568
R-008396091-000D	2310	389	CUCUCUUCAGAACAGAGCC	GGCUCUGUUCUGAAGAGAGUU	2569
R-008396094-000E	2287	390	GCUUUCAGUUGAGCUGACC	B GCUUUCAGUUGAGCUGACCTT B	2570
R-008396094-000E	2287	390	GCUUUCAGUUGAGCUGACC	GGUCAGCUCAACUGAAAGCUU	2571
R-008396097-000F	1927	391	GGGUGGGACACAGCAGCAA	UUGCUGCUGUGUCCCACCCUU	2573
R-008396097-000F	1927	391	GGGUGGGACACAGCAGCAA	B GGGUGGGACACAGCAGCAATT B	2572
R-008396100-000Y	712	392	UGCCACACGUGCAAUCCCU	AGGGAUUGCACGUGUGGCAUU	2575
R-008396100-000Y	712	392	UGCCACACGUGCAAUCCCU	B UGCCACACGUGCAAUCCCUTT B	2574

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396103-000Z	2121	393	UCUGUGAACUUGCUCAGGA	B UCUGUGAACUUGCUCAGGA*TT* B	2576
R-008396103-000Z	2121	393	UCUGUGAACUUGCUCAGGA	UCCUGAGCAAGUUCACAGAUU	2577
R-008396106-000A	2898	394	UGAGUAAUGGUGUAGAACA	B UGAGUAAUGGUGUAGAACA*TT* B	2578
R-008396106-000A	2898	394	UGAGUAAUGGUGUAGAACA	UGUUCUACACCAUUACUCAUU	2579
R-008396109-000B	1799	395	GUUGGAUUGAUUCGAAAUC	B GUUGGAUUGAUUCGAAAUC*TT* B	2580
R-008396109-000B	1799	395	GUUGGAUUGAUUCGAAAUC	GAUUUCGAAUCAAUCCAACUU	2581
R-008396112-000H	1036	396	UACAACUCUCCACAACCUU	AAGGUUGUGGAGAGUUGUAUU	2583
R-008396112-000H	1036	396	UACAACUCUCCACAACCUU	B UACAACUCUCCACAACCUU*TT* B	2582
R-008396115-000J	449	397	CAAGUCCUGUAUGAGUGGG	CCCACUCAUACAGGACUUGUU	2585
R-008396115-000J	449	397	CAAGUCCUGUAUGAGUGGG	B CAAGUCCUGUAUGAGUGGG*TT* B	2584
R-008396118-000K	1452	398	AGGAAGGGAUGGAAGGUCU	B AGGAAGGGAUGGAAGGUCU*TT* B	2586
R-008396118-000K	1452	398	AGGAAGGGAUGGAAGGUCU	AGACCUUCCAUCCCUUCCUUU	2587
R-008396124-000T	1203	399	AGCUCAUCAUACUGGCUAG	B AGCUCAUCAUACUGGCUAG*TT* B	2588
R-008396124-000T	1203	399	AGCUCAUCAUACUGGCUAG	CUAGCCAGUAUGAUGAGCUUU	2589
R-008396130-000A	1357	400	GCAAGCUUUAGGACUUCAC	GUGAAGUCCUAAAGCUUGCUU	2591
R-008396130-000A	1357	400	GCAAGCUUUAGGACUUCAC	B GCAAGCUUUAGGACUUCAC*TT* B	2590
R-008396133-00B	1512	401	AUGUGGUCACCUGUGCAGC	GCUGCACAGGUGACCACAUUU	2593
R-008396133-00B	1512	401	AUGUGGUCACCUGUGCAGC	B AUGUGGUCACCUGUGCAGC*TT* B	2592
R-008396136-000C	275	402	ACUCAAGCUGAUUUGAUGG	B ACUCAAGCUGAUUUGAUGG*TT* B	2594
R-008396136-000C	275	402	ACUCAAGCUGAUUUGAUGG	CCAUCAAAUCAGCUUGAGUUU	2595
R-008396139-000D	299	403	GACAUGGCCAUGGAACCAG	CUGGUUCCAUGGCCAUGUCUU	2597
R-008396139-000D	299	403	GACAUGGCCAUGGAACCAG	B GACAUGGCCAUGGAACCAG*TT* B	2596
R-008396142-000K	1241	404	GUAAAUAUAAUGAGGACCU	B GUAAAUAUAAUGAGGACCU*TT* B	2598
R-008396142-000K	1241	404	GUAAAUAUAAUGAGGACCU	AGGUCCUCAUUAUAUUUACUU	2599
R-008396145-000L	1961	405	CGCAUGGAAGAAAUAGUUG	CAACUAUUUCUUCCAUGCGUU	2601
R-008396145-000L	1961	405	CGCAUGGAAGAAAUAGUUG	B CGCAUGGAAGAAAUAGUUG*TT* B	2600
R-008396148-000M	1436	406	GAUGCUGCAACUAAACAGG	B GAUGCUGCAACUAAACAGG*TT* B	2602
R-008396148-000M	1436	406	GAUGCUGCAACUAAACAGG	CCUGUUUAGUUGCAGCAUCUU	2603
R-008396151-000U	2469	407	UGAUGGAACAUGAGAUGGG	B UGAUGGAACAUGAGAUGGG*TT* B	2604
R-008396151-000U	2469	407	UGAUGGAACAUGAGAUGGG	CCCAUCUCAUGUUCCAUCAUU	2605
R-008396154-000V	760	408	CCAGGUGGUGGUUAAUAAG	B CCAGGUGGUGGUUAAUAAG*TT* B	2606
R-008396154-000V	760	408	CCAGGUGGUGGUUAAUAAG	CUUAUUAACCACCACCUGGUU	2607
R-008396157-000W	2504	141	GCUGACUAUCCAGUUGAUG	CAUCAACUGGAUAGUCAGCUU	2609
R-008396157-000W	2504	141	GCUGACUAUCCAGUUGAUG	B GCUGACUAUCCAGUUGAUG*TT* B	2608
R-008396160-000C	2257	409	UGAGGACAAGCCACAAGAU	AUCUUGUGGCUUGUCCUCAUU	2611
R-008396160-000C	2257	409	UGAGGACAAGCCACAAGAU	B UGAGGACAAGCCACAAGAU*TT* B	2610
R-008396163-000D	952	410	ACUGGCCAUCUUUAAGUCU	AGACUUAAAGAUGGCCAGUUU	2613

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396163-000D	952	410	ACUGGCCAUCUUUAAGUCU	B ACUGGCCAUCUUUAAGUCUTT B	2612
R-008396166-000E	2283	411	AACGGCUUUCAGUUGAGCU	B AACGGCUUUCAGUUGAGCUTT B	2614
R-008396166-000E	2283	411	AACGGCUUUCAGUUGAGCU	AGCUCAACUGAAAGCCGUUUU	2615
R-008396169-000F	1649	62	ACUGAGCCUGCCAUCUGUG	G ACUGAGCCUGCCAUCUGUGTT B	2616
R-008396169-000F	1649	62	ACUGAGCCUGCCAUCUGUG	CACAGAUGGCAGGCUCAGUUU	2617
R-008396172-000M	2014	8	GGAUGUUCACAACCGAAUU	AAUUCGGUUGUGAACAUCCUU	2619
R-008396172-000M	2014	8	GGAUGUUCACAACCGAAUU	B GGAUGUUCACAACCGAAUUTT B	2618
R-008396175-000N	1794	412	CUACUGUUGGAUUGAUUCG	CGAAUCAAUCCAACAGUAGUU	2621
R-008396175-000N	1794	412	CUACUGUUGGAUUGAUUCG	B CUACUGUUGGAUUGAUUCGTT B	2620
R-008396178-000P	1745	413	GUUGUGGUUAAGCUCUUAC	B GUUGUGGUUAAGCUCUUACTT B	2622
R-008396178-000P	1745	413	GUUGUGGUUAAGCUCUUAC	GUAAGAGCUUAACCACAACUU	2623
R-008396181-000W	1211	414	AUACUGGCUAGUGGUGGAC	GUCCACCACUAGCCAGUAUUU	2625
R-008396181-000W	1211	414	AUACUGGCUAGUGGUGGAC	B AUACUGGCUAGUGGUGGACTT B	2624
R-008396184-000X	2549	415	GACCUCAUGGAUGGGCUGC	B GACCUCAUGGAUGGGCUGCTT B	2626
R-008396184-000X	2549	415	GACCUCAUGGAUGGGCUGC	GCAGCCCAUCCAUGAGGUCUU	2627
R-008396187-000Y	2007	416	UAGCUCGGGAUGUUCACAA	UUGUGAACAUCCCGAGCUAUU	2629
R-008396187-000Y	2007	416	UAGCUCGGGAUGUUCACAA	B UAGCUCGGGAUGUUCACAATT B	2628
R-008396190-000E	2474	417	GAACAUGAGAUGGGUGGCC	B GAACAUGAGAUGGGUGGCCTT B	2630
R-008396190-000E	2474	417	GAACAUGAGAUGGGUGGCC	GGCCACCCAUCUCAUGUUCUU	2631
R-008396193-000F	1712	418	CAGAAUGCAGUUCGCCUUC	GAAGGCGAACUGCAUUCUGUU	2633
R-008396193-000F	1712	418	CAGAAUGCAGUUCGCCUUC	B CAGAAUGCAGUUCGCCUUCTT B	2632
R-008396196-000G	1919	419	ACGUCCAUGGGUGGGACAC	B ACGUCCAUGGGUGGGACACTT B	2634
R-008396196-000G	1919	419	ACGUCCAUGGGUGGGACAC	GUGUCCCACCCAUGGACGUUU	2635
R-008396199-000H	1000	420	UGGUUCACCAGUGGAUUCU	AGAAUCCACUGGUGAACCAUU	2637
R-008396199-000H	1000	420	UGGUUCACCAGUGGAUUCU	B UGGUUCACCAGUGGAUUCUTT B	2636
R-008396202-000A	2392	421	AUAUCGCCAGGAUGAUCCU	AGGAUCAUCCUGGCGAUAUUU	2639
R-008396202-000A	2392	421	AUAUCGCCAGGAUGAUCCU	B AUAUCGCCAGGAUGAUCCUTT B	2638
R-008396205-000B	1449	422	AACAGGAAGGGAUGGAAGG	B AACAGGAAGGGAUGGAAGGTT B	2640
R-008396205-000B	1449	422	AACAGGAAGGGAUGGAAGG	CCUUCCAUCCCUUCCUGUUUU	2641
R-008396208-000C	2294	423	GUUGAGCUGACCAGCUCUC	GAGAGCUGGUCAGCUCAACUU	2643
R-008396208-000C	2294	423	GUUGAGCUGACCAGCUCUC	B GUUGAGCUGACCAGCUCUCTT B	2642
R-008396211-000J	1135	424	AAAUGUUAAAUUCUUGGCU	B AAAUGUUAAAUUCUUGGCUTT B	2644
R-008396211-000J	1135	424	AAAUGUUAAAUUCUUGGCU	AGCCAAGAAUUUAACAUUUUU	2645
R-008396214-000K	822	14	GACACGCUAUCAUGCGUUC	B GACACGCUAUCAUGCGUUCTT B	2646
R-008396214-000K	822	14	GACACGCUAUCAUGCGUUC	GAACGCAUGAUAGCGUGUCUU	2647
R-008396217-000L	1333	425	GGCUAUUGUAGAAGCUGGU	ACCAGCUUCUACAAUAGCCUU	2649

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396217-000L	1333	425	GGCUAUUGUAGAAGCUGGU	B GGCUAUUGUAGAAGCUGGUTT B	2648
R-008396220-000T	1743	426	CAGUUGUGGUUAAGCUCUU	AAGAGCUUAACCACAACUGUU	2651
R-008396220-000T	1743	426	CAGUUGUGGUUAAGCUCUU	B CAGUUGUGGUUAAGCUCUUTT B	2650
R-008396223-000U	600	427	CUACACAGUUUGAUGCUGC	GCAGCAUCAAACUGUGUAGUU	2653
R-008396223-000U	600	427	CUACACAGUUUGAUGCUGC	B CUACACAGUUUGAUGCUGCTT B	2652
R-008396226-000V	970	428	UGGAGGCAUUCCUGCCCUG	CAGGGCAGGAAUGCCUCCAUU	2655
R-008396226-000V	970	428	UGGAGGCAUUCCUGCCCUG	B UGGAGGCAUUCCUGCCCUGTT B	2654
R-008396229-000W	3137	429	GGACAGUUUACCAGUUGCC	B GGACAGUUUACCAGUUGCCTT B	2656
R-008396229-000W	3137	429	GGACAGUUUACCAGUUGCC	GGCAACUGGUAAAGUGUCCUU	2657
R-008396232-000C	372	430	UCCAUUCUGGUGCCACUAC	GUAGUGGCACCAGAAUGGAUU	2659
R-008396232-000C	372	430	UCCAUUCUGGUGCCACUAC	B UCCAUUCUGGUGCCACUACTT B	2659
R-008396235-000D	1761	431	UACACCCACCAUCCCACUG	B UACACCCACCAUCCCACUGTT B	2660
R-008396235-000D	1761	431	UACACCCACCAUCCCACUG	CAGUGGGAUGGUGGGUGUAUU	2661
R-008396238-000E	1650	432	CUGAGCCUGCCAUCUGUGC	GCACAGAUGGCAGGCUCAGUU	2663
R-008396238-000E	1650	432	CUGAGCCUGCCAUCUGUGC	B CUGAGCCUGCCAUCUGUGCTT B	2662
R-008396241-000L	972	433	GAGGCAUUCCUGCCCUGGU	B GAGGCAUUCCUGCCCUGGUTT B	2664
R-008396241-000L	972	433	GAGGCAUUCCUGCCCUGGU	ACCAGGGCAGGAAUGCCUCUU	2665
R-008396244-000M	1147	434	CUUGGCUAUUACGACAGAC	GUCUGUCGUAAUAGCCAAGUU	2667
R-008396244-000M	1147	434	CUUGGCUAUUACGACAGAC	B CUUGGCUAUUACGACAGACTT B	2666
R-008396247-000N	565	435	CCCUGAGACAUUAGAUGAG	B CCCUGAGACAUUAGAUGAGTT B	2668
R-008396247-000N	565	435	CCCUGAGACAUUAGAUGAG	CUCAUCUAAUGUCUCAGGGUU	2669
R-008396250-000V	525	436	AUGCAAUGACUCGAGCUCA	B AUGCAAUGACUCGAGCUCATT B	2670
R-008396250-000V	525	436	AUGCAAUGACUCGAGCUCA	UGAGCUCGAGUCAUUGCAUUU	2671
R-008396253-000W	1599	437	UAGAGGCUCUUGUGCGUAC	B UAGAGGCUCUUGUGCGUACTT B	2672
R-008396253-000W	1599	437	UAGAGGCUCUUGUGCGUAC	GUACGCACAAGAGCCUCUAUU	2673
R-008396256-000X	2199	438	UUCACUCUAGGAAUGAAGG	B UUCACUCUAGGAAUGAAGGTT B	2674
R-008396256-000X	2199	438	UUCACUCUAGGAAUGAAGG	CCUUCAUUCCUAGAGUGAAUU	2675
R-008396259-000Y	2261	439	GACAAGCCACAAGAUUACA	B GACAAGCCACAAGAUUACATT B	2676
R-008396259-000Y	2261	439	GACAAGCCACAAGAUUACA	UGUAAUCUUGUGGCUUGUCUU	2677
R-008396262-000E	705	440	CAGAACUUGCCACACGUGC	B CAGAACUUGCCACACGUGCTT B	2678
R-008396262-000E	705	440	CAGAACUUGCCACACGUGC	GCACGUGUGGCAAGUUCUGUU	2679
R-008396265-000F	916	441	GACCUUGCAUAACCUUUCC	B GACCUUGCAUAACCUUUCCTT B	2680
R-008396265-000F	916	441	GACCUUGCAUAACCUUUCC	GGAAAGGUUAUGCAAGGUCUU	2681
R-008396268-000G	385	442	CACUACCACAGCUCCUUCU	AGAAGGAGCUGUGGUAGUGUU	2683
R-008396268-000G	385	442	CACUACCACAGCUCCUUCU	B CACUACCACAGCUCCUUCUTT B	2682
R-008396271-000N	3076	443	CUAUUUGGGAUAUGUAUGG	B CUAUUUGGGAUAUGUAUGGTT B	2684
R-008396271-000N	3076	443	CUAUUUGGGAUAUGUAUGG	CCAUACAUAUCCCAAAUAGUU	2685

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396274-000P	1396	444	UCUUGUUCAGAACUGUCUU	B UCUUGUUCAGAACUGUCUUTT B	2686
R-008396274-000P	1396	444	UCUUGUUCAGAACUGUCUU	AAGACAGUUCUGAACAAGAUU	2687
R-008396277-000R	2447	445	GAUGCCUUGGGUAUGGACC	GGUCCAUACCCAAGGCAUCUU	2689
R-008396277-000R	2447	445	GAUGCCUUGGGUAUGGACC	B GAUGCCUUGGGUAUGGACCTT B	2688
R-008396280-000X	1338	446	UUGUAGAAGCUGGUGGAAU	B UUGUAGAAGCUGGUGGAAUTT B	2690
R-008396280-000X	1338	446	UUGUAGAAGCUGGUGGAAU	AUUCCACCAGCUUCUACAAUU	2691
R-008396283-000Y	2215	447	AGGUGUGGCGACAUAUGCA	UGCAUAUGUCGCCACACCUUU	2693
R-008396283-000Y	2215	447	AGGUGUGGCGACAUAUGCA	B AGGUGUGGCGACAUAUGCATT B	2692
R-008396286-000Z	722	448	GCAAUCCCUGAACUGACAA	B GCAAUCCCUGAACUGACAATT B	2694
R-008396286-000Z	722	448	GCAAUCCCUGAACUGACAA	UUGUCAGUUCAGGGAUUGCUU	2695
R-008396289-000A	1316	449	UGCUCUAGUAAUAAGCCGG	CCGGCUUAUUACUAGAGCAUU	2697
R-008396289-000A	1316	449	UGCUCUAGUAAUAAGCCGG	B UGCUCUAGUAAUAAGCCGGTT B	2697
R-008396292-000G	1687	450	CCGACACCAAGAAGCAGAG	B CCGACACCAAGAAGCAGAGTT B	2698
R-008396292-000G	1687	450	CCGACACCAAGAAGCAGAG	CUCUGCUUCUUGGUGUCGGUU	2699
R-008396295-000H	697	451	AGAUGAUGCAGAACUUGCC	B AGAUGAUGCAGAACUUGCCTT B	2700
R-008396295-000H	697	451	AGAUGAUGCAGAACUUGCC	GGCAAGUUCUGCAUCAUCUUU	2701
R-008396298-000J	2517	452	UUGAUGGGCUGCCAGAUCU	B UUGAUGGGCUGCCAGAUCUTT B	2702
R-008396298-000J	2517	452	UUGAUGGGCUGCCAGAUCU	AGAUCUGGCAGCCCAUCAAUU	2703
R-008396301-000B	1685	453	AGCCGACACCAAGAAGCAG	B AGCCGACACCAAGAAGCAGTT B	2704
R-008396301-000B	1685	453	AGCCGACACCAAGAAGCAG	CUGCUUCUUGGUGUCGGCUUU	2705
R-008396304-000C	3090	454	UAUGGGUAGGGUAAAUCAG	CUGAUUUACCCUACCCAUAUU	2707
R-008396304-000C	3090	454	UAUGGGUAGGGUAAAUCAG	B UAUGGGUAGGGUAAAUCAGTT B	2706
R-008396307-000D	1205	455	CUCAUCAUACUGGCUAGUG	B CUCAUCAUACUGGCUAGUGTT B	2708
R-008396307-000D	1205	455	CUCAUCAUACUGGCUAGUG	CACUAGCCAGUAUGAUGAGUU	2709
R-008396310-000K	1153	456	UAUUACGACAGACUGCCUU	B UAUUACGACAGACUGCCUUTT B	2710
R-008396310-000K	1153	456	UAUUACGACAGACUGCCUU	AAGGCAGUCUGUCGUAAUAUU	2711
R-008396313-000L	723	457	CAAUCCCUGAACUGACAAA	B CAAUCCCUGAACUGACAAATT B	2712
R-008396313-000L	723	457	CAAUCCCUGAACUGACAAA	UUUGUCAGUUCAGGGAUUGUU	2713
R-008396316-000M	1468	458	UCUCCUUGGGACUCUUGUU	AACAAGAGUCCCAAGGAGAUU	2715
R-008396316-000M	1468	458	UCUCCUUGGGACUCUUGUU	B UCUCCUUGGGACUCUUGUUTT B	2714
R-008396319-000N	2480	459	GAGAUGGGUGGCCACCACC	B GAGAUGGGUGGCCACCACCTT B	2716
R-008396319-000N	2480	459	GAGAUGGGUGGCCACCACC	GGUGGUGGCCACCCAUCUCUU	2717
R-008396322-000V	1856	460	CAGGGUGCCAUUCCACGAC	B CAGGGUGCCAUUCCACGACTT B	2718
R-008396322-000V	1856	460	CAGGGUGCCAUUCCACGAC	GUCGUGGAAUGGCACCCUGUU	2719
R-008396325-000W	2193	461	AGUUACUUCACUCUAGGAA	B AGUUACUUCACUCUAGGAATT B	2720
R-008396325-000W	2193	461	AGUUACUUCACUCUAGGAA	UUCCUAGAGUGAAGUAACUUU	2721

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396328-000X	2355	462	UUGGACUUGAUAUUGGUGC	B UUGGACUUGAUAUUGGUGC*TT* B	2722
R-008396328-000X	2355	462	UUGGACUUGAUAUUGGUGC	GCACCAAUAUCAAGUCCAAUU	2723
R-008396331-000D	1995	463	CCCUUCACAUCCUAGCUCG	CGAGCUAGGAUGUGAAGGGUU	2725
R-008396331-000D	1995	463	CCCUUCACAUCCUAGCUCG	B CCCUUCACAUCCUAGCUCG*TT* B	2724
R-008396334-000E	821	464	AGACACGCUAUCAUGCGUU	B AGACACGCUAUCAUGCGUU*TT* B	2726
R-008396334-000E	821	464	AGACACGCUAUCAUGCGUU	AACGCAUGAUAGCGUGUCUUU	2727
R-008396337-000F	1715	465	AAUGCAGUUCGCCUUCACU	B AAUGCAGUUCGCCUUCACU*TT* B	2728
R-008396337-000F	1715	465	AAUGCAGUUCGCCUUCACU	AGUGAAGGCGAACUGCAUUUU	2729
R-008396340-000M	1172	466	CUUAUGGCAACCAAGAAAG	CUUUCUUGGUUGCCAUAAGUU	2731
R-008396340-000M	1172	466	CUUAUGGCAACCAAGAAAG	B CUUAUGGCAACCAAGAAAG*TT* B	2730
R-008396343-000N	445	467	CUCCCAAGUCCUGUAUGAG	B CUCCCAAGUCCUGUAUGAG*TT* B	2732
R-008396343-000N	445	467	CUCCCAAGUCCUGUAUGAG	CUCAUACAGGACUUGGGAGUU	2733
R-008396346-000P	1759	468	CUUACACCCACCAUCCCAC	GUGGGAUGGUGGGUGUAAGUU	2735
R-008396346-000P	1759	468	CUUACACCCACCAUCCCAC	B CUUACACCCACCAUCCCAC*TT* B	2734
R-008396349-000R	1461	469	UGGAAGGUCUCCUUGGGAC	B UGGAAGGUCUCCUUGGGAC*TT* B	2736
R-008396349-000R	1461	469	UGGAAGGUCUCCUUGGGAC	GUCCCAAGGAGACCUUCCAUU	2737
R-008396342-000X	1993	470	AGCCCUUCACAUCCUAGCU	AGCUAGGAUGUGAAGGGCUUU	2739
R-008396342-000X	1993	470	AGCCCUUCACAUCCUAGCU	B AGCCCUUCACAUCCUAGCU*TT* B	2738
R-008396355-000Y	2558	471	GAUGGGCUGCCUCCAGGUG	B GAUGGGCUGCCUCCAGGUG*TT* B	2740
R-008396355-000Y	2558	471	GAUGGGCUGCCUCCAGGUG	CACCUGGAGGCAGCCCAUCUU	2741
R-008396358-000Z	1488	472	AGCUUCUGGGUUCAGAUGA	B AGCUUCUGGGUUCAGAUGA*TT* B	2742
R-008396358-000Z	1488	472	AGCUUCUGGGUUCAGAUGA	UCAUCUGAACCCAGAAGCUUU	2743
R-008396361-000F	1652	473	GAGCCUGCCAUCUGUGCUC	B GAGCCUGCCAUCUGUGCUC*TT* B	2744
R-008396361-000F	1652	473	GAGCCUGCCAUCUGUGCUC	GAGCACAGAUGGCAGGCUCUU	2745
R-008396364-000G	963	474	UUAAGUCUGGAGGCAUUCC	B UUAAGUCUGGAGGCAUUCC*TT* B	2746
R-008396364-000G	963	474	UUAAGUCUGGAGGCAUUCC	GGAAUGCCUCCAGACUUAAUU	2747
R-008396367-000H	1520	475	ACCUGUGCAGCUGGAAUUC	B ACCUGUGCAGCUGGAAUUC*TT* B	2748
R-008396367-000H	1520	475	ACCUGUGCAGCUGGAAUUC	GAAUUCCAGCUGCACAGGUUU	2749
R-008396370-000P	1828	476	UCCCGCAAAUCAUGCACCU	AGGUGCAUGAUUUGCGGGAUU	2751
R-008396370-000P	1828	476	UCCCGCAAAUCAUGCACCU	B UCCCGCAAAUCAUGCACCU*TT* B	2750
R-008396373-000R	2214	477	AAGGUGUGGCGACAUAUGC	B AAGGUGUGGCGACAUAUGC*TT* B	2752
R-008396373-000R	2214	477	AAGGUGUGGCGACAUAUGC	GCAUAUGUCGCCACACCUUUU	2753
R-008396376-000S	2155	478	AGCUAUUGAAGCUGAGGGA	UCCCUCAGCUUCAAUAGCUUU	2755
R-008396376-000S	2155	478	AGCUAUUGAAGCUGAGGGA	B AGCUAUUGAAGCUGAGGGA*TT* B	2754
R-008396379-000T	332	479	GUUAGUCACUGGCAGCAAC	GUUGCUGCCAGUGACUAACUU	2757
R-008396379-000T	332	479	GUUAGUCACUGGCAGCAAC	B GUUAGUCACUGGCAGCAAC*TT* B	2756
R-008396382-000Z	2545	74	CCAGGACCUCAUGGAUGGG	CCCAUCCAUGAGGUCCUGGUU	2759

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396382-000Z	2545	74	CCAGGACCUCAUGGAUGGG	B CCAGGACCUCAUGGAUGGGTT B	2758
R-008396385-000A	1878	180	UUCAGUUGCUUGUUCGUGC	B UUCAGUUGCUUGUUCGUGCTT B	2760
R-008396385-000A	1878	180	UUCAGUUGCUUGUUCGUGC	GCACGAACAAGCAACUGAAUU	2761
R-008396388-000B	1789	106	AAAGGCUACUGUUGGAUUG	CAAUCCAACAGUAGCCUUUUU	2763
R-008396388-000B	1789	106	AAAGGCUACUGUUGGAUUG	B AAAGGCUACUGUUGGAUUGTT B	2762
R-008396391-000H	2547	168	AGGACCUCAUGGAUGGGCU	B AGGACCUCAUGGAUGGGCUTT B	2764
R-008396391-000H	2547	168	AGGACCUCAUGGAUGGGCU	AGCCCAUCCAUGAGGUCCUUU	2765
R-008396394-000J	1573	481	GAUGAUGGUCUGCCAAGUG	B GAUGAUGGUCUGCCAAGUGTT B	2766
R-008396394-000J	1573	481	GAUGAUGGUCUGCCAAGUG	CACUUGGCAGACCAUCAUCUU	2767
R-008396397-000K	1446	482	CUAAACAGGAAGGGAUGGA	B CUAAACAGGAAGGGAUGGATT B	2768
R-008396397-000K	1446	482	CUAAACAGGAAGGGAUGGA	UCCAUCCCUUCCUGUUUAGUU	2769
R-008396400-000C	1868	483	CCACGACUAGUUCAGUUGC	GCAACUGAACUAGUCGUGGUU	2771
R-008396400-000C	1868	483	CCACGACUAGUUCAGUUGC	B CCACGACUAGUUCAGUUGCTT B	2770
R-008396403-000D	1873	484	ACUAGUUCAGUUGCUUGUU	AACAAGCAACUGAACUAGUUU	2773
R-008396403-000D	1873	484	ACUAGUUCAGUUGCUUGUU	B ACUAGUUCAGUUGCUUGUUTT B	2772
R-008396406-000E	1002	485	GUUCACCAGUGGAUUCUGU	B GUUCACCAGUGGAUUCUGUTT B	2774
R-008396406-000E	1002	485	GUUCACCAGUGGAUUCUGU	ACAGAAUCCACUGGUGAACUU	2775
R-008396409-000F	408	486	GUGGUAAAGGCAAUCCUGA	B GUGGUAAAGGCAAUCCUGATT B	2776
R-008396409-000F	408	486	GUGGUAAAGGCAAUCCUGA	UCAGGAUUGCCUUUACCACUU	2777
R-008396412-000M	287	487	UUGAUGGAGUUGGACAUGG	CCAUGUCCAACUCCAUCAAUU	2779
R-008396412-000M	287	487	UUGAUGGAGUUGGACAUGG	B UUGAUGGAGUUGGACAUGGTT B	2778
R-008396415-000N	1492	119	UCUGGGUUCAGAUGAUAUA	UAUAUCAUCUGAACCCAGAUU	2781
R-008396415-000N	1492	119	UCUGGGUUCAGAUGAUAUA	B UCUGGGUUCAGAUGAUAUATT B	2780
R-008396418-000P	517	187	UGGACAGUAUGCAAUGACU	B UGGACAGUAUGCAAUGACUTT B	2782
R-008396418-000P	517	187	UGGACAGUAUGCAAUGACU	AGUCAUUGCAUACUGUCCAUU	2783
R-008396421-000W	447	177	CCCAAGUCCUGUAUGAGUG	B CCCAAGUCCUGUAUGAGUGTT B	2784
R-008396421-000W	447	177	CCCAAGUCCUGUAUGAGUG	CACUCAUACAGGACUUGGGUU	2785
R-008396424-000X	2128	488	ACUUGCUCAGGACAAGGAA	UUCCUUGUCCUGAGCAAGUUU	2787
R-008396424-000X	2128	488	ACUUGCUCAGGACAAGGAA	B ACUUGCUCAGGACAAGGAATT B	2786
R-008396427-000Y	2513	489	CCAGUUGAUGGGCUGCCAG	B CCAGUUGAUGGGCUGCCAGTT B	2788
R-008396427-000Y	2513	489	CCAGUUGAUGGGCUGCCAG	CUGGCAGCCCAUCAACUGGUU	2789
R-008396430-000E	1196	490	GAAAGCAAGCUCAUCAUAC	GUAUGAUGAGCUUGCUUUCUU	2791
R-008396430-000E	1196	490	GAAAGCAAGCUCAUCAUAC	B GAAAGCAAGCUCAUCAUACTT B	2790
R-008396433-000F	572	491	ACAUUAGAUGAGGGCAUGC	B ACAUUAGAUGAGGGCAUGCTT B	2792
R-008396433-000F	572	491	ACAUUAGAUGAGGGCAUGC	GCAUGCCCUCAUCUAAUGUUU	2793
R-008396436-000G	622	492	UCCCACUAAUGUCCAGCGU	B UCCCACUAAUGUCCAGCGUTT B	2794

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396436-000G	622	492	UCCCACUAAUGUCCAGCGU	ACGCUGGACAUUAGUGGGAUU	2795
R-008396439-000H	1187	493	GGCAACCAAGAAAGCAAGC	GCUUGCUUUCUUGGUUGCCUU	2797
R-008396439-000H	1187	493	GGCAACCAAGAAAGCAAGC	B GGCAACCAAGAAAGCAAGCTT B	2796
R-008396442-000P	2098	49	CCAAAGAGUAGCUGCAGGG	B CCAAAGAGUAGCUGCAGGGTT B	2798
R-008396442-000P	2098	49	CCAAAGAGUAGCUGCAGGG	CCCUGCAGCUACUCUUUGGUU	2799
R-008396445-000R	1971	494	AAAUAGUUGAAGGUUGUAC	B AAAUAGUUGAAGGUUGUACTT B	2800
R-008396445-000R	1971	494	AAAUAGUUGAAGGUUGUAC	GUACAACCUUCAACUAUUUUU	2801
R-008396448-000S	3083	495	GGAUAUGUAUGGGUAGGGU	ACCCUACCCAUACAUAUCCUU	2803
R-008396448-000S	3083	495	GGAUAUGUAUGGGUAGGGU	B GGAUAUGUAUGGGUAGGGUTT B	2802
R-008396454-000Z	2944	496	UAAUCUGAAUAAAGUGUAA	UUACACUUUAUUCAGAUUAUU	2805
R-008396454-000Z	2944	496	UAAUCUGAAUAAAGUGUAA	B UAAUCUGAAUAAAGUGUAATT B	2804
R-008396457-000A	1894	497	UGCACAUCAGGAUACCCAG	B UGCACAUCAGGAUACCCAGTT B	2806
R-008396457-000A	1894	497	UGCACAUCAGGAUACCCAG	CUGGGUAUCCUGAUGUGCAUU	2807
R-008396460-000G	1323	498	GUAAUAAGCCGGCUAUUGU	B GUAAUAAGCCGGCUAUUGUTT B	2808
R-008396460-000G	1323	498	GUAAUAAGCCGGCUAUUGU	ACAAUAGCCGGCUUAUUACUU	2809
R-008396469-000K	1202	499	AAGCUCAUCAUACUGGCUA	B AAGCUCAUCAUACUGGCUATT B	2810
R-008396469-000K	1202	499	AAGCUCAUCAUACUGGCUA	UAGCCAGUAUGAUGAGCUUUU	2811
R-008396472-000S	718	500	ACGUGCAAUCCCUGAACUG	CAGUUCAGGGAUUGCACGUUU	2813
R-008396472-000S	718	500	ACGUGCAAUCCCUGAACUG	B ACGUGCAAUCCCUGAACUGTT B	2812
R-008396475-000T	2097	46	UCCAAAGAGUAGCUGCAGG	CCUGCAGCUACUCUUUGGAUU	2815
R-008396475-000T	2097	46	UCCAAAGAGUAGCUGCAGG	B UCCAAAGAGUAGCUGCAGGTT B	2814
R-008396478-000U	1744	501	AGUUGUGGUUAAGCUCUUA	B AGUUGUGGUUAAGCUCUUATT B	2816
R-008396478-000U	1744	501	AGUUGUGGUUAAGCUCUUA	UAAGAGCUUAACCACAACUUU	2817
R-008396481-000A	756	502	AGGACCAGGUGGUGGUUAA	UUAACCACCACCUGGUCCUUU	2819
R-008396481-000A	756	502	AGGACCAGGUGGUGGUUAA	B AGGACCAGGUGGUGGUUAATT B	2818
R-008396484-000B	1317	503	GCUCUAGUAAUAAGCCGGC	GCCGGCUUAUUACUAGAGCUU	2821
R-008396484-000B	1317	503	GCUCUAGUAAUAAGCCGGC	B GCUCUAGUAAUAAGCCGGCTT B	2820
R-008396487-000C	284	504	GAUUUGAUGGAGUUGGACA	B GAUUUGAUGGAGUUGGACATT B	2822
R-008396487-000C	284	504	GAUUUGAUGGAGUUGGACA	UGUCCAACUCCAUCAAAUCUU	2823
R-008396490-000J	886	505	UGAUGUAGAAACAGCUCGU	B UGAUGUAGAAACAGCUCGUTT B	2824
R-008396490-000J	886	505	UGAUGUAGAAACAGCUCGU	ACGAGCUGUUUCUACAUCAUU	2825
R-008396493-000K	2430	506	CUGGUGGAUAUGGCCAGGA	B CUGGUGGAUAUGGCCAGGATT B	2826
R-008396493-000K	2430	506	CUGGUGGAUAUGGCCAGGA	UCCUGGCCAUAUCCACCAGUU	2827
R-008396496-000L	1207	507	CAUCAUACUGGCUAGUGGU	B CAUCAUACUGGCUAGUGGUTT B	2828
R-008396496-000L	1207	507	CAUCAUACUGGCUAGUGGU	ACCACUAGCCAGUAUGAUGUU	2829
R-008396499-000M	592	508	GAUCCCAUCUACACAGUUU	AAACUGUGUAGAUGGGAUCUU	2831
R-008396499-000M	592	508	GAUCCCAUCUACACAGUUU	B GAUCCCAUCUACACAGUUUTT B	2830

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396502-000E	824	509	CACGCUAUCAUGCGUUCUC	GAGAACGCAUGAUAGCGUGUU	2833
R-008396502-000E	824	509	CACGCUAUCAUGCGUUCUC	B CACGCUAUCAUGCGUUCUCTT B	2832
R-008396505-000F	519	510	GACAGUAUGCAAUGACUCG	B GACAGUAUGCAAUGACUCGTT B	2834
R-008396505-000F	519	510	GACAGUAUGCAAUGACUCG	CGAGUCAUUGCAUACUGUCUU	2835
R-008396508-000G	3166	511	AAGUUGUUGUAACCUGCUG	CAGCAGGUUACAACAACUUUU	2837
R-008396508-000G	3166	511	AAGUUGUUGUAACCUGCUG	B AAGUUGUUGUAACCUGCUGTT B	2836
R-008396511-000N	1151	512	GCUAUUACGACAGACUGCC	B GCUAUUACGACAGACUGCCTT B	2838
R-008396511-000N	1151	512	GCUAUUACGACAGACUGCC	GGCAGUCUGUCGUAAUAGCUU	2839
R-008396514-000P	2566	513	GCCUCCAGGUGACAGCAAU	B GCCUCCAGGUGACAGCAAUTT B	2840
R-008396514-000P	2566	513	GCCUCCAGGUGACAGCAAU	AUUGCUGUCACCUGGAGGCUU	2841
R-008396517-000R	453	514	UCCUGUAUGAGUGGGAACA	UGUUCCCACUCAUACAGGAUU	2843
R-008396517-000R	453	514	UCCUGUAUGAGUGGGAACA	B UCCUGUAUGAGUGGGAACATT B	2842
R-008396520-000X	587	515	AUGCAGAUCCCAUCUACAC	GUGUAGAUGGGAUCUGCAUUU	2845
R-008396520-000X	587	515	AUGCAGAUCCCAUCUACAC	B AUGCAGAUCCCAUCUACACTT B	2844
R-008396523-000Y	930	516	UUUCCCAUCAUCGUGAGGG	B UUUCCCAUCAUCGUGAGGGTT B	2846
R-008396523-000Y	930	516	UUUCCCAUCAUCGUGAGGG	CCCUCACGAUGAUGGGAAAUU	2847
R-008396526-000Z	1585	517	CCAAGUGGGUGGUAUAGAG	B CCAAGUGGGUGGUAUAGAGTT B	2848
R-008396526-000Z	1585	517	CCAAGUGGGUGGUAUAGAG	CUCUAUACCACCCACUUGGUU	2849
R-008396529-000A	915	518	GGACCUUGCAUAACCUUUC	B GGACCUUGCAUAACCUUUCTT B	2850
R-008396529-000A	915	518	GGACCUUGCAUAACCUUUC	GAAAGGUUAUGCAAGGUCCUU	2851
R-008396532-000G	446	519	UCCCAAGUCCUGUAUGAGU	ACUCAUACAGGACUUGGGAUU	2853
R-008396532-000G	446	519	UCCCAAGUCCUGUAUGAGU	B UCCCAAGUCCUGUAUGAGUTT B	2852
R-008396535-000H	1869	520	CACGACUAGUUCAGUUGCU	AGCAACUGAACUAGUCGUGUU	2855
R-008396535-000H	1869	520	CACGACUAGUUCAGUUGCU	B CACGACUAGUUCAGUUGCUTT B	2854
R-008396538-000J	1960	521	CCGCAUGGAAGAAAUAGUU	AACUAUUUCUUCCAUGCGGUU	2857
R-008396538-000J	1960	521	CCGCAUGGAAGAAAUAGUU	B CCGCAUGGAAGAAAUAGUUTT B	2856
R-008396541-000R	1708	522	GGCCCAGAAUGCAGUUCGC	B GGCCCAGAAUGCAGUUCGCTT B	2858
R-008396541-000R	1708	522	GGCCCAGAAUGCAGUUCGC	GCGAACUGCAUUCUGGGCCUU	2859
R-008396544-000S	306	523	CCAUGGAACCAGACAGAAA	UUUCUGUCUGGUUCCAUGGUU	2861
R-008396544-000S	306	523	CCAUGGAACCAGACAGAAA	B CCAUGGAACCAGACAGAAATT B	2860
R-PP8396550-000Z	2281	524	GAAACGGCUUUCAGUUGAG	B GAAACGGCUUUCAGUUGAGTT B	2862
R-PP8396550-000Z	2281	524	GAAACGGCUUUCAGUUGAG	CUCAACUGAAAGCCGUUUCUU	2863
R-008396553-000A	3082	525	GGGAUAUGUAUGGGUAGGG	B GGGAUAUGUAUGGGUAGGGTT B	2864
R-008396553-000A	3082	525	GGGAUAUGUAUGGGUAGGG	CCCUACCCAUACAUAUCCCUU	2865
R-008396556-000B	1473	526	UUGGGACUCUUGUUCAGCU	AGCUGAACAAGAGUCCCAAUU	2867
R-008396556-000B	1473	526	UUGGGACUCUUGUUCAGCU	B UUGGGACUCUUGUUCAGCUTT B	2866

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396559-000C	559	527	UAUGUUCCCUGAGACAUUA	UAAUGUCUCAGGGAACAUAUU	2869
R-008396559-000C	559	527	UAUGUUCCCUGAGACAUUA	B UAUGUUCCCUGAGACAUUATT B	2868
R-008396562-000J	1416	528	GGACUCUCAGGAAUCUUUC	B GGACUCUCAGGAAUCUUUCTT B	2870
R-008396562-000J	1416	528	GGACUCUCAGGAAUCUUUC	GAAAGAUUCCUGAGAGUCCUU	2871
R-008396565-000K	2145	529	AAGCUGCAGAAGCUAUUGA	B AAGCUGCAGAAGCUAUUGATT B	2872
R-008396565-000K	2145	529	AAGCUGCAGAAGCUAUUGA	UCAAUAGCUUCUGCAGCUUUU	2873
R-008396568-000L	1994	530	GCCCUUCACAUCCUAGCUC	B GCCCUUCACAUCCUAGCUCTT B	2874
R-008396568-000L	1994	530	GCCCUUCACAUCCUAGCUC	GAGCUAGGAUGUGAAGGGCUU	2875
R-008396571-000T	1611	27	UGCGUACUGUCCUUCGGGC	B UGCGUACUGUCCUUCGGGCTT B	2876
R-008396571-000T	1611	27	UGCGUACUGUCCUUCGGGC	GCCCGAAGGACAGUACGCAUU	2877
R-008396574-000U	1702	531	AGAGAUGGCCCAGAAUGCA	B AGAGAUGGCCCAGAAUGCATT B	2878
R-008396574-000U	1702	531	AGAGAUGGCCCAGAAUGCA	UGCAUUCUGGGCCAUCUCUUU	2879
R-008396577-000V	417	532	GCAAUCCUGAGGAAGAGGA	B GCAAUCCUGAGGAAGAGGATT B	2880
R-008396577-000V	417	532	GCAAUCCUGAGGAAGAGGA	UCCUCUUCCUCAGGAUUGCUU	2881
R-008396580-000B	2444	533	CAGGAUGCCUUGGGUAUGG	B CAGGAUGCCUUGGGUAUGGTT B	2882
R-008396580-000B	2444	533	CAGGAUGCCUUGGGUAUGG	CCAUACCCAAGGCAUCCUGUU	2883
R-008396586-000D	555	534	CUGCUAUGUUCCCUGAGAC	B CUGCUAUGUUCCCUGAGACTT B	2884
R-008396586-000D	555	534	CUGCUAUGUUCCCUGAGAC	GUCUCAGGGAACAUAGCAGUU	2885
R-008396589-000E	2019	535	UUCACAACCGAAUUGUUAU	B UUCACAACCGAAUUGUUAUTT B	2886
R-008396589-000E	2019	535	UUCACAACCGAAUUGUUAU	AUAACAAUUCGGUUGUGAAUU	2887
R-008396592-000L	1197	536	AAAGCAAGCUCAUCAUACU	B AAAGCAAGCUCAUCAUACUTT B	2888
R-008396592-000L	1197	536	AAAGCAAGCUCAUCAUACU	AGUAUGAUGAGCUUGCUUUUU	2889
R-008396595-000M	415	537	AGGCAAUCCUGAGGAAGAG	CUCUUCCUCAGGAUUGCCUUU	2891
R-008396595-000M	415	537	AGGCAAUCCUGAGGAAGAG	B AGGCAAUCCUGAGGAAGAGTT B	2890
R-008396598-000N	2061	538	UGUUUGUGCAGCUGCUUUA	B UGUuUGUGCAGCUGCUUUATT B	2892
R-008396598-000N	2061	538	UGUUUGUGCAGCUGCUUUA	UAAAGCAGCUGCACAAACAUU	2893
R-008396601-000F	1352	539	GGAAUGCAAGCUUUAGGAC	B GGAAUGCAAGCUUUAGGACTT B	2894
R-008396601-000F	1352	539	GGAAUGCAAGCUUUAGGAC	GUCCUAAAGCUUGCAUUCCUU	2895
R-008396604-000G	1502	135	GAUGAUAUAAAUGUGGUCA	UGACCACAUUUAUAUCAUCUU	2897
R-008396604-000G	1502	135	GAUGAUAUAAAUGUGGUCA	B GAUGAUAUAAAUGUGGUCATT B	2896
R-008396607-000H	1331	540	CCGGCUAUUGUAGAAGCUG	B CCGGCUAUUGUAGAAGCUGTT B	2898
R-008396607-000H	1331	540	CCGGCUAUUGUAGAAGCUG	CAGCUUCUACAAUAGCCGGUU	2899
R-008396610-000P	1325	541	AAUAAGCCGGCUAUUGUAG	B AAUAAGCCGGCUAUUGUAGTT B	2900
R-008396610-000P	1325	541	AAUAAGCCGGCUAUUGUAG	CUACAAUAGCCGGCUUAUUUU	2901
R-008396613-000R	1486	542	UCAGCUUCUGGGUUCAGAU	B UCAGCUUCUGGGUUCAGAUTT B	2902
R-008396613-000R	1486	542	UCAGCUUCUGGGUUCAGAU	AUCUGAACCCAGAAGCUGAUU	2903
R-008396616-000S	454	543	CCUGUAUGAGUGGGAACAG	B CCUGUAUGAGUGGGAACAGTT B	2904

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396616-000S	454	543	CCUGUAUGAGUGGGAACAG	CUGUUCCCACUCAUACAGGUU	2905
R-008396619-000T	490	544	CACUCAAGAACAAGUAGCU	B CACUCAAGAACAAGUAGCUTT B	2906
R-008396619-000T	490	544	CACUCAAGAACAAGUAGCU	AGCUACUUGUUCUUGAGUGUU	2907
R-008396622-000Z	1996	545	CCUUCACAUCCUAGCUCGG	B CCUUCACAUCCUAGCUCGGTT B	2908
R-008396622-000Z	1996	545	CCUUCACAUCCUAGCUCGG	CCGAGCUAGGAUGUGAAGGUU	2909
R-008396625-000A	1839	546	AUGCACCUUUGCGUGAGCA	B AUGCACCUUUGCGUGAGCATT B	2910
R-008396625-000A	1839	546	AUGCACCUUUGCGUGAGCA	UGCUCACGCAAAGGUGCAUUU	2911
R-008396628-000B	1888	547	UGUUCGUGCACAUCAGGAU	AUCCUGAUGUGCACGAACAUU	2913
R-008396628-000B	1888	547	UGUUCGUGCACAUCAGGAU	B UGUUCGUGCACAUCAGGAUTT B	2912
R-008396631-000H	1879	548	UCAGUUGCUUGUUCGUGCA	B UCAGUUGCUUGUUCGUGCATT B	2914
R-008396631-000H	1879	548	UCAGUUGCUUGUUCGUGCA	UGCACGAACAAGCAACUGAUU	2915
R-008396634-000J	2508	172	ACUAUCCAGUUGAUGGGCU	B ACUAUCCAGUUGAUGGGCUTT B	2916
R-008396634-000J	2508	172	ACUAUCCAGUUGAUGGGCU	AGCCCAUCAACUGGAUAGUUU	2917
R-008396637-000K	1829	549	CCCGCAAAUCAUGCACCUU	AAGGUGCAUGAUUUGCGGGUU	2919
R-008396637-000K	1829	549	CCCGCAAAUCAUGCACCUU	B CCCGCAAAUCAUGCACCUUTT B	2918
R-008396640-000S	281	550	GCUGAUUUGAUGGAGUUGG	B GCUGAUUUGAUGGAGUUGGTT B	2920
R-008396640-000S	281	550	GCUGAUUUGAUGGAGUUGG	CCAACUCCAUCAAAUCAGCUU	2921
R-008396643-000T	1598	551	AUAGAGGCUCUUGUGCGUA	UACGCACAAGAGCCUCUAUUU	2923
R-008396643-000T	1598	551	AUAGAGGCUCUUGUGCGUA	B AUAGAGGCUCUUGUGCGUATT B	2922
R-008396646-000U	2135	552	CAGGACAAGGAAGCUGCAG	B CAGGACAAGGAAGCUGCAGTT B	2924
R-008396646-000U	2135	552	CAGGACAAGGAAGCUGCAG	CUGCAGCUUCCUUGUCCUGUU	2925
R-008396649-000V	642	67	UGGCUGAACCAUCACAGAU	AUCUGUGAUGGUUCAGCCAUU	2927
R-008396649-000V	642	67	UGGCUGAACCAUCACAGAU	B UGGCUGAACCAUCACAGAUTT B	2926
R-008396652-000B	1755	553	AGCUCUUACACCCACCAUC	B AGCUCUUACACCCACCAUCTT B	2928
R-008396652-000B	1755	553	AGCUCUUACACCCACCAUC	GAUGGUGGGUGUAAGAGCUUU	2929
R-008396655-000C	651	554	CAUCACAGAUGCUGAAACA	B CAUCACAGAUGCUGAAACATT B	2930
R-008396655-000C	651	554	CAUCACAGAUGCUGAAACA	UGUUUCAGCAUCUGUGAUGUU	2931
R-008396658-000D	1335	555	CUAUUGUAGAAGCUGGUGG	CCACCAGCUUCUACAAUAGUU	2933
R-008396658-000D	1335	555	CUAUUGUAGAAGCUGGUGG	B CUAUUGUAGAAGCUGGUGGTT B	2932
R-008396661-000K	2541	556	AUGCCCAGGACCUCAUGGA	UCCAUGAGGUCCUGGGCAUUU	2935
R-008396661-000K	2541	556	AUGCCCAGGACCUCAUGGA	B AUGCCCAGGACCUCAUGGATT B	2934
R-008396664-000L	531	557	UGACUCGAGCUCAGAGGGU	B UGACUCGAGCUCAGAGGGUTT B	2936
R-008396664-000L	531	557	UGACUCGAGCUCAGAGGGU	ACCCUCUGAGCUCGAGUCAUU	2937
R-008396667-000M	606	558	AGUUUGAUGCUGCUCAUCC	B AGUUUGAUGCUGCUCAUCCTT B	2938
R-008396667-000M	606	558	AGUUUGAUGCUGCUCAUCC	GGAUGAGCAGCAUCAAACUUU	2939
R-008396670-000U	1620	559	UCCUUCGGGCUGGUGACAG	B UCCUUCGGGCUGGUGACAGTT B	2940

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396670-000U	1620	559	UCCUUCGGGCUGGUGACAG	CUGUCACCAGCCCGAAGGAUU	2941
R-008396673-000V	2211	560	AUGAAGGUGUGGCGACAUA	B AUGAAGGUGUGGCGACAUATT B	2942
R-008396673-000V	2211	560	AUGAAGGUGUGGCGACAUA	UAUGUCGCCACACCUUCAUUU	2943
R-008396676-000W	2293	561	AGUUGAGCUGACCAGCUCU	B AGUUGAGCUGACCAGCUCUTT B	2944
R-008396676-000W	2293	561	AGUUGAGCUGACCAGCUCU	AGAGCUGGUCAGCUCAACUUU	2945
R-008396679-000X	1511	65	AAUGUGGUCACCUGUGCAG	B AAUGUGGUCACCUGUGCAGTT B	2946
R-008396679-000X	1511	65	AAUGUGGUCACCUGUGCAG	CUGCACAGGUGACCACAUUUU	2947
R-008396682-000D	455	562	CUGUAUGAGUGGGAACAGG	B CUGUAUGAGUGGGAACAGGTT B	2948
R-008396682-000D	455	562	CUGUAUGAGUGGGAACAGG	CCUGUUCCCACUCAUACAGUU	2949
R-008396685-000E	540	563	CUCAGAGGGUACGAGCUGC	B CUCAGAGGGUACGAGCUGCTT B	2950
R-008396685-000E	540	563	CUCAGAGGGUACGAGCUGC	GCAGCUCGUACCCUCUGAGUU	2951
R-008396688-000F	416	564	GGCAAUCCUGAGGAAGAGG	CCUCUUCCUCAGGAUUGCCUU	2953
R-008396688-000F	416	564	GGCAAUCCUGAGGAAGAGG	B GGCAAUCCUGAGGAAGAGGTT B	2952
R-008396691-000M	1669	130	UCUUCGUCAUCUGACCAGC	GCUGGUCAGAUGACGAAGAUU	2955
R-008396691-000M	1669	130	UCUUCGUCAUCUGACCAGC	B UCUUCGUCAUCUGACCAGCTT B	2954
R-008396694-000N	1210	565	CAUACUGGCUAGUGGUGGA	B CAUACUGGCAUGUGGUGGATT B	2956
R-008396694-000N	1210	565	CAUACUGGCUAGUGGUGGA	UCCACCACUAGCCAGUAUGUU	2957
R-008396697-000P	2262	566	ACAAGCCACAAGAUUACAA	UUGUAAUCUUGUGGCUUGUUU	2959
R-008396697-000P	2262	566	ACAAGCCACAAGAUUACAA	B ACAAGCCACAAGAUUACAATT B	2958
R-008396700-000G	1604	567	GCUCUUGUGCGUACUGUCC	GGACAGUACGCACAAGAGCUU	2961
R-008396700-000G	1604	567	GCUCUUGUGCGUACUGUCC	B GCUCUUGUGCGUACUGUCCTT B	2960
R-008396703-000H	435	568	AUGUGGAUACCUCCCAAGU	B AUGUGGAUACCUCCCAAGUTT B	2962
R-008396703-000H	435	568	AUGUGGAUACCUCCCAAGU	ACUUGGGAGGUAUCCACAUUU	2963
R-008396706-000J	2060	569	UUGUUUGUGCAGCUGCUUU	B UUGUUUGUGCAGCUGCUUUTT B	2964
R-008396706-000J	2060	569	UUGUUUGUGCAGCUGCUUU	AAAGCAGCUGCACAAACAAUU	2965
R-008396709-000K	2225	570	ACAUAUGCAGCUGCUGUUU	B ACAUAUGCAGCUGCUGUUUTT B	2966
R-008396709-000K	2225	570	ACAUAUGCAGCUGCUGUUU	AAACAGCAGCUGCAUAUGUUU	2967
R-008396712-000S	2510	47	UAUCCAGUUGAUGGGCUGC	B UAUCCAGUUGAUGGGCUGCTT B	2968
R-008396712-000S	2510	47	UAUCCAGUUGAUGGGCUGC	GCAGCCCAUCAACUGGAUAUU	2969
R-008396715-000T	481	571	UCAGUCCUUCACUCAAGAA	UUCUUGAGUGAAGGACUGAUU	2971
R-008396715-000T	481	571	UCAGUCCUUCACUCAAGAA	B UCAGUCCUUCACUCAAGAATT B	2970
R-008396718-000U	917	572	ACCUUGCAUAACCUUUCCC	B ACCUUGCAUAACCUUUCCCTT B	2972
R-008396718-000U	917	572	ACCUUGCAUAACCUUUCCC	GGGAAAGGUUAUGCAAGGUUU	2973
R-008396721-000A	2221	573	GGCGACAUAUGCAGCUGCU	B GGCGACAUAUGCAGCUGCUTT B	2974
R-008396721-000A	2221	573	GGCGACAUAUGCAGCUGCU	AGCAGCUGCAUAUGUCGCCUU	2975
R-008396724-000B	849	574	UGGUGUCUGCUAUUGUACG	CGUACAAUAGCAGACACCAUU	2977
R-008396724-000B	849	574	UGGUGUCUGCUAUUGUACG	B UGGUGUCUGCUAUUGUACGTT B	2976

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396727-000C	562	575	GUUCCCUGAGACAUUAGAU	B GUUCCCUGAGACAUUAGAUTT B	2978
R-008396727-000C	562	575	GUUCCCUGAGACAUUAGAU	AUCUAAUGUCUCAGGGAACUU	2979
R-003896730-000J	617	140	GCUCAUCCCACUAAUGUCC	GGACAUUAGUGGGAUGAGCUU	2981
R-003896730-000J	617	140	GCUCAUCCCACUAAUGUCC	B GCUCAUCCCACUAAUGUCCTT B	2980
R-008396733-000K	1787	576	AUAAAGGCUACUGUUGGAU	B AUAAAGGCUACUGUUGGAUTT B	2982
R-008396733-000K	1787	576	AUAAAGGCUACUGUUGGAU	AUCCAACAGUAGCCUUUAUUU	2983
R-008396736-000L	1860	57	GUGCCAUUCCACGACUAGU	ACUAGUCGUGGAAUGGCACUU	2985
R-008396736-000L	1860	57	GUGCCAUUCCACGACUAGU	B GUGCCAUUCCACGACUAGUTT B	2984
R-008396739-000M	1590	578	UGGGUGGUAUAGAGGCUCU	B UGGGUGGUAUAGAGGCUCUTT B	2986
R-008396739-000M	1590	578	UGGGUGGUAUAGAGGCUCU	AGAGCCUCUAUACCACCCAUU	2987
R-008396742-000U	955	579	GGCCAUCUUUAAGUCUGGA	UCCAGACUUAAAGAUGGCCUU	2989
R-008396742-000U	955	579	GGCCAUCUUUAAGUCUGGA	B GGCCAUCUUUAAGUCUGGATT B	2988
R-008396745-000V	2365	580	UAUUGGUGCCCAGGGAGAA	B UAUUGGUGCCCAGGGAGAATT B	2990
R-008396745-000V	2365	580	UAUUGGUGCCCAGGGAGAA	UUCUCCCUGGGCACCAAUAUU	2991
R-008396748-000W	534	581	CUCGAGCUCAGAGGGUACG	B CUCGAGCUCAGAGGGUACGTT B	2992
R-008396748-000W	534	581	CUCGAGCUCAGAGGGUACG	CGUACCCUCUGAGCUCGAGUU	2993
R-008396751-000C	706	582	AGAACUUGCCACACGUGCA	UGCACGUGUGGCAAGUUCUUU	2995
R-008396751-000C	706	582	AGAACUUGCCACACGUGCA	B AGAACUUGCCACACGUGCATT B	2994
R-008396754-000D	1740	583	UACCAGUUGUGGUUAAGCU	B UACCAGUUGUGGUUAAGCUTT B	2996
R-008396754-000D	1740	583	UACCAGUUGUGGUUAAGCU	AGCUUAACCACAACUGGUAUU	2997
R-008396757-000E	638	584	CGUUUGGCUGAACCAUCAC	B CGUUUGGCUGAACCAUCACTT B	2998
R-008396757-000E	638	584	CGUUUGGCUGAACCAUCAC	GUGAUGGUUCAGCCAAACGUU	2999
R-008396760-000L	1334	585	GCUAUUGUAGAAGCUGGUG	CACCAGCUUCUACAAUAGCUU	3001
R-008396760-000L	1334	585	GCUAUUGUAGAAGCUGGUG	B GCUAUUGUAGAAGCUGGUGTT B	3000
R-008396763-000M	971	586	GGAGGCAUUCCUGCCCUGG	B GGAGGCAUUCCUGCCCUGGTT B	3002
R-008396763-000M	971	586	GGAGGCAUUCCUGCCCUGG	CCAGGGCAGGAAUGCCUCCUU	3003
R-008396766-000N	2493	587	ACCACCCUGGUGCUGACUA	UAGUCAGCACCAGGGUGGUUU	3005
R-008396766-000N	2493	587	ACCACCCUGGUGCUGACUA	B ACCACCCUGGUGCUGACUATT B	3004
R-008396769-000P	1814	588	AAUCUUGCCCUUUGUCCCG	B AAUCUUGCCCUUUGUCCCGTT B	3006
R-008396769-000P	1814	588	AAUCUUGCCCUUUGUCCCG	CGGGACAAAGGGCAAGAUUUU	3007
R-008396772-000W	1088	589	CGUUUAGCUGGUGGGCUGC	GCAGCCCACCAGCUAAACGUU	3009
R-008396772-000W	1088	589	CGUUUAGCUGGUGGGCUGC	B CGUUUAGCUGGUGGGCUGCTT B	3008
R-008396775-000X	2292	590	CAGUUGAGCUGACCAGCUC	GAGCUGGUCAGCUCAACUGUU	3011
R-008396775-000X	2292	590	CAGUUGAGCUGACCAGCUC	B CAGUUGAGCUGACCAGCUCTT B	3010
R-008396778-000Y	1504	591	UGAUAUAAAUGUGGUCACC	GGUGACCACAUUUAUAUCAUU	3013
R-008396778-000Y	1504	591	UGAUAUAAAUGUGGUCACC	B UGAUAUAAAUGUGGUCACCTT B	3012

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396781-000E	404	592	CUGAGUGGUAAAGGCAAUC	GAUUGCCUUUACCACUCAGUU	3015
R-008396781-000E	404	592	CUGAGUGGUAAAGGCAAUC	B CUGAGUGGUAAAGGCAAUCTT B	3014
R-008396784-000F	1301	593	AAGGUGCUAUCUGUCUGCU	AGCAGACAGAUAGCACCUUUU	3017
R-008396784-000F	1301	593	AAGGUGCUAUCUGUCUGCU	B AAGGUGCUAUCUGUCUGCUTT B	3016
R-008396787-000G	2004	594	UCCUAGCUCGGGAUGUUCA	UGAACAUCCCGAGCUAGGAUU	3019
R-008396787-000G	2004	594	UCCUAGCUCGGGAUGUUCA	B UCCUAGCUCGGGAUGUUCATT B	3018
R-008396790-000N	853	6	GUCUGCUAUUGUACGUACC	GGUACGUACAAUAGCAGACUU	3021
R-008396790-000N	853	6	GUCUGCUAUUGUACGUACC	B GUCUGCUAUUGUACGUACCTT B	3020
R-008396793-000P	277	595	UCAAGCUGAUUUGAUGGAG	B UCAAGCUGAUUUGAUGGAGTT B	3022
R-008396793-000P	277	595	UCAAGCUGAUUUGAUGGAG	CUCCAUCAAAUCAGCUUGAUU	3023
R-008396795-000R	2304	596	CCAGCUCUCUCUUCAGAAC	GUUCUGAAGAGAGAGCUGGUU	3025
R-008396795-000R	2304	596	CCAGCUCUCUCUUCAGAAC	B CCAGCUCUCUCUUCAGAACTT B	3024
R-008396799-000S	300	597	ACAUGGCCAUGGAACCAGA	B ACAUGGCCAUGGAACCAGATT B	3026
R-008396799-000S	300	597	ACAUGGCCAUGGAACCAGA	UCUGGUUCCAUGGCCAUGUUU	3027
R-008396802-000J	1906	598	UACCCAGCGCCGUACGUCC	B UACCCAGCGCCGUACGUCCTT B	3028
R-008396802-000J	1906	598	UACCCAGCGCCGUACGUCC	GGACGUACGGCGCUGGGUAUU	3029
R-008396805-000K	1973	599	AUAGUUGAAGGUUGUACCG	CGGUACAACCUUCAACUAUUU	3031
R-008396805-000K	1973	599	AUAGUUGAAGGUUGUACCG	B AUAGUUGAAGGUUGUACCGTT B	3030
R-008396808-000L	1360	600	AGCUUUAGGACUUCACCUG	B AGCUUUAGGACUUCACCUGTT B	3032
R-008396808-000L	1360	600	AGCUUUAGGACUUCACCUG	CAGGUGAAGUCCUAAAGCUUU	3033
R-008396811-000T	2094	601	ACAUCCAAAGAGUAGCUGC	GCAGCUACUCUUUGGAUGUUU	3035
R-008396811-000T	2094	601	ACAUCCAAAGAGUAGCUGC	B ACAUCCAAAGAGUAGCUGCTT B	3034
R-008396814-000U	920	602	UUGCAUAACCUUUCCCAUC	B UUGCAUAACCUUUCCCAUCTT B	3036
R-008396814-000U	920	602	UUGCAUAACCUUUCCCAUC	GAUGGGAAAGGUUAUGCAAUU	3037
R-008396817-000V	1707	603	UGGCCCAGAAUGCAGUUCG	CGAACUGCAUUCUGGGCCAUU	3039
R-008396817-000V	1707	603	UGGCCCAGAAUGCAGUUCG	B UGGCCCAGAAUGCAGUUCGTT B	3038
R-008396820-000B	1808	604	AUUCGAAAUCUUGCCCUUU	B AUUCGAAAUCUUGCCCUUUTT B	3040
R-008396820-000B	1808	604	AUUCGAAAUCUUGCCCUUU	AAAGGGCAAGAUUUCGAAUUU	3041
R-008396823-000C	1326	605	AUAAGCCGGCUAUUGUAGA	UCUACAAUAGCCGGCUUAUUU	3043
R-008396823-000C	1326	605	AUAAGCCGGCUAUUGUAGA	B AUAAGCCGGCUAUUGUAGATT B	3042
R-008396826-000D	1158	606	CGACAGACUGCCUUCAAAU	B CGACAGACUGCCUUCAAAUTT B	3044
R-008396826-000D	1158	606	CGACAGACUGCCUUCAAAU	AUUUGAAGGCAGUCUGUCGUU	3045
R-008396829-000E	781	607	UGCAGUUAUGGUCCAUCAG	B UGCAGUUAUGGUCCAUCAGTT B	3046
R-008396829-000E	781	607	UGCAGUUAUGGUCCAUCAG	CUGAUGGACCAUAACUGCAUU	3047
R-008396832-000L	607	608	GUUUGAUGCUGCUCAUCCC	B GUUUGAUGCUGCUCAUCCCTT B	3048
R-008396832-000L	607	608	GUUUGAUGCUGCUCAUCCC	GGGAUGAGCAGCAUCAAACUU	3049
R-008396835-000M	627	609	CUAAUGUCCAGCGUUUGGC	GCCAAACGCUGGACAUUAGUU	3051

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396835-000M	627	609	CUAAUGUCCAGCGUUUGGC	B CUAAUGUCCAGCGUUUGGCTT B	3050
R-008396838-000N	500	610	CAAGUAGCUGAUAUUGAUG	B CAAGUAGCUGAUAUUGAUGTT B	3052
R-008396838-000N	500	610	CAAGUAGCUGAUAUUGAUG	CAUCAAUAUCAGCUACUUGUU	3053
R-008396841-000V	2185	611	UCUGACAGAGUUACUUCAC	B UCUGACAGAGUUACUUCACTT B	3054
R-008396841-000V	2185	611	UCUGACAGAGUUACUUCAC	GUGAAGUAACUCUGUCAGAUU	3055
R-008396844-000W	1592	612	GGUGGUAUAGAGGCUCUUG	B GGUGGUAUAGAGGCUCUUGTT B	3056
R-008396844-000W	1592	612	GGUGGUAUAGAGGCUCUUG	CAAGAGCCUCUAUACCACCUU	3057
R-008396847-000X	758	613	GACCAGGUGGUGGUUAAUA	B GACCAGGUGGUGGUUAAUATT B	3058
R-008396847-000X	758	613	GACCAGGUGGUGGUUAAUA	UAUUAACCACCACCUGGUCUU	3059
R-008396850-000D	2551	614	CCUCAUGGAUGGGCUGCCU	B CCUCAUGGAUGGGCUGCCUTT B	3060
R-008396850-000D	2551	614	CCUCAUGGAUGGGCUGCCU	AGGCAGCCCAUCCAUGAGGUU	3061
R-008396853-000E	1409	615	UGUCUUUGGACUCUCAGGA	B UGUCUUUGGACUCUCAGGATT B	3062
R-008396853-000E	1409	615	UGUCUUUGGACUCUCAGGA	UCCUGAGAGUCCAAAGACAUU	3063
R-008396856-000F	497	616	GAACAAGUAGCUGAUAUUG	B GAACAAGUAGCUGAUAUUGTT B	3064
R-008396856-000F	497	616	GAACAAGUAGCUGAUAUUG	CAAUAUCAGCUACUUGUUCUU	3065
R-008396859-000G	381	617	GUGCCACUACCACAGCUCC	B GUGCCACUACCACAGCUCCTT B	3066
R-008396859-000G	381	617	GUGCCACUACCACAGCUCC	GGAGCUGUGGUAGUGGCACUU	3067
R-008396862-000N	1841	618	GCACCUUUGCGUGAGCAGG	CCUGCUCACGCAAAGGUGCUU	3069
R-008396862-000N	1841	618	GCACCUUUGCGUGAGCAGG	B GCACCUUUGCGUGAGCAGGTT B	3068
R-008396865-000P	1368	619	GACUUCACCUGACAGAUCC	B GACUUCACCUGACAGAUCCTT B	3070
R-008396865-000P	1368	619	GACUUCACCUGACAGAUCC	GGAUCUGUCAGGUGAAGUCUU	3071
R-008396868-000R	2047	620	AAAUACCAUUCCAUUGUUU	AAACAAUGGAAUGGUAUUUUU	3073
R-008396868-000R	2047	620	AAAUACCAUUCCAUUGUUU	B AAAUACCAUUCCAUUGUUUTT B	3072
R-008396871-000X	492	621	CUCAAGAACAAGUAGCUGA	B CUCAAGAACAAGUAGCUGATT B	3074
R-008396871-000X	492	621	CUCAAGAACAAGUAGCUGA	UCAGCUACUUGUUCUUGAGUU	3075
R-008396874-000Y	832	126	CAUGCGUUCUCCUCAGAUG	B CAUGCGUUCUCCUCAGAUGTT B	3076
R-008396874-000Y	832	126	CAUGCGUUCUCCUCAGAUG	CAUCUGAGGAGAACGCAUGUU	3077
R-008396877-000Z	2118	622	UCCUCUGUGAACUUGCUCA	B UCCUCUGUGAACUUGCUCATT B	3078
R-008396877-000Z	2118	622	UCCUCUGUGAACUUGCUCA	UGAGCAAGUUCACAGAGGAUU	3079
R-008396880-000F	968	623	UCUGGAGGCAUUCCUGCCC	GGGCAGGAAUGCCUCCAGAUU	3081
R-008396880-000F	968	623	UCUGGAGGCAUUCCUGCCC	B UCUGGAGGCAUUCCUGCCCTT B	3080
R-008396883-000G	965	624	AAGUCUGGAGGCAUUCCUG	CAGGAAUGCCUCCAGACUUUU	3083
R-008396883-000G	965	624	AAGUCUGGAGGCAUUCCUG	B AAGUCUGGAGGCAUUCCUGTT B	3082
R-008396886-000H	1977	625	UUGAAGGUUGUACCGGAGC	GCUCCGGUACAACCUUCAAUU	3085
R-008396886-000H	1977	625	UUGAAGGUUGUACCGGAGC	B UUGAAGGUUGUACCGGAGCTT B	3084
R-008396889-000J	2001	626	ACAUCCUAGCUCGGGAUGU	B ACAUCCUAGCUCGGGAUGUTT B	3086

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396889-000J	2001	626	ACAUCCUAGCUCGGGAUGU	ACAUCCCGAGCUAGGAUGUUU	3087
R-008396892-000R	1191	627	ACCAAGAAAGCAAGCUCAU	B ACCAAGAAAGCAAGCUCAUTT B	3088
R-008396892-000R	1191	627	ACCAAGAAAGCAAGCUCAU	AUGAGCUUGCUUUCUUGGUUU	3089
R-008396895-000S	640	628	UUUGGCUGAACCAUCACAG	B UUUGGCUGAACCAUCACAGTT B	3090
R-008396895-000S	640	628	UUUGGCUGAACCAUCACAG	CUGUGAUGGUUCAGCCAAAUU	3091
R-008396898-000T	715	629	CACACGUGCAAUCCCUGAA	B CACACGUGCAAUCCCUGAATT B	3092
R-008396898-000T	715	629	CACACGUGCAAUCCCUGAA	UUCAGGGAUUGCACGUGUGUU	3093
R-008396901-000K	1204	630	GCUCAUCAUACUGGCUAGU	ACUAGCCAGUAUGAUGAGCUU	3095
R-008396901-000K	1204	630	GCUCAUCAUACUGGCUAGU	B GCUCAUCAUACUGGCUAGUTT B	3094
R-008396904-000L	3093	631	GGGUAGGGUAAAUCAGUAA	B GGGUAGGGUAAAUCAGUAATT B	3096
R-008396904-000L	3093	631	GGGUAGGGUAAAUCAGUAA	UUACUGAUUUACCCUACCCUU	3097
R-008396907-000M	1371	632	UUCACCUGACAGAUCCAAG	CUUGGAUCUGUCAGGUGAAUU	3099
R-008396907-000M	1371	632	UUCACCUGACAGAUCCAAG	B UUCACCUGACAGAUCCAAGTT B	3098
R-008396910-000U	1424	121	AGGAAUCUUUCAGAUGCUG	B AGGAAUCUUUCAGAUGCUGTT B	3100
R-008396910-000U	1424	121	AGGAAUCUUUCAGAUGCUG	CAGCAUCUGAAAGAUUCCUUU	3101
R-008396913-000V	860	161	AUUGUACGUACCAUGCAGA	B AUUGUACGUACCAUGCAGATT B	3102
R-008396913-000V	860	161	AUUGUACGUACCAUGCAGA	UCUGCAUGGUACGUACAAUUU	3103
R-008396916-000W	409	633	UGGUAAAGGCAAUCCUGAG	B UGGUAAAGGCAAUCCUGAGTT B	3104
R-008396916-000W	409	633	UGGUAAAGGCAAUCCUGAG	CUCAGGAUUGCCUUUACCAUU	3105
R-008396919-000X	1143	7	AAUUCUUGGCUAUUACGAC	GUCGUAAUAGCCAAGAAUUUU	3107
R-008396919-000X	1143	7	AAUUCUUGGCUAUUACGAC	B AAUUCUUGGCUAUUACGACTT B	3106
R-008396922-000D	2405	634	GAUCCUAGCUAUCGUUCUU	B GAUCCUAGCUAUCGUUCUUTT B	3108
R-008396922-000D	2405	634	GAUCCUAGCUAUCGUUCUU	AAGAACGAUAGCUAGGAUCUU	3109
R-008396928-000F	1671	635	UUCGUCAUCUGACCAGCCG	CGGCUGGUCAGAUGACGAAUU	3111
R-008396928-000F	1671	635	UUCGUCAUCUGACCAGCCG	B UUCGUCAUCUGACCAGCCGTT B	3110
R-008396931-000M	1427	636	AAUCUUUCAGAUGCUGCAA	B AAUCUUUCAGAUGCUGCAATT B	3112
R-008396931-000M	1427	636	AAUCUUUCAGAUGCUGCAA	UUGCAGCAUCUGAAAGAUUUU	3113
R-008396934-000N	1717	637	UGCAGUUCGCCUUCACUAU	AUAGUGAAGGCGAACUGCAUU	3115
R-008396934-000N	1717	637	UGCAGUUCGCCUUCACUAU	B UGCAGUUCGCCUUCACUAUTT B	3114
R-008396937-000P	2400	638	AGGAUGAUCCUAGCUAUCG	CGAUAGCUAGGAUCAUCCUUU	3117
R-008396937-000P	2400	638	AGGAUGAUCCUAGCUAUCG	B AGGAUGAUCCUAGCUAUCGTT B	3116
R-008396940-000W	2305	639	CAGCUCUCUCUUCAGAACA	B CAGCUCUCUCUUCAGAACATT B	3118
R-008396940-000W	2305	639	CAGCUCUCUCUUCAGAACA	UGUUCUGAAGAGAGAGCUGUU	3119
R-008396943-000X	1928	640	GGUGGGACACAGCAGCAAU	B GGUGGGACACAGCAGCAAUTT B	3120
R-008396943-000X	1928	640	GGUGGGACACAGCAGCAAU	AUUGCUGCUGUGUCCCACCUU	3121
R-008396946-000Y	2399	641	CAGGAUGAUCCUAGCUAUC	B CAGGAUGAUCCUAGCUAUCTT B	3122
R-008396946-000Y	2399	641	CAGGAUGAUCCUAGCUAUC	GAUAGCUAGGAUCAUCCUGUU	3123

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008396949-000Z	426	642	AGGAAGAGGAUGUGGAUAC	B AGGAAGAGGAUGUGGAUACTT B	3124
R-008396949-000Z	426	642	AGGAAGAGGAUGUGGAUAC	GUAUCCACAUCCUCUUCCUUU	3125
R-008396952-000F	1309	643	AUCUGUCUGCUCUAGUAAU	AUUACUAGAGCAGACAGAUUU	3127
R-008396952-000F	1309	643	AUCUGUCUGCUCUAGUAAU	B AUCUGUCUGCUCUAGUAAUTT B	3126
R-008396955-000G	925	644	UAACCUUUCCCAUCAUCGU	B UAACCuUUCCCAUCAUCGUTT B	3128
R-008396955-000G	925	644	UAACCUUUCCCAUCAUCGU	ACGAUGAUGGGAAAGGUUAUU	3129
R-008396958-000H	2072	645	CUGCUUUAUUCUCCCAUUG	CAAUGGGAGAAUAAAGCAGUU	3131
R-008396958-000H	2072	645	CUGCUUUAUUCUCCCAUUG	B CUGCUUUAUUCUCCCAUUGTT B	3130
R-008396964-000R	2939	646	AAUUGUAAUCUGAAUAAAG	B AAUUGUAAUCUGAAUAAAGTT B	3132
R-008396964-000R	2939	646	AAUUGUAAUCUGAAUAAAG	CUUUAUUCAGAUUACAAUUUU	3133
R-008396973-000Z	1480	647	UCUUGUUCAGCUUCUGGGU	B UCUUGUUCAGCUUCUGGGUTT B	3134
R-008396973-000Z	1480	647	UCUUGUUCAGCUUCUGGGU	ACCCAGAAGCUGAACAAGAUU	3135
R-008396976-000A	1889	648	GUUCGUGCACAUCAGGAUA	B GUUCGUGCACAUCAGGAUATT B	3136
R-008396976-000A	1889	648	GUUCGUGCACAUCAGGAUA	UAUCCUGAUGUGCACGAACUU	3137
R-008396979-000B	699	649	AUGAUGCAGAACUUGCCAC	B AUGAUGCAGAACUUGCCACTT B	3138
R-008396979-000B	699	649	AUGAUGCAGAACUUGCCAC	GUGGCAAGUUCUGCAUCAUUU	3139
R-008396982-000H	506	650	GCUGAUAUUGAUGGACAGU	B GCUGAUAUUGAUGGACAGUTT B	3140
R-008396982-000H	506	650	GCUGAUAUUGAUGGACAGU	ACUGUCCAUCAAUAUCAGCUU	3141
R-008396985-000J	1750	651	GGUUAAGCUCUUACACCCA	UGGGUGUAAGAGCUUAACCUU	3143
R-008396985-000J	1750	651	GGUUAAGCUCUUACACCCA	B GGUUAAGCUCUUACACCCATT B	3142
R-008396988-000K	1820	652	GCCCUUUGUCCCGCAAAUC	B GCCCUUUGUCCCGCAAAUCTT B	3144
R-008396988-000K	1820	652	GCCCUUUGUCCCGCAAAUC	GAUUUGCGGGACAAAGGGCUU	3145
R-008396991-000S	541	653	UCAGAGGGUACGAGCUGCU	AGCAGCUCGUACCCUCUGAUU	3147
R-008396991-000S	541	653	UCAGAGGGUACGAGCUGCU	B UCAGAGGGUACGAGCUGCUTT B	3146
R-008396994-000T	880	102	UACAAAUGAUGUAGAAACA	B UACAAAUGAUGUAGAAACATT B	3148
R-008396994-000T	880	102	UACAAAUGAUGUAGAAACA	UGUUUCUACAUCAUUUGUAUU	3149
R-008396997-000U	665	654	AAACAUGCAGUUGUAAACU	B AAACAUGCAGUUGUAAACUTT B	3150
R-008396997-000U	665	654	AAACAUGCAGUUGUAAACU	AGUUUACAACUGCAUGUUUUU	3151
R-008397000-000H	1817	655	CUUGCCCUUUGUCCCGCAA	UUGCGGGACAAAGGGCAAGUU	3153
R-008397000-000H	1817	655	CUUGCCCUUUGUCCCGCAA	B CUUGCCCUUUGUCCCGCAATT B	3152
R-008397003-000J	2275	656	UUACAAGAAACGGCUUUCA	UGAAAGCCGUUUCUUGUAAUU	3155
R-008397003-000J	2275	656	UUACAAGAAACGGCUUUCA	B UUACAAGAAACGGCUUUCATT B	3154
R-008397006-000K	2426	657	CACUCUGGUGGAUAUGGCC	GGCCAUAUCCACCAGAGUGUU	3157
R-008397006-000K	2426	657	CACUCUGGUGGAUAUGGCC	B CACUCUGGUGGAUAUGGCCTT B	3156
R-008397009-000L	958	658	CAUCUUUAAGUCUGGAGGC	B CAUCUUUAAGUCUGGAGGCTT B	3158
R-008397009-000L	958	658	CAUCUUUAAGUCUGGAGGC	GCCUCCAGACUUAAAGAUGUU	3159

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397012-000T	1657	659	UGCCAUCUGUGCUCUUCGU	B UGCCAUCUGUGCUCUUCGUTT B	3160
R-008397012-000T	1657	659	UGCCAUCUGUGCUCUUCGU	ACGAAGAGCACAGAUGGCAUU	3161
R-008397015-000U	1146	660	UCUUGGCUAUUACGACAGA	UCUGUCGUAAUAGCCAAGAUU	3163
R-008397015-000U	1146	660	UCUUGGCUAUUACGACAGA	B UCUUGGCUAUUACGACAGATT B	3162
R-008397018-000V	3078	661	AUUUGGGAUAUGUAUGGGU	B AUUUGGGAUAUGUAUGGGUTT B	3164
R-008397018-000V	3078	661	AUUUGGGAUAUGUAUGGGU	ACCCAUACAUAUCCCAAAUUU	3165
R-008397021-000B	1008	662	CAGUGGAUUCUGUGUUGUU	AACAACACAGAAUCCACUGUU	3167
R-008397021-000B	1008	662	CAGUGGAUUCUGUGUUGUU	B CAGUGGAUUCUGUGUUGUUTT B	3166
R-008397024-000C	1621	663	CCUUCGGGCUGGUGACAGG	CCUGUCACCAGCCCGAAGGUU	3169
R-008397024-000C	1621	663	CCUUCGGGCUGGUGACAGG	B CCUUCGGGCUGGUGACAGGTT B	3168
R-008397027-000D	1932	664	GGACACAGCAGCAAUUUGU	B GGACACAGCAGCAAUUUGUTT B	3170
R-008397027-000D	1932	664	GGACACAGCAGCAAUUUGU	ACAAAUUGCUGCUGUGUCCUU	3171
R-008397030-000K	1909	665	CCAGCGCCGUACGUCCAUG	CAUGGACGUACGGCGCUGGUU	3173
R-008397030-000K	1909	665	CCAGCGCCGUACGUCCAUG	B CCAGCGCCGUACGUCCAUGTT B	3172
R-008397033-000L	2279	666	AAGAAACGGCUUUCAGUUG	CAACUGAAAGCCGUUUCUUUU	3175
R-008397033-000L	2279	666	AAGAAACGGCUUUCAGUUG	B AAGAAACGGCUUUCAGUUGTT B	3174
R-008397036-000M	574	667	AUUAGAUGAGGGCAUGCAG	B AUUAGAUGAGGGCAUGCAGTT B	3176
R-008397036-000M	574	667	AUUAGAUGAGGGCAUGCAG	CUGCAUGCCCUCAUCUAAUUU	3177
R-008397039-000N	2303	668	ACCAGCUCUCUCUUCAGAA	UUCUGAAGAGAGAGCUGGUUU	3179
R-008397039-000N	2303	668	ACCAGCUCUCUCUUCAGAA	B ACCAGCUCUCUCUUCAGAATT B	3178
R-008397042-000V	784	669	AGUUAUGGUCCAUCAGCUU	B AGUUAUGGUCCAUCAGCUUTT B	3180
R-008397042-000V	784	669	AGUUAUGGUCCAUCAGCUU	AAGCUGAUGGACCAUAACUUU	3181
R-008397045-000W	2507	670	GACUAUCCAGUUGAUGGGC	GCCCAUCAACUGGAUAGUCUU	3183
R-008397045-000W	2507	670	GACUAUCCAGUUGAUGGGC	B GACUAUCCAGUUGAUGGGCTT B	3182
R-008397048-000X	995	671	AUGCUUGGUUCACCAGUGG	B AUGCUUGGUUCACCAGUGGTT B	3184
R-008397048-000X	995	671	AUGCUUGGUUCACCAGUGG	CCACUGGUGAACCAAGCAUUU	3185
R-008397051-000D	2006	672	CUAGCUCGGGAUGUUCACA	UGUGAACAUCCCGAGCUAGUU	3187
R-008397051-000D	2006	672	CUAGCUCGGGAUGUUCACA	B CUAGCUCGGGAUGUUCACATT B	3186
R-008397054-000E	1857	673	CUCUUACACCCACCAUCCC	GGGAUGGUGGGUGUAAGAGUU	3189
R-008397054-000E	1857	673	CUCUUACACCCACCAUCCC	B CUCUUACACCCACCAUCCCTT B	3188
R-008397057-000F	2129	674	CUUGCUCAGGACAAGGAAG	B CUUGCUCAGGACAAGGAAGTT B	3190
R-008397057-000F	2129	674	CUUGCUCAGGACAAGGAAG	CUUCCUUGUCCUGAGCAAGUU	3191
R-008397060-000M	2272	675	AGAUUACAAGAAACGGCUU	B AGAUUACAAGAAACGGCUUTT B	3192
R-008397060-000M	2272	675	AGAUUACAAGAAACGGCUU	AAGCCGUUUCUUGUAAUCUUU	3193
R-008397063-000N	389	676	ACCACAGCUCCUUCUCUGA	B ACCACAGCUCCUUCUCUGATT B	3194
R-008397063-000N	389	676	ACCACAGCUCCUUCUCUGA	UCAGAGAAGGAGCUGUGGUUU	3195
R-008397066-000P	708	176	AACUUGCCACACGUGCAAU	B AACUUGCCACACGUGCAAUTT B	3196

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397066-000P	708	176	AACUUGCCACACGUGCAAU	AUUGCACGUGUGGCAAGUUUU	3197
R-008397069-000R	1435	677	AGAUGCUGCAACUAAACAG	CUGUUUAGUUGCAGCAUCUUU	3199
R-008397069-000R	1435	677	AGAUGCUGCAACUAAACAG	B AGAUGCUGCAACUAAACAGTT B	3198
R-008397072-000X	1247	34	AUAAUGAGGACCUAUACUU	B AUAAUGAGGACCUAUACUUTT B	3200
R-008397072-000X	1247	34	AUAAUGAGGACCUAUACUU	AAGUAUAGGUCCUCAUUAUUU	3201
R-008397075-000Y	1752	678	UUAAGCUCUUACACCCACC	GGUGGGUGUAAGAGCUUAAUU	3203
R-008397075-000Y	1752	678	UUAAGCUCUUACACCCACC	B UUAAGCUCUUACACCCACCTT B	3202
R-008397078-000Z	773	679	AAUAAGGCUGCAGUUAUGG	CCAUAACUGCAGCCUUAUUUU	3205
R-008397078-000Z	773	679	AAUAAGGCUGCAGUUAUGG	B AAUAAGGCUGCAGUUAUGGTT B	3204
R-008397081-000F	3080	680	UUGGGAUAUGUAUGGGUAG	CUACCCAUACAUAUCCCAAUU	3207
R-008397081-000F	3080	680	UUGGGAUAUGUAUGGGUAG	B UUGGGAUAUGUAUGGGUAGTT B	3206
R-008397084-000G	3174	681	GUAACCUGCUGUGAUACGA	B GUAACCUGCUGUGAUACGATT B	3208
R-008397084-000G	3174	681	GUAACCUGCUGUGAUACGA	UCGUAUCACAGCAGGUUACUU	3209
R-008397087-000H	1578	682	UGGUCUGCCAAGUGGGUGG	B UGGUCUGCCAAGUGGGUGGTT B	3210
R-008397087-000H	1578	682	UGGUCUGCCAAGUGGGUGG	CCACCCACUUGGCAGACCAUU	3211
R-008397090-000P	398	683	CCUUCUCUGAGUGGUAAAG	B CCUUCUCUGAGUGGUAAAGTT B	3212
R-008397090-000P	398	683	CCUUCUCUGAGUGGUAAAG	CUUUACCACUCAGAGAAGGUU	3213
R-008397083-000R	2153	684	GAAGCUAUUGAAGCUGAGG	CCUCAGCUUCAAUAGCUUCUU	3215
R-008397083-000R	2153	684	GAAGCUAUUGAAGCUGAGG	B GAAGCUAUUGAAGCUGAGGTT B	3214
R-008397096-000S	702	685	AUGCAGAACUUGCCACACG	CGUGUGGCAAGUUCUGCAUUU	3217
R-008397096-000S	702	685	AUGCAGAACUUGCCACACG	B AUGCAGAACUUGCCACACGTT B	3216
R-008397099-000T	503	686	GUAGCUGAUAUUGAUGGAC	B GUAGCUGAUAUUGAUGGACTT B	3218
R-008397099-000T	503	686	GUAGCUGAUAUUGAUGGAC	GUCCAUCAAUAUCAGCUACUU	3219
R-008397102-000K	276	687	CUCAAGCUGAUUUGAUGGA	B CUCAAGCUGAUUUGAUGGATT B	3220
R-008397102-000K	276	687	CUCAAGCUGAUUUGAUGGA	UCCAUCAAAUCAGCUUGAGUU	3221
R-008397105-000L	1962	688	GCAUGGAAGAAAUAGUUGA	B GCAUGGAAGAAAUAGUUGATT B	3222
R-008397105-000L	1962	688	GCAUGGAAGAAAUAGUUGA	UCAACUAUUUCUUCCAUGCUU	3223
R-008397108-000M	1347	689	CUGGUGGAAUGCAAGCUUU	B CUGGUGGAAUGCAAGCUUUTT B	3224
R-008397108-000M	1347	689	CUGGUGGAAUGCAAGCUUU	AAAGCUUGCAUUCCACCAGUU	3225
R-008397111-000U	2544	690	CCCAGGACCUCAUGGAUGG	CCAUCCAUGAGGUCCUGGGUU	3227
R-008397111-000U	2544	690	CCCAGGACCUCAUGGAUGG	B CCCAGGACCUCAUGGAUGGTT B	3226
R-008397114-000V	3079	691	UUUGGGAUAUGUAUGGGUA	B UUUGGGAUAUGUAUGGGUATT B	3228
R-008397114-000V	3079	691	UUUGGGAUAUGUAUGGGUA	UACCCAUACAUAUCCCAAAUU	3229
R-008397117-000W	3164	692	CAAAGUUGUUGUAACCUGC	GCAGGUUACAACAACUUUGUU	3231
R-008397117-000W	3164	692	CAAAGUUGUUGUAACCUGC	B CAAAGUUGUUGUAACCUGCTT B	3230
R-008397120-000C	2026	693	CCGAAUUGUUAUCAGAGGA	B CCGAAUUGUUAUCAGAGGATT B	3232

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397120-000C	2026	693	CCGAAUUGUUAUCAGAGGA	UCCUCUGAUAACAAUUCGGUU	3233
R-008397123-000D	2938	694	UAAUUGUAAUCUGAAUAAA	B UAAUUGUAAUCUGAAUAAATT B	3234
R-008397123-000D	2938	694	UAAUUGUAAUCUGAAUAAA	UUUAUUCAGAUUACAAUUAUU	3235
R-008397126-000E	2940	695	AUUGUAAUCUGAAUAAAGU	ACUUUAUUCAGAUUACAAUUU	3237
R-008397126-000E	2940	695	AUUGUAAUCUGAAUAAAGU	B AUUGUAAUCUGAAUAAAGUTT B	3236
R-008397129-000F	2027	696	CGAAUUGUUAUCAGAGGAC	B CGAAUUGUUAUCAGAGGACTT B	3238
R-008397129-000F	2027	696	CGAAUUGUUAUCAGAGGAC	GUCCUCUGAUAACAAUUCGUU	3239
R-008397132-000M	448	697	CCAAGUCCUGUAUGAGUGG	CCACUCAUACAGGACUUGGUU	3241
R-008397132-000M	448	697	CCAAGUCCUGUAUGAGUGG	B CCAAGUCCUGUAUGAGUGGTT B	3240
R-008397135-000N	1328	698	AAGCCGGCUAUUGUAGAAG	B AAGCCGGCUAUUGUAGAAGTT B	3242
R-008397135-000N	1328	698	AAGCCGGCUAUUGUAGAAG	CUUCUACAAUAGCCGGCUUUU	3243
R-008397138-000P	1970	33	GAAAUAGUUGAAGGUUGUA	UACAACCUUCAACUAUUUCUU	3245
R-008397138-000P	1970	33	GAAAUAGUUGAAGGUUGUA	B GAAAUAGUUGAAGGUUGUATT B	3244
R-008397141-000W	2406	699	AUCCUAGCUAUCGUUCUUU	AAAGAACGAUAGCUAGGAUUU	3247
R-008397141-000W	2406	699	AUCCUAGCUAUCGUUCUUU	B AUCCUAGCUAUCGUUCUUUTT B	3246
R-008397144-000X	924	700	AUAACCUUUCCCAUCAUCG	B AUAACCUUUCCCAUCAUCGTT B	3248
R-008397144-000X	924	700	AUAACCUUUCCCAUCAUCG	CGAUGAUGGGAAAGGUUAUUU	3249
R-008397147-000Y	1584	701	GCCAAGUGGGUGGUAUAGA	UCUAUACCACCCACUUGGCUU	3251
R-008397147-000Y	1584	701	GCCAAGUGGGUGGUAUAGA	B GCCAAGUGGGUGGUAUAGATT B	3250
R-008397150-000E	1871	702	CGACUAGUUCAGUUGCUUG	B CGACUAGUUCAGUUGCUUGTT B	3252
R-008397150-000E	1871	702	CGACUAGUUCAGUUGCUUG	CAAGCAACUGAACUAGUCGUU	3253
R-008397153-000F	999	703	UUGGUUCACCAGUGGAUUC	B UUGGUUCACCAGUGGAUUCTT B	3254
R-008397153-000F	999	703	UUGGUUCACCAGUGGAUUC	GAAUCCACUGGUGAACCAAUU	3255
R-008397156-000G	1400	704	GUUCAGAACUGUCUUUGGA	UCCAAAGACAGUUCUGAACUU	3257
R-008397156-000G	1400	704	GUUCAGAACUGUCUUUGGA	B GUUCAGAACUGUCUUUGGATT B	3256
R-008397159-000H	3180	705	UGCUGUGAUACGAUGCUUC	GAAGCAUCGUAUCACAGCAUU	3259
R-008397159-000H	3180	705	UGCUGUGAUACGAUGCUUC	B UGCUGUGAUACGAUGCUUCTT B	3258
R-008397162-000P	2569	706	UCCAGGUGACAGCAAUCAG	CUGAUUGCUGUCACCUGGAUU	3261
R-008397162-000P	2569	706	UCCAGGUGACAGCAAUCAG	B UCCAGGUGACAGCAAUCAGTT B	3260
R-008397165-000R	787	707	UAUGGUCCAUCAGCUUUCU	AGAAAGCUGAUGGACCAUAUU	3263
R-008397165-000R	787	707	UAUGGUCCAUCAGCUUUCU	B UAUGGUCCAUCAGCUUUCUTT B	3262
R-008397168-000S	1861	708	UGCCAUUCCACGACUAGUU	B UGCCAUUCCACGACUAGUUTT B	3264
R-008397168-000S	1861	708	UGCCAUUCCACGACUAGUU	AACUAGUCGUGGAAUGGCAUU	3265
R-008397171-000Y	1190	709	AACCAAGAAAGCAAGCUCA	UGAGCUUGCUUUCUUGGUUUU	3267
R-008397171-000Y	1190	709	AACCAAGAAAGCAAGCUCA	B AACCAAGAAAGCAAGCUCATT B	3266
R-008397174-000Z	1557	710	AUAAUUAUAAGAACAAGAU	AUCUUGUUCUUAUAAUUAUUU	3269
R-008397174-000Z	1557	710	AUAAUUAUAAGAACAAGAU	B AUAAUUAUAAGAACAAGAUTT B	3268

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397177-000Z	1751	711	GUUAAGCUCUUACACCCAC	B GUUAAGCUCUUACACCCACTT B	3270
R-008397177-000Z	1751	711	GUUAAGCUCUUACACCCAC	GUGGGUGUAAGAGCUUAACUU	3271
R-008397180-000G	2897	712	UUGAGUAAUGGUGUAGAAC	B UUGAGUAAUGGUGUAGAACTT B	3272
R-008397180-000G	2897	712	UUGAGUAAUGGUGUAGAAC	GUUCUACACCAUUACUCAAUU	3273
R-008397183-000H	2217	713	GUGUGGCGACAUAUGCAGC	GCUGCAUAUGUCGCCACACUU	3275
R-008397183-000H	2217	713	GUGUGGCGACAUAUGCAGC	B GUGUGGCGACAUAUGCAGCTT B	3274
R-008397186-000J	2302	714	GACCAGCUCUCUCUUCAGA	UCUGAAGAGAGAGCUGGUCUU	3277
R-008397186-000J	2302	714	GACCAGCUCUCUCUUCAGA	B GACCAGCUCUCUCUUCAGATT B	3276
R-008397189-000K	1984	715	UUGUACCGGAGCCCUUCAC	GUGAAGGGCUCCGGUACAAUU	3279
R-008397189-000K	1984	715	UUGUACCGGAGCCCUUCAC	B UUGUACCGGAGCCCUUCACTT B	3278
R-008397192-000S	302	716	AUGGCCAUGGAACCAGACA	B AUGGCCAUGGAACCAGACATT B	3280
R-008397192-000S	302	716	AUGGCCAUGGAACCAGACA	UGUCUGGUUCCAUGGCCAUUU	3281
R-008397195-000T	2431	717	UGGUGGAUAUGGCCAGGAU	B UGGUGGAUAUGGCCAGGAUTT B	3282
R-008397195-000T	2431	717	UGGUGGAUAUGGCCAGGAU	AUCCUGGCCAUAUCCACCAUU	3283
R-008397198-000U	2183	718	CCUCUGACAGAGUUACUUC	GAAGUAACUCUGUCAGAGGUU	3285
R-008397198-000U	2183	718	CCUCUGACAGAGUUACUUC	B CCUCUGACAGAGUUACUUCTT B	3284
R-008397201-000L	2403	719	AUGAUCCUAGCUAUCGUUC	GAACGAUAGCUAGGAUCAUUU	3287
R-008397201-000L	2403	719	AUGAUCCUAGCUAUCGUUC	B AUGAUCCUAGCUAUCGUUCTT B	3286
R-008397204-000M	788	720	AUGGUCCAUCAGCUUUCUA	B AUGGUCCAUCAGCUUUCUATT B	3288
R-008397204-000M	788	720	AUGGUCCAUCAGCUUUCUA	UAGAAAGCUGAUGGACCAUUU	3289
R-008397207-000N	1476	721	GGACUCUUGUUCAGCUUCU	B GGACUCUUGUUCAGCUUCUTT B	3290
R-008397207-000N	1476	721	GGACUCUUGUUCAGCUUCU	AGAAGCUGAACAAGAGUCCUU	3291
R-008397210-000V	827	722	GCUAUCAUGCGUUCUCCUC	B GCUAUCAUGCGUUCUCCUCTT B	3292
R-008397210-000V	827	722	GCUAUCAUGCGUUCUCCUC	GAGGAGAACGCAUGAUAGCUU	3293
R-008397213-000W	2299	723	GCUGACCAGCUCUCUCUUC	B GCUGACCAGCUCUCUCUUCTT B	3294
R-008397213-000W	2299	723	GCUGACCAGCUCUCUCUUC	GAAGAGAGAGCUGGUCAGCUU	3295
R-008397216-000X	1891	724	UCGUGCACAUCAGGAUACC	B UCGUGCACAUCAGGAUACCTT B	3296
R-008397216-000X	1891	724	UCGUGCACAUCAGGAUACC	GGUAUCCUGAUGUGCACGAUU	3297
R-008397219-000Y	2196	725	UACUUCACUCUAGGAAUGA	UCAUUCCUAGAGUGAAGUAUU	3299
R-008397219-000Y	2196	725	UACUUCACUCUAGGAAUGA	B UACUUCACUCUAGGAAUGATT B	3298
R-008397222-000E	663	726	UGAAACAUGCAGUUGUAAA	UUUACAACUGCAUGUUUCAUU	3301
R-008397222-000E	663	726	UGAAACAUGCAGUUGUAAA	B UGAAACAUGCAGUUGUAAATT B	3300
R-008397225-000F	1028	727	UAUGCCAUUACAACUCUCC	GGAGAGUUGUAAUGGCAUAUU	3303
R-008397225-000F	1028	727	UAUGCCAUUACAACUCUCC	B UAUGCCAUUACAACUCUCCTT B	3302
R-008397228-000G	2032	728	UGUUAUCAGAGGACUAAAU	AUUUAGUCCUCUGAUAACAUU	3305
R-008397228-000G	2032	728	UGUUAUCAGAGGACUAAAU	B UGUUAUCAGAGGACUAAAUTT B	3304

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397231-000N	1459	729	GAUGGAAGGUCUCCUUGGG	B GAUGGAAGGUCUCCUUGGGTT B	3306
R-008397231-000N	1459	729	GAUGGAAGGUCUCCUUGGG	CCCAAGGAGACCUUCCAUCUU	3307
R-008397234-000P	2095	730	CAUCCAAAGAGUAGCUGCA	UGCAGCUACUCUUUGGAUGUU	3309
R-008397234-000P	2095	730	CAUCCAAAGAGUAGCUGCA	B CAUCCAAAGAGUAGCUGCATT B	3308
R-008397237-000R	1686	731	GCCGACACCAAGAAGCAGA	B GCCGACACCAAGAAGCAGATT B	3310
R-008397237-000R	1686	731	GCCGACACCAAGAAGCAGA	UCUGCUUCUUGGUGUCGGCUU	3311
R-008397240-000X	1412	732	CUUUGGACUCUCAGGAAUC	B CUUUGGACUCUCAGGAAUCTT B	3312
R-008397240-000X	1412	732	CUUUGGACUCUCAGGAAUC	GAUUCCUGAGAGUCCAAAGUU	3313
R-008397243-000Y	2473	733	GGAACAUGAGAUGGGUGGC	GCCACCCAUCUCAUGUUCCUU	3315
R-008397243-000Y	2473	733	GGAACAUGAGAUGGGUGGC	B GGAACAUGAGAUGGGUGGCTT B	3314
R-008397246-000Z	1080	734	UGGCAGUGCGUUUAGCUGG	CCAGCUAAACGCACUGCCAUU	3317
R-008397246-000Z	1080	734	UGGCAGUGCGUUUAGCUGG	B UGGCAGUGCGUUUAGCUGGTT B	3316
R-008397249-000Z	2143	735	GGAAGCUGCAGAAGCUAUU	AAUAGCUUCUGCAGCUUCCUU	3319
R-008397249-000Z	2143	735	GGAAGCUGCAGAAGCUAUU	B GGaAGCUGCAGAAGCUAUUTT B	3318
R-008397252-000G	2203	736	CUCUAGGAAUGAAGGUGUG	B CUCUAGGAAUGAAGGUGUGTT B	3320
R-008397252-000G	2203	736	CUCUAGGAAUGAAGGUGUG	CACACCUUCAUUCCUAGAGUU	3321
R-008397255-000H	548	737	GUACGAGCUGCUAUGUUCC	B GUACGAGCUGCUAUGUUCCTT B	3322
R-008397255-000H	548	737	GUACGAGCUGCUAUGUUCC	GGAACAUAGCAGCUCGUACUU	3323
R-008397258-000J	2050	45	UACCAUUCCAUUGUUUGUG	CACAAACAAUGGAAUGGUAUU	3325
R-008397258-000J	2050	45	UACCAUUCCAUUGUUUGUG	B UACCAUUCCAUUGUUUGUGTT B	3324
R-008397261-000R	1867	738	UCCACGACUAGUUCAGUUG	B UCCACGACUAGUUCAGUUGTT B	3326
R-008397261-000R	1867	738	UCCACGACUAGUUCAGUUG	CAACUGAACUAGUCGUGGAUU	3327
R-008397264-000S	842	739	CCUCAGAUGGUGUCUGCUA	B CCUCAGAUGGUGUCUGCUATT B	3328
R-008397264-000S	842	739	CCUCAGAUGGUGUCUGCUA	UAGCAGACACCAUCUGAGGUU	3329
R-008397267-000T	2120	740	CUCUGUGAACUUGCUCAGG	CCUGAGCAAGUUCACAGAGUU	3331
R-008397267-000T	2120	740	CUCUGUGAACUUGCUCAGG	B CUCUGUGAACUUGCUCAGGTT B	3330
R-008397270-000Z	782	741	GCAGUUAUGGUCCAUCAGC	B GCAGUUAUGGUCCAUCAGCTT B	3332
R-008397270-000Z	782	741	GCAGUUAUGGUCCAUCAGC	GCUGAUGGACCAUAACUGCUU	3333
R-008397273-000Z	1758	742	UCUUACACCCACCAUCCCA	UGGGAUGGUGGGUGUAAGAUU	3335
R-008397273-000Z	1758	742	UCUUACACCCACCAUCCCA	B UCUUACACCCACCAUCCCATT B	3334
R-008397276-000B	2396	743	CGCCAGGAUGAUCCUAGCU	B CGCCAGGAUGAUCCUAGCUTT B	3336
R-008397276-000B	2396	743	CGCCAGGAUGAUCCUAGCU	AGCUAGGAUCAUCCUGGCGUU	3337
R-008397279-000C	1373	744	CACCUGACAGAUCCAAGUC	GACUUGGAUCUGUCAGGUGUU	3339
R-008397279-000C	1373	744	CACCUGACAGAUCCAAGUC	B CACCUGACAGAUCCAAGUCTT B	3338
R-008397282-000J	1518	745	UCACCUGUGCAGCUGGAAU	B UCACCUGUGCAGCUGGAAUTT B	3340
R-008397282-000J	1518	745	UCACCUGUGCAGCUGGAAU	AUUCCAGCUGCACAGGUGAUU	3341
R-008397285-000K	2557	746	GGAUGGGCUGCCUCCAGGU	ACCUGGAGGCAGCCCAUCCUU	3343

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397285-000K	2557	746	GGAUGGGCUGCCUCCAGGU	B GGAUGGGCUGCCUCCAGGUTT B	3342
R-008397288-000L	1987	747	UACCGGAGCCCUUCACAUC	B UACCGGAGCCCUUCACAUCTT B	3344
R-008397288-000L	1987	747	UACCGGAGCCCUUCACAUC	GAUGUGAAGGGCUCCGGUAUU	3345
R-008397291-000T	568	748	UGAGACAUUAGAUGAGGGC	GCCCUCAUCUAAUGUCUCAUU	3347
R-008397291-000T	568	748	UGAGACAUUAGAUGAGGGC	B UGAGACAUUAGAUGAGGGCTT B	3346
R-008397294-000U	2201	749	CACUCUAGGAAUGAAGGUG	B CACUCUAGGAAUGAAGGUGTT B	3348
R-008397294-000U	2201	749	CACUCUAGGAAUGAAGGUG	CACCUUCAUUCCUAGAGUGUU	3349
R-008397297-000V	609	750	UUGAUGCUGCUCAUCCCAC	GUGGGAUGAGCAGCAUCAAUU	3351
R-008397297-000V	609	750	UUGAUGCUGCUCAUCCCAC	B UUGAUGCUGCUCAUCCCACTT B	3350
R-008397300-000M	400	751	UUCUCUGAGUGGUAAAGGC	GCCUUUACCACUCAGAGAAUU	3353
R-008397300-000M	400	751	UUCUCUGAGUGGUAAAGGC	B UUCUCUGAGUGGUAAAGGCTT B	3352
R-008397303-000N	331	752	UGUUAGUCACUGGCAGCAA	UUGCUGCCAGUGACUAACAUU	3355
R-008397303-000N	331	752	UGUUAGUCACUGGCAGCAA	B UGUUAGUCACUGGCAGCAATT B	3354
R-008397306-000P	1967	753	GAAGAAAUAGUUGAAGGUU	AACCUUCAACUAUUUCUUCUU	3357
R-008397306-000P	1967	753	GAAGAAAUAGUUGAAGGUU	B GAAGAAAUAGUUGAAGGUUTT B	3356
R-008397309-000R	2198	754	CUUCACUCUAGGAAUGAAG	CUUCAUUCCUAGAGUGAAGUU	3359
R-008397309-000R	2198	754	CUUCACUCUAGGAAUGAAG	B CUUCACUCUAGGAAUGAAGTT B	3358
R-008397312-000X	1493	755	CUGGGUUCAGAUGAUAUAA	UUAUAUCAUCUGAACCCAGUU	3361
R-008397312-000X	1493	755	CUGGGUUCAGAUGAUAUAA	B CUGGGUUCAGAUGAUAUAATT B	3360
R-008397315-000Y	2260	756	GGACAAGCCACAAGAUUAC	GUAAUCUUGUGGCUUGUCCUU	3363
R-008397315-000Y	2260	756	GGACAAGCCACAAGAUUAC	B GGACAAGCCACAAGAUUACTT B	3362
R-008397318-000Z	2496	757	ACCCUGGUGCUGACUAUCC	B ACCCUGGUGCUGACUAUCCTT B	3364
R-008397318-000Z	2496	757	ACCCUGGUGCUGACUAUCC	GGAUAGUCAGCACCAGGGUUU	3365
R-008397321-000F	2361	758	UUGAUAUUGGUGCCCAGGG	B UUGAUAUUGGUGCCCAGGGTT B	3366
R-008397321-000F	2361	758	UUGAUAUUGGUGCCCAGGG	CCCUGGGCACCAAUAUCAAUU	3367
R-008397324-000G	443	759	ACCUCCCAAGUCCUGUAUG	CAUACAGGACUUGGGAGGUUU	3369
R-008397324-000G	443	759	ACCUCCCAAGUCCUGUAUG	B ACCUCCCAAGUCCUGUAUGTT B	3368
R-008397327-000H	523	760	GUAUGCAAUGACUCGAGCU	B GUAUGCAAUGACUCGAGCUTT B	3370
R-008397327-000H	523	760	GUAUGCAAUGACUCGAGCU	AGCUCGAGUCAUUGCAUACUU	3371
R-008397330-000P	1742	761	CCAGUUGUGGUUAAGCUCU	B CCAGUUGUGGUUAAGCUCUTT B	3372
R-008397330-000P	1742	761	CCAGUUGUGGUUAAGCUCU	AGAGCUUAACCACAACUGGUU	3373
R-008397333-000R	530	762	AUGACUCGAGCUCAGAGGG	B AUGACUCGAGCUCAGAGGGTT B	3374
R-008397333-000R	530	762	AUGACUCGAGCUCAGAGGG	CCCUCUGAGCUCGAGUCAUUU	3375
R-008397336-000S	3169	763	UUGUUGUAACCUGCUGUGA	B UUGUUGUAACCUGCUGUGATT B	3376
R-008397336-000S	3169	763	UUGUUGUAACCUGCUGUGA	UCACAGCAGGUUACAACAAUU	3377
R-008397339-000T	1385	764	CCAAGUCAACGUCUUGUUC	B CCAAGUCAACGUCUUGUUCTT B	3378

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397339-000T	1385	764	CCAAGUCAACGUCUUGUUC	GAACAAGACGUUGACUUGGUU	3379
R-008397342-000Z	2123	131	UGUGAACUUGCUCAGGACA	B UGUGAACUUGCUCAGCACATT B	3380
R-008397342-000Z	2123	131	UGUGAACUUGCUCAGGACA	UGUCCUGAGCAAGUUCACAUU	3381
R-008397345-000Z	2036	765	AUCAGAGGACUAAAUACCA	B AUCAGAGGACUAAAUACCATT B	3382
R-008397345-000Z	2036	765	AUCAGAGGACUAAAUACCA	UGGUAUUUAGUCCUCUGAUUU	3383
R-008397348-000B	3088	766	UGUAUGGGUAGGGUAAAUC	GAUUUACCCUACCCAUACAUU	3385
R-008397348-000B	3088	766	UGUAUGGGUAGGGUAAAUC	B UGUAUGGGUAGGGUAAAUCTT B	3384
R-008397351-000H	2051	56	ACCAUUCCAUUGUUUGUGC	GCACAAACAAUGGAAUGGUUU	3387
R-008397351-000H	2051	56	ACCAUUCCAUUGUUUGUGC	B ACCAUUCCAUUGUUUGUGCTT B	3386
R-008397354-000J	288	170	UGAUGGAGUUGGACAUGGC	GCCAUGUCCAACUCCAUCAUU	3389
R-008397354-000J	288	170	UGAUGGAGUUGGACAUGGC	B UGAUGGAGUUGGACAUGGCTT B	3388
R-008397357-000K	1850	767	CGUGAGCAGGGUGCCAUUC	B CGUGAGCAGGGUGCCAUUCTT B	3390
R-008397357-000K	1850	767	CGUGAGCAGGGUGCCAUUC	GAAUGGCACCCUGCUCACGUU	3391
R-008397360-000S	2548	82	GGACCUCAUGGAUGGGCUG	B GGACCUCAUGGAUGGGCUGTT B	3392
R-008397360-000S	2548	82	GGACCUCAUGGAUGGGCUG	CAGCCCAUCCAUGAGGUCCUU	3393
R-008397363-000T	2518	768	UGAUGGGCUGCCAGAUCUG	B UGAUGGGCUGCCAGAUCUGTT B	3394
R-008397363-000T	2518	768	UGAUGGGCUGCCAGAUCUG	CAGAUCUGGCAGCCCAUCAUU	3395
R-008397366-000U	1886	769	UGAUGGGCUGCCAGAUCUG	B CUUGUUCGUGCACAUCAGGTT B	3396
R-008397366-000U	1886	769	UGAUGGGCUGCCAGAUCUG	CCUGAUGUGCACGAACAAGUU	3397
R-008397369-000V	650	770	CUUGUUCGUGCACAUCAGG	GUUUCAGCAUCUGUGAUGGUU	3399
R-008397369-000V	650	770	CUUGUUCGUGCACAUCAGG	B CCAUCACAGAUGCUGAAACTT B	3398
R-008397372-000B	3139	771	ACAGUUUACCAGUUGCCUU	AAGGCAACUGGUAAACUGUUU	3401
R-008397372-000B	3139	771	ACAGUUUACCAGUUGCCUU	B ACAGUUUACCAGUUGCCUUTT B	3400
R-008397375-000C	2025	772	ACCGAAUUGUUAUCAGAGG	CCUCUGAUAACAAUUCGGUUU	3403
R-008397375-000C	2025	772	ACCGAAUUGUUAUCAGAGG	B ACCGAAUUGUUAUCAGAGGTT B	3402
R-008397378-000D	1082	773	GCAGUGCGUUUAGCUGGUG	CACCAGCUAAACGCACUGCUU	3405
R-008397378-000D	1082	773	GCAGUGCGUUUAGCUGGUG	B GCAGUGCGUUUAGCUGGUGTT B	3404
R-008397381-000K	2475	774	AACAUGAGAUGGGUGGCCA	UGGCCACCCAUCUCAUGUUUU	3407
R-008397381-000K	2475	774	AACAUGAGAUGGGUGGCCA	B AACAUGAGAUGGGUGGCCATT B	3406
R-008397384-000L	1375	775	CCUGACAGAUCCAAGUCAA	UUGACUUGGAUCUGUCAGGUU	3409
R-008397384-000L	1375	775	CCUGACAGAUCCAAGUCAA	B CCUGACAGAUCCAAGUCAATT B	3408
R-008397387-000M	2013	776	GGGAUGUUCACAACCGAAU	B GGGAUGUUCACAACCGAAUTT B	3410
R-008397387-000M	2013	776	GGGAUGUUCACAACCGAAU	AUUCGGUUGUGAACAUCCCUU	3411
R-008397390-000U	1236	41	CUUUAGUAAAUAUAAUGAG	CUCAUUAUAUUUACUAAAGUU	3413
R-008397390-000U	1236	41	CUUUAGUAAAUAUAAUGAG	B CUUUAGUAAAUAUAAUGAGTT B	3412
R-008397393-000V	1653	128	AGCCUGCCAUCUGUGCUCU	B AGCCUGCCAUCUGUGCUCUTT B	3414
R-008397393-000V	1653	128	AGCCUGCCAUCUGUGCUCU	AGAGCACAGAUGGCAGGCUUU	3415

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397396-000W	1802	777	GGAUUGAUUCGAAAUCUUG	B GGAUUGAUUCGAAAUCUUGTT B	3416
R-008397396-000W	1802	777	GGAUUGAUUCGAAAUCUUG	CAAGAUUUCGAAUCAAUCCUU	3417
R-008397399-000X	2144	778	GAAGCUGCAGAAGCUAUUG	CAAUAGCUUCUGCAGCUUCUU	3419
R-008397399-000X	2144	778	GAAGCUGCAGAAGCUAUUG	B GAAGCUGCAGAAGCUAUUGTT B	3418
R-008397402-000P	529	779	AAUGACUCGAGCUCAGAGG	B AAUGACUCGAGCUCAGAGGTT B	3420
R-008397402-000P	529	779	AAUGACUCGAGCUCAGAGG	CCUCUGAGCUCGAGUCAUUUU	3421
R-008397405-000R	1482	780	UUGUUCAGCUUCUGGGUUC	GAACCCAGAAGCUGAACAAUU	3423
R-008397405-000R	1482	780	UUGUUCAGCUUCUGGGUUC	B UUGUUCAGCUUCUGGGUUCTT B	3422
R-008397408-000S	1546	781	CCUCACUUGCAAUAAUUAU	B CCUCACUUGCAAUAAUUAUTT B	3424
R-008397408-000S	1546	781	CCUCACUUGCAAUAAUUAU	AUAAUUAUUGCAAGUGAGGUU	3425
R-008397411-000Y	845	782	CAGAUGGUGUCUGCUAUUG	CAAUAGCAGACACCAUCUGUU	3427
R-008397411-000Y	845	782	CAGAUGGUGUCUGCUAUUG	B CAGAUGGUGUCUGCUAUUGTT B	3426
R-008397414-000Z	487	783	CUUCACUCAAGAACAAGUA	B CUUCACUCAAGAACAAGUATT B	3428
R-008397414-000Z	487	783	CUUCACUCAAGAACAAGUA	UACUUGUUCUUGAGUGAAGUU	3429
R-008397417-000A	652	784	AUCACAGAUGCUGAAACAU	AUGUUUCAGCAUCUGUGAUUU	3431
R-008397417-000A	652	784	AUCACAGAUGCUGAAACAU	B AUCACAGAUGCUGAAACAUTT B	3430
R-008397420-000G	1720	785	AGUUCGCCUUCACUAUGGA	UCCAUAGUGAAGGCGAACUUU	3433
R-008397420-000G	1720	785	AGUUCGCCUUCACUAUGGA	B AGUUCGCCUUCACUAUGGATT B	3432
R-008397423-000H	951	786	UACUGGCCAUCUUUAAGUC	GACUUAAAGAUGGCCAGUAUU	3435
R-008397423-000H	951	786	UACUGGCCAUCUUUAAGUC	B UACUGGCCAUCUUUAAGUCTT B	3434
R-008397426-000J	1232	787	CAAGCUUUAGUAAAUAUAA	UUAUAUUUACUAAAGCUUGUU	3437
R-008397426-000J	1232	787	CAAGCUUUAGUAAAUAUAA	B CAAGCUUUAGUAAAUAUAATT B	3436
R-008397429-000K	2269	28	ACAAGAUUACAAGAAACGG	B ACAAGAUUACAAGAAACGGTT B	3438
R-008397429-000K	2269	28	ACAAGAUUACAAGAAACGG	CCGUUUCUUGUAAUCUUGUUU	3439
R-008397432-000S	2265	788	AGCCACAAGAUUACAAGAA	B AGCCACAAGAUUACAAGAATT B	3440
R-008397432-000S	2265	788	AGCCACAAGAUUACAAGAA	UUCUUGUAAUCUUGUGGCUUU	3441
R-008397435-000T	1698	789	AAGCAGAGAUGGCCCAGAA	B AAGCAGAGAUGGCCCAGAATT B	3442
R-008397435-000T	1698	789	AAGCAGAGAUGGCCCAGAA	UUCUGGGCCAUCUCUGCUUUU	3443
R-008397438-000U	701	790	GAUGCAGAACUUGCCACAC	GUGUGGCAAGUUCUGCAUCUU	3445
R-008397438-000U	701	790	GAUGCAGAACUUGCCACAC	B GAUGCAGAACUUGCCACACTT B	3444
R-008397441-000A	1428	791	AUCUUUCAGAUGCUGCAAC	GUUGCAGCAUCUGAAAGAUUU	3447
R-008397441-000A	1428	791	AUCUUUCAGAUGCUGCAAC	B AUCUUUCAGAUGCUGCAACTT B	3446
R-008397444-000B	1930	792	UGGGACACAGCAGCAAUUU	B UGGGACACAGCAGCAAUUUTT B	3448
R-008397444-000B	1930	792	UGGGACACAGCAGCAAUUU	AAAUUGCUGCUGUGUCCCAUU	3449
R-008397447-000C	1379	793	ACAGAUCCAAGUCAACGUC	GACGUUGACUUGGAUCUGUUU	3451
R-008397447-000C	1379	793	ACAGAUCCAAGUCAACGUC	B ACAGAUCCAAGUCAACGUCTT B	3450

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397450-000J	1936	794	ACAGCAGCAAUUUGUGGAG	B ACAGCAGCAAUUUGUGGAGTT B	3452
R-008397450-000J	1936	794	ACAGCAGCAAUUUGUGGAG	CUCCACAAAUUGCUGCUGUUU	3453
R-008397453-000K	1441	795	UGCAACUAAACAGGAAGGG	CCCUUCCUGUUUAGUUGCAUU	3455
R-008397453-000K	1441	795	UGCAACUAAACAGGAAGGG	B UGCAACUAAACAGGAAGGGTT B	3454
R-008397456-000L	2132	796	GCUCAGGACAAGGAAGCUG	CAGCUUCCUUGUCCUGAGCUU	3457
R-008397456-000L	2132	796	GCUCAGGACAAGGAAGCUG	B GCUCAGGACAAGGAAGCUGTT B	3456
R-008397459-000M	2443	165	CCAGGAUGCCUUGGGUAUG	B CCAGGAUGCCUUGGGUAUGTT B	3458
R-008397459-000M	2443	165	CCAGGAUGCCUUGGGUAUG	CAUACCCAAGGCAUCCUGGUU	3459
R-008397462-000U	1800	163	UUGGAUUGAUUCGAAAUCU	AGAUUUCGAAUCAAUCCAAUU	3461
R-008397462-000U	1800	163	UUGGAUUGAUUCGAAAUCU	B UUGGAUUGAUUCGAAAUCUTT B	3460
R-008397465-000V	403	185	UCUGAGUGGUAAAGGCAAU	AUUGCCUUUACCACUCAGAUU	3463
R-008397465-000V	403	185	UCUGAGUGGUAAAGGCAAU	B UCUGAGUGGUAAAGGCAAUTT B	3462
R-008397468-000W	1007	105	CCAGUGGAUUCUGUGUUGU	ACAACACAGAAUCCACUGGUU	3465
R-008397468-000W	1007	105	CCAGUGGAUUCUGUGUUGU	B CCAGUGGAUUCUGUGUUGUTT B	3464
R-008397471-000C	1057	113	AUUACAUCAAGAAGGAGCU	AGCUCCUUCUUGAUGUAAUUU	3467
R-008397471-000C	1057	113	AUUACAUCAAGAAGGAGCU	B AUUACAUCAAGAAGGAGCUTT B	3466
R-008397474-000D	2267	87	CCACAAGAUUACAAGAAAC	B CCACAAGAUUACAAGAAACTT B	3468
R-008397474-000D	2267	87	CCACAAGAUUACAAGAAAC	GUUUCUUGUAAUCUUGUGGUU	3469
R-008397477-000E	1240	158	AGUAAAUAUAAUGAGGACC	B AGUAAAUAUAAUGAGGACCTT B	3470
R-008397477-000E	1240	158	AGUAAAUAUAAUGAGGACC	GGUCCUCAUUAUAUUUACUUU	3471
R-008397480-000L	2043	797	GACUAAAUACCAUUCCAUU	AAUGGAAUGGUAUUUAGUCUU	3473
R-008397480-000L	2043	797	GACUAAAUACCAUUCCAUU	B GACUAAAUACCAUUCCAUUTT B	3472
R-008397483-000M	608	798	UUUGAUGCUGCUCAUCCCA	UGGGAUGAGCAGCAUCAAAUU	3475
R-008397483-000M	608	798	UUUGAUGCUGCUCAUCCCA	B UUUGAUGCUGCUCAUCCCATT B	3474
R-008397486-000N	341	799	UGGCAGCAACAGUCUUACC	B UGGCAGCAACAGUCUUACCTT B	3476
R-008397486-000N	341	799	UGGCAGCAACAGUCUUACC	GGUAAGACUGUUGCUGCCAUU	3477
R-008397489-000P	1194	800	AAGAAAGCAAGCUCAUCAU	B AAGAAAGCAAGCUCAUCAUTT B	3478
R-008397489-000P	1194	800	AAGAAAGCAAGCUCAUCAU	AUGAUGAGCUUGCUUUCUUUU	3479
R-008397492-000W	2350	801	UGAUCUUGGACUUGAUAUU	B UGAUCUUGGACUUGAUAUUTT B	3480
R-008397492-000W	2350	801	UGAUCUUGGACUUGAUAUU	AAUAUCAAGUCCAAGAUCAUU	3481
R-008397495-000X	2948	802	CUGAAUAAAGUGUAACAAU	B CUGAAUAAAGUGUAACAAUTT B	3482
R-008397495-000X	2948	802	CUGAAUAAAGUGUAACAAU	AUUGUUACACUUUAUUCAGUU	3483
R-008397507-000T	2044	803	ACUAAAUACCAUUCCAUUG	B ACUAAAUACCAUUCCAUUGTT B	3484
R-008397507-000T	2044	803	ACUAAAUACCAUUCCAUUG	CAAUGGAAUGGUAUUUAGUUU	3485
R-008397510-000Z	621	804	AUCCCACUAAUGUCCAGCG	CGCUGGACAUUAGUGGGAUUU	3487
R-008397510-000Z	621	804	AUCCCACUAAUGUCCAGCG	B AUCCCACUAAUGUCCAGCGTT B	3486
R-008397513-000Z	384	805	CCACUACCACAGCUCCUUC	B CCACUACCACAGCUCCUUCTT B	3488

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397513-000Z	384	805	CCACUACCACAGCUCCUUC	GAAGGAGCUGUGGUAGUGGUU	3489
R-008397516-000B	1898	806	CAUCAGGAUACCCAGCGCC	B CAUCAGGAUACCCAGCGCCTT B	3490
R-008397516-000B	1898	806	CAUCAGGAUACCCAGCGCC	GGCGCUGGGUAUCCUGAUGUU	3491
R-008397519-000C	1795	15	UACUGUUGGAUUGAUUCGA	UCGAAUCAAUCCAACAGUAUU	3493
R-008397519-000C	1795	15	UACUGUUGGAUUGAUUCGA	B UACUGUUGGAUUGAUUCGATT B	3492
R-008397522-000J	653	807	UCACAGAUGCUGAAACAUG	CAUGUUUCAGCAUCUGUGAUU	3495
R-008397522-000J	653	807	UCACAGAUGCUGAAACAUG	B UCACAGAUGCUGAAACAUGTT B	3494
R-008397525-000K	1846	808	UUUGCGUGAGCAGGGUGCC	GGCACCCUGCUCACGCAAAUU	3497
R-008397525-000K	1846	808	UUUGCGUGAGCAGGGUGCC	B UUUGCGUGAGCAGGGUGCCTT B	3496
R-008397528-000L	2348	809	GCUGAUCUUGGACUUGAUA	UAUCAAGUCCAAGAUCAGCUU	3499
R-008397528-000L	2348	809	GCUGAUCUUGGACUUGAUA	B GCUGAUCUUGGACUUGAUATT B	3498
R-008397531-000T	1798	19	UGUUGGAUUGAUUCGAAAU	AUUUCGAAUCAAUCCAACAUU	3501
R-008397531-000T	1798	19	UGUUGGAUUGAUUCGAAAU	B UGUUGGAUUGAUUCGAAAUTT B	3500
R-008397534-000U	1150	810	GGCUAUUACGACAGACUGC	B GGCUAUUACGACAGACUGCTT B	3502
R-008397534-000U	1150	810	GGCUAUUACGACAGACUGC	GCAGUCUGUCGUAAUAGCCUU	3503
R-008397537-000V	1009	180	AGUGGAUUCUGUGUUGUUU	AAACAACACAGAAUCCACUUU	3505
R-008397537-000V	1009	180	AGUGGAUUCUGUGUUGUUU	B AGUGGAUUCUGUGUUGUUUTT B	3504
R-008397540-000B	654	178	CACAGAUGCUGAAACAUGC	B CACAGAUGCUGAAACAUGCTT B	3506
R-008397540-000B	654	178	CACAGAUGCUGAAACAUGC	GCAUGUUUCAGCAUCUGUGUU	3507
R-008397543-000C	298	811	GGACAUGGCCAUGGAACCA	B GGACAUGGCCAUGGAACCATT B	3508
R-008397543-000C	298	811	GGACAUGGCCAUGGAACCA	UGGUUCCAUGGCCAUGUCCUU	3509
R-008397546-000D	1568	812	AACAAGAUGAUGGUCUGCC	B AACAAGAUGAUGGUCUGCCTT B	3510
R-008397546-000D	1568	812	AACAAGAUGAUGGUCUGCC	GGCAGACCAUCAUCUUGUUUU	3511
R-008397549-000E	1058	813	UUACAUCAAGAAGGAGCUA	B UUACAUCaAGAAGGAGCUATT B	3512
R-008397549-000E	1058	813	UUACAUCAAGAAGGAGCUA	UAGCUCCUUCUUGAUGUAAUU	3513
R-008397552-000L	1835	814	AAUCAUGCACCUUUGCGUG	B AAUCAUGCACCUUUGCGUGTT B	3514
R-008397552-000L	1835	814	AAUCAUGCACCUUUGCGUG	CACGCAAAGGUGCAUGAUUUU	3515
R-008397555-000M	1832	815	GCAAAUCAUGCACCUUUGC	B GCAAAUCAUGCACCUUUGCTT B	3516
R-008397555-000M	1832	815	GCAAAUCAUGCACCUUUGC	GCAAAGGUGCAUGAUUUGCUU	3517
R-008397558-000N	2550	55	ACCUCAUGGAUGGGCUGCC	GGCAGCCCAUCCAUGAGGUUU	3519
R-008397558-000N	2550	55	ACCUCAUGGAUGGGCUGCC	B ACCUCAUGGAUGGGCUGCCTT B	3518
R-008397561-000V	406	816	GAGUGGUAAAGGCAAUCCU	AGGAUUGCCUUUACCACUCUU	3521
R-008397561-000V	406	816	GAGUGGUAAAGGCAAUCCU	B GAGUGGUAAAGGCAAUCCUTT B	3520
R-008397564-000W	1723	817	UCGCCUUCACUAUGGACUA	B UCGCCUUCACUAUGGACUATT B	3522
R-008397564-000W	1723	817	UCGCCUUCACUAUGGACUA	UAGUCCAUAGUGAAGGCGAUU	3523
R-008397567-000X	371	818	AUCCAUUCUGGUGCCACUA	UAGUGGCACCAGAAUGGAUUU	3525

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397567-000X	371	818	AUCCAUUCUGGUGCCACUA	B AUCCAUUCUGGUGCCACUA*TT* B	3524
R-008397570-000D	1899	819	AUCAGGAUACCCAGCGCCG	CGGCGCUGGGUAUCCUGAUUU	3527
R-008397570-000D	1899	819	AUCAGGAUACCCAGCGCCG	B AUCAGGAUACCCAGCGCCG*TT* B	3526
R-008397573-000E	522	820	AGUAUGCAAUGACUCGAGC	B AGUAUGCAAUGACUCGAGC*TT* B	3528
R-008397573-000E	522	820	AGUAUGCAAUGACUCGAGC	GCUCGAGUCAUUGCAUACUUU	3529
R-008397576-000F	2285	821	CGGCUUUCAGUUGAGCUGA	B CGGCUUUCAGUUGAGCUGA*TT* B	3530
R-008397576-000F	2285	821	CGGCUUUCAGUUGAGCUGA	UCAGCUCAACUGAAAGCCGUU	3531
R-008397579-000G	779	822	GCUGCAGUUAUGGUCCAUC	GAUGGACCAUAACUGCAGCUU	3533
R-008397579-000G	779	822	GCUGCAGUUAUGGUCCAUC	B GCUGCAGUUAUGGUCCAUC*TT* B	3532
R-008397582-000N	2896	823	AUUGAGUAAUGGUGUAGAA	B AUUGAGUAAUGGUGUAGAA*TT* B	3534
R-008397582-000N	2896	823	AUUGAGUAAUGGUGUAGAA	UUCUACACCAUUACUCAAUUU	3535
R-008397588-000R	2943	824	GUAAUCUGAAUAAAGUGUA	UACACUUUAUUCAGAUUACUU	3537
R-008397588-000R	2943	824	GUAAUCUGAAUAAAGUGUA	B GUAAUCUGAAUAAAGUGUA*TT* B	3536
R-008397591-000X	513	825	UUGAUGGACAGUAUGCAAU	B UUGAUGGACAGUAUGCAAU*TT* B	3538
R-008397591-000X	513	825	UUGAUGGACAGUAUGCAAU	AUUGCAUACUGUCCAUCAAUU	3539
R-008397594-000Y	3084	826	GAUAUGUAUGGGUAGGGUA	B GAUAUGUAUGGGUAGGGUA*TT* B	3540
R-008397594-000Y	3084	826	GAUAUGUAUGGGUAGGGUA	UACCCUACCCAUACAUAUCUU	3541
R-008397597-000Z	1567	827	GAACAAGAUGAUGGUCUGC	B GAACAAGAUGAUGGUCUGC*TT* B	3542
R-008397597-000Z	1567	827	GAACAAGAUGAUGGUCUGC	GCAGACCAUCAUCUUGUUCUU	3543
R-008397600-000S	2034	828	UUAUCAGAGGACUAAAUAC	B UUAUCAGAGGACUAAAUAC*TT* B	3544
R-008397600-000S	2034	828	UUAUCAGAGGACUAAAUAC	GUAUUUAGUCCUCUGAUAAUU	3545
R-008397603-000T	1003	829	UUCACCAGUGGAUUCUGUG	B UUCACCAGUGGAUUCUGUG*TT* B	3546
R-008397603-000T	1003	829	UUCACCAGUGGAUUCUGUG	CACAGAAUCCACUGGUGAAUU	3547
R-008397606-000U	1980	830	AAGGUUGUACCGGAGCCCU	AGGGCUCCGGUACAACCUUUU	3549
R-008397606-000U	1980	830	AAGGUUGUACCGGAGCCCU	B AAGGUUGUACCGGAGCCCU*TT* B	3548
R-008397609-000V	1340	831	GUAGAAGCUGGUGGAAUGC	GCAUUCCACCAGCUUCUACUU	3551
R-008397609-000V	1340	831	GUAGAAGCUGGUGGAAUGC	B GUAGAAGCUGGUGGAAUGC*TT* B	3550
R-008397612-000B	1437	832	AUGCUGCAACUAAACAGGA	B AUGCUGCAACUAAACAGGA*TT* B	3552
R-008397612-000B	1437	832	AUGCUGCAACUAAACAGGA	UCCUGUUUAGUUGCAGCAUUU	3553
R-008397615-000C	2499	145	CUGGUGCUGACUAUCCAGU	B CUGGUGCUGACUAUCCAGU*TT* B	3554
R-008397615-000C	2499	145	CUGGUGCUGACUAUCCAGU	ACUGGAUAGUCAGCACCAGUU	3555
R-008396718-000D	785	64	GUUAUGGUCCAUCAGCUUU	AAAGCUGAUGGACCAUAACUU	3557
R-008396718-000D	785	64	GUUAUGGUCCAUCAGCUUU	B GUUAUGGUCCAUCAGCUUU*TT* B	3556
R-008397621-000K	2425	833	UCACUCUGGUGGAUAUGGC	B UCACUCUGGUGGAUAUGGC*TT* B	3558
R-008397621-000K	2425	833	UCACUCUGGUGGAUAUGGC	GCCAUAUCCACCAGAGUGAUU	3559
R-008397624-000L	282	834	CUGAUUUGAUGGAGUUGGA	UCCAACUCCAUCAAAUCAGUU	3561
R-008397624-000L	282	834	CUGAUUUGAUGGAGUUGGA	B CUGAUUUGAUGGAGUUGGA*TT* B	3560

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397627-000M	1206	835	UCAUCAUACUGGCUAGUGG	B UCAUCAUACUGGCUAGUGGTT B	3562
R-008397627-000M	1206	835	UCAUCAUACUGGCUAGUGG	CCACUAGCCAGUAUGAUGAUU	3563
R-008397630-000U	1885	836	GCUUGUUCGUGCACAUCAG	CUGAUGUGCACGAACAAGCUU	3565
R-008397630-000U	1885	836	GCUUGUUCGUGCACAUCAG	B GCUUGUUCGUGCACAUCAGTT B	3564
R-008397633-000V	1314	837	UCUGCUCUAGUAAUAAGCC	B UCUGCUCUAGUAAUAAGCCTT B	3566
R-008397633-000V	1314	837	UCUGCUCUAGUAAUAAGCC	GGCUUAUUACUAGAGCAGAUU	3567
R-008397636-000W	2388	174	UUGGAUAUCGCCAGGAUGA	B UUGGAUAUCGCCAGGAUGATT B	3568
R-008397636-000W	2388	174	UUGGAUAUCGCCAGGAUGA	UCAUCCUGGCGAUAUCCAAUU	3569
R-008397639-000X	1308	838	UAUCUGUCUGCUCUAGUAA	B UAUCUGUCUGCUCUAGUAATT B	3570
R-008397639-000X	1308	838	UAUCUGUCUGCUCUAGUAA	UUACUAGAGCAGACAGAUAUU	3571
R-008397642-000D	1200	839	GCAAGCUCAUCAUACUGGC	GCCAGUAUGAUGAGCUUGCUU	3573
R-008397642-000D	1200	839	GCAAGCUCAUCAUACUGGC	B GCAAGCUCAUCAUACUGGCTT B	3572
R-008397645-000E	543	840	AGAGGGUACGAGCUGCUAU	B AGAGGGUACGAGCUGCUAUTT B	3574
R-008397645-000E	543	840	AGAGGGUACGAGCUGCUAU	AUAGCAGCUCGUACCCUCUUU	3575
R-008397648-000F	1609	841	UGUGCGUACUGUCCUUCGG	B UGUGCGUACUGUCCUUCGGTT B	3576
R-008397648-000F	1609	841	UGUGCGUACUGUCCUUCGG	CCGAAGGACAGUACGCACAUU	3577
R-008397651-000M	1453	842	GGAAGGGAUGGAAGGUCUC	B GGAAGGGAUGGAAGGUCUCTT B	3578
R-008397651-000M	1453	842	GGAAGGGAUGGAAGGUCUC	GAGACCUUCCAUCCCUUCCUU	3579
R-008397654-000N	2127	138	AACUUGCUCAGGACAAGGA	B AACUUGCUCAGGACAAGGATT B	3580
R-008397654-000N	2127	138	AACUUGCUCAGGACAAGGA	UCCUUGUCCUGAGCAAGUUUU	3581
R-008397657-000P	833	843	AUGCGUUCUCCUCAGAUGG	B AUGCGUUCUCCUCAGAUGGTT B	3582
R-008397657-000P	833	843	AUGCGUUCUCCUCAGAUGG	CCAUCUGAGGAGAACGCAUUU	3583
R-008397660-000W	2188	844	GACAGAGUUACUUCACUCU	B GACAGAGUUACUUCACUCUTT B	3584
R-008397660-000W	2188	844	GACAGAGUUACUUCACUCU	AGAGUGAAGUAACUCUGUCUU	3585
R-008397663-000X	1148	845	UUGGCUAUUACGACAGACU	B UUGGCUAUUACGACAGACUTT B	3586
R-008397663-000X	1148	845	UUGGCUAUUACGACAGACU	AGUCUGUCGUAAUAGCCAAUU	3587
R-008397666-000Y	1736	846	GGACUACCAGUUGUGGUUA	B GGACUACCAGUUGUGGUUATT B	3588
R-008397666-000Y	1736	846	GGACUACCAGUUGUGGUUA	UAACCACAACUGGUAGUCCUU	3589
R-008397669-000Z	1401	847	UUCAGAACUGUCUUUGGAC	GUCCAAAGACAGUUCUGAAUU	3591
R-008397669-000Z	1401	847	UUCAGAACUGUCUUUGGAC	B UUCAGAACUGUCUUUGGACTT B	3590
R-008397672-000F	1677	848	AUCUGACCAGCCGACACCA	UGGUGUCGGCUGGUCAGAUUU	3593
R-008397672-000F	1677	848	AUCUGACCAGCCGACACCA	B AUCUGACCAGCCGACACCATT B	3592
R-008397675-000G	1934	849	ACACAGCAGCAAUUUGUGG	B ACACAGCAGCAAUUUGUGGTT B	3594
R-008397675-000G	1934	849	ACACAGCAGCAAUUUGUGG	CCACAAAUUGCUGCUGUGUUU	3595
R-008397678-000H	388	850	UACCACAGCUCCUUCUCUG	CAGAGAAGGAGCUGUGGUAUU	3597
R-008397678-000H	388	850	UACCACAGCUCCUUCUCUG	B UACCACAGCUCCUUCUCUGTT B	3596

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397681-000P	1920	851	CGUCCAUGGGUGGGACACA	B CGUCCAUGGGUGGGACACATT B	3598
R-008397681-000P	1920	851	CGUCCAUGGGUGGGACACA	UGUGUCCCACCCAUGGACGUU	3599
R-008397684-000R	1747	852	UGUGGUUAAGCUCUUACAC	GUGUAAGAGCUUAACCACAUU	3601
R-008397684-000R	1747	852	UGUGGUUAAGCUCUUACAC	B UGUGGUUAAGCUCUUACACTT B	3600
R-008397687-000S	861	853	UUGUACGUACCAUGCAGAA	B UUGUACGUACCAUGCAGAATT B	3602
R-008397687-000S	861	853	UUGUACGUACCAUGCAGAA	UUCUGCAUGGUACGUACAAUU	3603
R-008397690-000Y	1904	854	GAUACCCAGCGCCGUACGU	B GAUACCCAGCGCCGUACGUTT B	3604
R-008397690-000Y	1904	854	GAUACCCAGCGCCGUACGU	ACGUACGGCGCUGGGUAUCUU	3605
R-008397693-000Z	831	855	UCAUGCGUUCUCCUCAGAU	B UCAUGCGUUCUCCUCAGAUTT B	3606
R-008397693-000Z	831	855	UCAUGCGUUCUCCUCAGAU	AUCUGAGGAGAACGCAUGAUU	3607
R-008397696-000A	1895	856	GCACAUCAGGAUACCCAGC	GCUGGGUAUCCUGAUGUGCUU	3609
R-008397696-000A	1895	856	GCACAUCAGGAUACCCAGC	B GCACAUCAGGAUACCCAGCTT B	3608
R-008397699-000B	2273	857	GAUUACAAGAAACGGCUUU	AAAGCCGUUUCUUGUAAUCUU	3611
R-008397699-000B	2273	857	GAUUACAAGAAACGGCUUU	B GAUUACAAGAAACGGCUUUTT B	3610
R-008397702-000U	1738	858	ACUACCAGUUGUGGUUAAG	B ACUACCAGUUGUGGUUAAGTT B	3612
R-008397702-000U	1738	858	ACUACCAGUUGUGGUUAAG	CUUAACCACAACUGGUAGUUU	3613
R-008397705-000V	1395	859	GUCUUGUUCAGAACUGUCU	B GUCUUGUUCAGAACUGUCUTT B	3614
R-008397705-000V	1395	859	GUCUUGUUCAGAACUGUCU	AGACAGUUCUGAACAAGACUU	3615
R-008397708-000W	1675	860	UCAUCUGACCAGCCGACAC	B UCAUCUGACCAGCCGACACTT B	3616
R-008397708-000W	1675	860	UCAUCUGACCAGCCGACAC	GUGUCGGCUGGUCAGAUGAUU	3617
R-008397711-000C	1845	861	CUUUGCGUGAGCAGGGUGC	B CUUUGCGUGAGCAGGGUGCTT B	3618
R-008397711-000C	1845	861	CUUUGCGUGAGCAGGGUGC	GCACCCUGCUCACGCAAAGUU	3619
R-008397714-000D	1408	862	CUGUCUUUGGACUCUCAGG	CCUGAGAGUCCAAAGACAGUU	3621
R-008397714-000D	1408	862	CUGUCUUUGGACUCUCAGG	B CUGUCUUUGGACUCUCAGGTT B	3620
R-008397717-000E	1059	863	UACAUCAAGAAGGAGCUAA	B UACAUCAAGAAGGAGCUAATT B	3622
R-008397717-000E	1059	863	UACAUCAAGAAGGAGCUAA	UUAGCUCCUUCUUGAUGUAUU	3623
R-008397720-000L	1381	864	AGAUCCAAGUCAACGUCUU	AAGACGUUGACUUGGAUCUUU	3625
R-008397720-000L	1381	864	AGAUCCAAGUCAACGUCUU	B AGAUCCAAGUCAACGUCUUTT B	3624
R-008397723-000M	1386	865	CAAGUCAACGUCUUGUUCA	B CAAGUCAACGUCUUGUUCATT B	3626
R-008397723-000M	1386	865	CAAGUCAACGUCUUGUUCA	UGAACAAGACGUUGACUUGUU	3627
R-008397726-000N	1470	866	UCCUUGGGACUCUUGUUCA	UGAACAAGAGUCCCAAGGAUU	3629
R-008397726-000N	1470	866	UCCUUGGGACUCUUGUUCA	B UCCUUGGGACUCUUGUUCATT B	3628
R-008397729-000P	1349	867	GGUGGAAUGCAAGCUUUAG	CUAAAGCUUGCAUUCCACCUU	3631
R-008397729-000P	1349	867	GGUGGAAUGCAAGCUUUAG	B GGUGGAAUGCAAGCUUUAGTT B	3630
R-008397732-000W	1440	868	CUGCAACUAAACAGGAAGG	CCUUCCUGUUUAGUUGCAGUU	3633
R-008397732-000W	1440	868	CUGCAACUAAACAGGAAGG	B CUGCAACUAAACAGGAAGGTT B	3632
R-008397735-000X	1364	869	UUAGGACUUCACCUGACAG	CUGUCAGGUGAAGUCCUAAUU	3635

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397735-000X	1364	869	UUAGGACUUCACCUGACAG	B UUAGGACUUCACCUGACAGTT B	3634
R-008397738-000Y	502	870	AGUAGCUGAUAUUGAUGGA	B AGUAGCUGAUAUUGAUGGATT B	3636
R-008397738-000Y	502	870	AGUAGCUGAUAUUGAUGGA	UCCAUCAAUAUCAGCUACUUU	3637
R-008397741-000E	1246	871	UAUAAUGAGGACCUAUACU	AGUAUAGGUCCUCAUUAUAUU	3639
R-008397741-000E	1246	871	UAUAAUGAGGACCUAUACU	B UAUAAUGAGGACCUAUACUTT B	3638
R-008397744-000F	3178	872	CCUGCUGUGAUACGAUGCU	AGCAUCGUAUCACAGCAGGUU	3641
R-008397744-000F	3178	872	CCUGCUGUGAUACGAUGCU	B CCUGCUGUGAUACGAUGCUTT B	3640
R-008397747-000G	2483	873	AUGGGUGGCCACCACCCUG	B AUGGGUGGCCACCACCCUGTT B	3642
R-008397747-000G	2483	873	AUGGGUGGCCACCACCCUG	CAGGGUGGUGGCCACCCAUUU	3643
R-008397750-000N	1417	874	GACUCUCAGGAAUCUUUCA	B GACUCUCAGGAAUCUUUCATT B	3644
R-008397750-000N	1417	874	GACUCUCAGGAAUCUUUCA	UGAAAGAUUCCUGAGAGUCUU	3645
R-008397753-000P	1893	875	GUGCACAUCAGGAUACCCA	B GUGCACAUCAGGAUACCCATT B	3646
R-008397753-000P	1893	875	GUGCACAUCAGGAUACCCA	UGGGUAUCCUGAUGUGCACUU	3647
R-008397756-000R	817	876	UUCCAGACACGCUAUCAUG	CAUGAUAGCGUGUCUGGAAUU	3649
R-008397756-000R	817	876	UUCCAGACACGCUAUCAUG	B UUCCAGACACGCUAUCAUGTT B	3648
R-008397759-000S	711	877	UUGCCACACGUGCAAUCCC	GGGAUUGCACGUGUGGCAAUU	3651
R-008397759-000S	711	877	UUGCCACACGUGCAAUCCC	B UUGCCACACGUGCAAUCCCTT B	3650
R-008397762-000Y	1433	878	UCAGAUGCUGCAACUAAAC	GUUUAGUUGCAGCAUCUGAUU	3653
R-008397762-000Y	1433	878	UCAGAUGCUGCAACUAAAC	B UCAGAUGCUGCAACUAAACTT B	3652
R-008397765-000Z	1362	879	CUUUAGGACUUCACCUGAC	GUCAGGUGAAGUCCUAAAGUU	3655
R-008397765-000Z	1362	879	CUUUAGGACUUCACCUGAC	B CUUUAGGACUUCACCUGACTT B	3654
R-008397768-000A	1838	880	CAUGCACCUUUGCGUGAGC	B CAUGCACCUUUGCGUGAGCTT B	3656
R-008397768-000A	1838	880	CAUGCACCUUUGCGUGAGC	GCUCACGCAAAGGUGCAUGUU	3657
R-008397771-000G	1037	881	ACAACUCUCCACAACCUUU	AAAGGUUGUGGAGAGUUGUUU	3659
R-008397771-000G	1037	881	ACAACUCUCCACAACCUUU	B ACAACUCUCCACAACCUUUTT B	3658
R-008397774-000H	1474	882	UGGGACUCUUGUUCAGCUU	B UGGGACUCUUGUUCAGCUUTT B	3660
R-008397774-000H	1474	882	UGGGACUCUUGUUCAGCUU	AAGCUGAAACAAGAGUCCCAUU	3661
R-008397777-000J	997	883	GCUUGGUUCACCAGUGGAU	B GCUUGGUUCACCAGUGGAUTT B	3662
R-008397777-000J	997	883	GCUUGGUUCACCAGUGGAU	AUCCACUGGUGAACCAAGCUU	3663
R-008397780-000R	931	884	UUCCCAUCAUCGUGAGGGC	B UUCCCAUCAUCGUGAGGGCTT B	3664
R-008397780-000R	931	884	UUCCCAUCAUCGUGAGGGC	GCCCUCACGAUGAUGGGAAUU	3665
R-008397783-000S	1313	885	GUCUGCUCUAGUAAUAAGC	GCUUAUUACUAGAGCAGACUU	3667
R-008397783-000S	1313	885	GUCUGCUCUAGUAAUAAGC	B GUCUGCUCUAGUAAUAAGCTT B	3666
R-008397786-000T	1487	886	CAGCUUCUGGGUUCAGAUG	B CAGCUUCUGGGUUCAGAUGTT B	3668
R-008397786-000T	1487	886	CAGCUUCUGGGUUCAGAUG	CAUCUGAACCCAGAAGCUGUU	3669
R-008397789-000U	1673	887	CGUCAUCUGACCAGCCGAC	B CGUCAUCUGACCAGCCGACTT B	3670

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397789-000U	1673	887	CGUCAUCUGACCAGCCGAC	GUCGGCUGGUCAGAUGACGUU	3671
R-008397792-000A	561	888	UGUUCCCUGAGACAUUAGA	UCUAAUGUCUCAGGGAACAUU	3673
R-008397792-000A	561	888	UGUUCCCUGAGACAUUAGA	B UGUUCCCUGAGACAUUAGATT B	3672
R-008397795-000B	1188	889	GCAACCAAGAAAGCAAGCU	B GCAACCAAGAAAGCAAGCUTT B	3674
R-008397795-000B	1188	889	GCAACCAAGAAAGCAAGCU	AGCUUGCUUUCUUGGUUGCUU	3675
R-008397798-000C	292	890	GGAGUUGGACAUGGCCAUG	B GGAGUUGGACAUGGCCAUGTT B	3676
R-008397798-000C	292	890	GGAGUUGGACAUGGCCAUG	CAUGGCCAUGUCCAACUCCUU	3677
R-008397801-000V	1958	891	GUCCGCAUGGAAGAAAUAG	B GUCCGCAUGGAAGAAAUAGTT B	3678
R-008397801-000V	1958	891	GUCCGCAUGGAAGAAAUAG	CUAUUUCUUCCAUGCGGACUU	3679
R-008397804-000W	2349	892	CUGAUCUUGGACUUGAUAU	B CUGAUCUUGGACUUGAUAUTT B	3680
R-008397804-000W	2349	892	CUGAUCUUGGACUUGAUAU	AUAUCAAGUCCAAGAUCAGUU	3681
R-008397807-000X	1460	893	AUGGAAGGUCUCCUUGGGA	UCCCAAGGAGACCUUCCAUUU	3683
R-008397807-000X	1460	893	AUGGAAGGUCUCCUUGGGA	B AUGGAAGGUCUCCUUGGGATT B	3682
R-008397810-000D	1579	894	GAUGGUCUGCCAAGUGGGU	B GAUGGUCUGCCaAGUGGGUTT B	3684
R-008397810-000D	1579	894	GAUGGUCUGCCAAGUGGGU	ACCCACUUGGCAGACCAUCUU	3685
R-008397813-000E	536	4	CGAGCUCAGAGGGUACGAG	B CGAGCUCAGAGGGUACGAGTT B	3686
R-008397813-000E	536	4	CGAGCUCAGAGGGUACGAG	CUCGUACCCUCUGAGCUCGUU	3687
R-008397816-000F	690	895	ACUAUCAAGAUGAUGCAGA	UCUGCAUCAUCUUGAUAGUUU	3689
R-008397816-000F	690	895	ACUAUCAAGAUGAUGCAGA	B ACUAUCAAGAUGAUGCAGATT B	3688
R-008397819-000F	655	896	ACAGAUGCUGAAACAUGCA	B ACAGAUGCUGAAACAUGCATT B	3690
R-008397819-000F	655	896	ACAGAUGCUGAAACAUGCA	UGCAUGUUUCAGCAUCUGUUU	3691
R-008397822-000N	2290	897	UUCAGUUGAGCUGACCAGC	GCUGGUCAGCUCAACUGAAUU	3693
R-008397822-000N	2290	897	UUCAGUUGAGCUGACCAGC	B UUCAGUUGAGCUGACCAGCTT B	3692
R-008397825-000P	1600	898	AGAGGCUCUUGUGCGUACU	B AGAGGCUCUUGUGCGUACUTT B	3694
R-008397825-000P	1600	898	AGAGGCUCUUGUGCGUACU	AGUACGCACAAGAGCCUGUUU	3695
R-008397828-000R	2432	899	GGUGGAUAUGGCCAGGAUG	CAUCCUGGCCAUAUCCACCUU	3697
R-008397828-000R	2432	899	GGUGGAUAUGGCCAGGAUG	B GGUGGAUAUGGCCAGGAUGTT B	3696
R-008397831-000X	710	900	CUUGCCACACGUGCAAUCC	B CUUGCCACACGUGCAAUCCTT B	3698
R-008397831-000X	710	900	CUUGCCACACGUGCAAUCC	GGAUUGCACGUGUGGCAAGUU	3699
R-008397834-000Y	1714	901	GAAUGCAGUUCGCCUUCAC	B GAAUGCAGUUCGCCUUCACTT B	3700
R-008397834-000Y	1714	901	GAAUGCAGUUCGCCUUCAC	GUGAAGGCGAACUGCAUUCUU	3701
R-008397837-000Z	2005	902	CCUAGCUCGGGAUGUUCAC	B CCUAGCUCGGGAUGUUCACTT B	3702
R-008397837-000Z	2005	902	CCUAGCUCGGGAUGUUCAC	GUGAACAUCCCGAGCUAGGUU	3703
R-008397840-000F	1728	903	UUCACUAUGGACUACCAGU	B UUCACUAUGGACUACCAGUTT B	3704
R-008397840-000F	1728	903	UUCACUAUGGACUACCAGU	ACUGGUAGUCCAUAGUGAAUU	3705
R-008397843-000G	2482	904	GAUGGGUGGCCACCACCCU	AGGGUGGUGGCCACCCAUCUU	3707
R-008397843-000G	2482	904	GAUGGGUGGCCACCACCCU	B GAUGGGUGGCCACCACCCUTT B	3706

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397846-000H	768	905	UGGUUAAUAAGGCUGCAGU	B UGGUUAAUAAGGCUGCAGUTT B	3708
R-008397846-000H	768	905	UGGUUAAUAAGGCUGCAGU	ACUGCAGCCUUAUUAACCAUU	3709
R-008397849-000J	693	906	AUCAAGAUGAUGCAGAACU	B AUCAAGAUGAUGCAGAACUTT B	3710
R-008397849-000J	693	906	AUCAAGAUGAUGCAGAACU	AGUUCUGCAUCAUCUUGAUUU	3711
R-008397852-000R	3179	907	CUGCUGUGAUACGAUGCUU	B CUGCUGUGAUACGAUGCUUTT B	3712
R-008397852-000R	3179	907	CUGCUGUGAUACGAUGCUU	AAGCAUCGUAUCACAGCAGUU	3713
R-008397855-000S	1549	89	CACUUGCAAUAAUUAUAAG	CUUAUAAUUAUUGCAAGUGUU	3715
R-008397855-000S	1549	89	CACUUGCAAUAAUUAUAAG	B CACUUGCAAUAAUUAUAAGTT B	3714
R-008397858-000T	1792	167	GGCUACUGUUGGAUUGAUU	AAUCAAUCCAACAGUAGCCUU	3717
R-008397858-000T	1792	167	GGCUACUGUUGGAUUGAUU	B GGCUACUGUUGGAUUGAUUTT B	3716
R-008397861-000Z	2448	908	AUGCCUUGGGUAUGGACCC	GGGUCCAUACCCAAGGCAUUU	3719
R-008397861-000Z	2448	908	AUGCCUUGGGUAUGGACCC	B AUGCCUUGGGUAUGGACCCTT B	3718
R-008397864-000A	3183	909	UGUGAUACGAUGCUUCAAG	B UGUGAUACGAUGCUUCAAGTT B	3720
R-008397864-000A	3183	909	UGUGAUACGAUGCUUCAAG	CUUGAAGCAUCGUAUCACAUU	3721
R-008397867-000B	1293	910	GAGUGCUGAAGGUGCUAUC	GAUAGCACCUUCAGCACUCUU	3723
R-008397867-000B	1293	910	GAGUGCUGAAGGUGCUAUC	B GAGUGCUGAAGGUGCUAUCTT B	3722
R-008397870-000H	544	911	GAGGGUACGAGCUGCUAUG	CAUAGCAGCUCGUACCCUCUU	3725
R-008397870-000H	544	911	GAGGGUACGAGCUGCUAUG	B GAGGGUACGAGCUGCUAUGTT B	3724
R-008397873-000J	1676	26	CAUCUGACCAGCCGACACC	GGUGUCGGCUGGUCAGAUGUU	3727
R-008397873-000J	1676	26	CAUCUGACCAGCCGACACC	B CAUCUGACCAGCCGACACCTT B	3726
R-008397876-000K	2937	912	UUAAUUGUAAUCUGAAUAA	B UUAAUUGUAAUCUGAAUAATT B	3728
R-008397876-000K	2937	912	UUAAUUGUAAUCUGAAUAA	UUAUUCAGAUUACAAUUAAUU	3729
R-008397879-000L	1691	913	CACCAAGAAGCAGAGAUGG	CCAUCUCUGCUUCUUGGUGUU	3731
R-008397879-000L	1691	913	CACCAAGAAGCAGAGAUGG	B CACCAAGAAGCAGAGAUGGTT B	3730
R-008397882-000T	2195	120	UUACUUCACUCUAGGAAUG	B UUACUUCACUCUAGGAAUGTT B	3732
R-008397882-000T	2195	120	UUACUUCACUCUAGGAAUG	CAUUCCUAGAGUGAAGUAAUU	3733
R-008397885-000U	1356	186	UGCAAGCUUUAGGACUUCA	B UGCAAGCUUUAGGACUUCATT B	3734
R-008397885-000U	1356	186	UGCAAGCUUUAGGACUUCA	UGAAGUCCUAAAGCUUGCAUU	3735
R-008397888-000V	557	184	GCUAUGUUCCCUGAGACAU	AUGUCUCAGGGAACAUAGCUU	3737
R-008397888-000V	557	184	GCUAUGUUCCCUGAGACAU	B GCUAUGUUCCCUGAGACAUTT B	3736
R-008397897-000E	1353	914	GAAUGCAAGCUUUAGGACU	AGUCCUAAAGCUUGCAUUCUU	3739
R-008397897-000E	1353	914	GAAUGCAAGCUUUAGGACU	B GAAUGCAAGCUUUAGGACUTT B	3738
R-008397900-000W	1843	915	ACCUUUGCGUGAGCAGGGU	B ACCUUUGCGUGAGCAGGGUTT B	3740
R-008397900-000W	1843	915	ACCUUUGCGUGAGCAGGGU	ACCCUGCUCACGCAAAGGUUU	3741
R-008397903-000X	1302	916	AGGUGCUAUCUGUCUGCUC	B AGGUGCUAUCUGUCUGCUCTT B	3742
R-008397903-000X	1302	916	AGGUGCUAUCUGUCUGCUC	GAGCAGACAGAUAGCACCUUU	3743

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397906-000Y	2130	917	UUGCUCAGGACAAGGAAGC	B UUGCUCAGGACAAGGAAGC*TT* B	3744
R-008397906-000Y	2130	917	UUGCUCAGGACAAGGAAGC	GCUUCCUUGUCCUGAGCAA<u>UU</u>	3745
R-008397909-000Z	2165	918	GCUGAGGGAGCCACAGCUC	B GCUGAGGGAGCCACAGCUC*TT* B	3746
R-008397909-000Z	2165	918	GCUGAGGGAGCCACAGCUC	GAGCUGUGGCUCCCUCAGC<u>UU</u>	3747
R-008397912-000F	387	919	CUACCACAGCUCCUUCUCU	B CUACCACAGCUCCUUCUCU*TT* B	3748
R-008397912-000F	387	919	CUACCACAGCUCCUUCUCU	AGAGAAGGAGCUGUGGUAG<u>UU</u>	3749
R-008397915-000G	2472	920	UGGAACAUGAGAUGGGUGG	CCACCCAUCUCAUGUUCCA<u>UU</u>	3751
R-008397915-000G	2472	920	UGGAACAUGAGAUGGGUGG	B UGGAACAUGAGAUGGGUGG*TT* B	3750
R-008397918-000H	857	921	GCUAUUGUACGUACCAUGC	B GCUAUUGUACGUACCAUGC*TT* B	3752
R-008397918-000H	857	921	GCUAUUGUACGUACCAUGC	GCAUGGUACGUACAAUAGC<u>UU</u>	3753
R-008397921-000P	1816	922	UCUUGCCCUUUGUCCCGCA	UGCGGGACAAAGGGCAAGA<u>UU</u>	3755
R-008397921-000P	1816	922	UCUUGCCCUUUGUCCCGCA	B UCUUGCCCUUUGUCCCGCA*TT* B	3754
R-008397924-000R	1561	923	UUAUAAGAACAAGAUGAUG	CAUCAUCUUGUUCUUAUAA<u>UU</u>	3757
R-008397924-000R	1561	923	UUAUAAGAACAAGAUGAUG	B UUAUAAGAACAAGAUGAUG*TT* B	3756
R-008397927-000S	811	924	GGAAGCUUCCAGACACGCU	B GGAAGCUUCCAGACACGCU*TT* B	3758
R-008397927-000S	811	924	GGAAGCUUCCAGACACGCU	AGCGUGUCUGGAAGCUUCC<u>UU</u>	3759
R-008397930-000Y	1327	925	UAAGCCGGCUAUUGUAGAA	B UAAGCCGGCUAUUGUAGAA*TT* B	3760
R-008397930-000Y	1327	925	UAAGCCGGCUAUUGUAGAA	UUCUACAAUAGCCGGCUUA<u>UU</u>	3761
R-008397933-000Z	757	926	GGACCAGGUGGUGGUUAAU	B GGACCAGGUGGUGGUUAAU*TT* B	3762
R-008397933-000Z	757	926	GGACCAGGUGGUGGUUAAU	AUUAACCACCACCUGGUCC<u>UU</u>	3763
R-008397936-000A	507	927	CUGAUAUUGAUGGACAGUA	B CUGAUAUUGAUGGACAGUA*TT* B	3764
R-008397936-000A	507	927	CUGAUAUUGAUGGACAGUA	UACUGUCCAUCAAUAUCAG<u>UU</u>	3765
R-008397939-000B	3092	928	UGGGUAGGGUAAAUCAGUA	B UGGGUAGGGUAAAUCAGUA*TT* B	3766
R-008397939-000B	3092	928	UGGGUAGGGUAAAUCAGUA	UACUGAUUUACCCUACCCA<u>UU</u>	3767
R-008397942-000H	2359	929	ACUUGAUAUUGGUGCCCAG	B ACUUGAUAUUGGUGCCCAG*TT* B	3768
R-008397942-000H	2359	929	ACUUGAUAUUGGUGCCCAG	CUGGGCACCAAUAUCAAGU<u>UU</u>	3769
R-008397945-000J	1753	930	UAAGCUCUUACACCCACCA	B UAAGCUCUUACACCCACCA*TT* B	3770
R-008397945-000J	1753	930	UAAGCUCUUACACCCACCA	UGGUGGGUGUAAGAGCUUA<u>UU</u>	3771
R-008397948-000K	273	931	CUACUCAAGCUGAUUUGAU	AUCAAAUCAGCUUGAGUAG<u>UU</u>	3773
R-008397948-000K	273	931	CUACUCAAGCUGAUUUGAU	B CUACUCAAGCUGAUUUGAU*TT* B	3772
R-008397951-000S	1859	932	GGUGCCAUUCCACGACUAG	CUAGUCGUGGAAUGGCACC<u>UU</u>	3775
R-008397951-000S	1859	932	GGUGCCAUUCCACGACUAG	B GGUGCCAUUCCACGACUAG*TT* B	3774
R-008397954-000T	296	933	UUGGACAUGGCCAUGGAAC	B UUGGACAUGGCCAUGGAAC*TT* B	3776
R-008397954-000T	296	933	UUGGACAUGGCCAUGGAAC	GUUCCAUGGCCAUGUCCAA<u>UU</u>	3777
R-008397957-000U	615	934	CUGCUCAUCCCACUAAUGU	ACAUUAGUGGGAUGAGCAG<u>UU</u>	3779
R-008397957-000U	615	934	CUGCUCAUCCCACUAAUGU	B CUGCUCAUCCCACUAAUGU*TT* B	3778
R-008397960-000A	301	935	CAUGGCCAUGGAACCAGAC	GUCUGGUUCCAUGGCCAUG<u>UU</u>	3781

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008397960-000A	301	935	CAUGGCCAUGGAACCAGAC	B CAUGGCCAUGGAACCAGACTT B	3780
R-008397963-000B	1184	936	UAUGGCAACCAAGAAAGCA	B UAUGGCAACCAAGAAAGCATT B	3782
R-008397963-000B	1184	936	UAUGGCAACCAAGAAAGCA	UGCUUUCUUGGUUGCCAUAUU	3783
R-008397966-000C	1006	937	ACCAGUGGAUUCUGUGUUG	B ACCAGUGGAUUCUGUGUUGTT B	3784
R-008397966-000C	1006	937	ACCAGUGGAUUCUGUGUUG	CAACACAGAAUCCACUGGUUU	3785
R-008397969-000D	2189	938	ACAGAGUUACUUCACUCUA	B ACAGAGUUACUUCACUCUATT B	3786
R-008397969-000D	2189	938	ACAGAGUUACUUCACUCUA	UAGAGUGAAGUAACUCUGUUU	3787
R-008397972-000K	1365	939	UAGGACUUCACCUGACAGA	UCUGUCAGGUGAAGUCCUAUU	3789
R-008397972-000K	1365	939	UAGGACUUCACCUGACAGA	B UAGGACUUCACCUGACAGATT B	3788
R-008397975-000L	2442	940	GCCAGGAUGCCUUGGGUAU	B GCCAGGAUGCCUUGGGUAUTT B	3790
R-008397975-000L	2442	940	GCCAGGAUGCCUUGGGUAU	AUACCCAAGGCAUCCUGGCUU	3791
R-008397978-000M	1249	941	AAUGAGGACCUAUACUUAC	B AAUGAGGACCUAUACUUACTT B	3792
R-008397978-000M	1249	941	AAUGAGGACCUAUACUUAC	GUAAGUAUAGGUCCUCAUUUU	3793
R-008397981-000U	1144	942	AUUCUUGGCUAUUACGACA	B AUUCUUGGCUAUUACGACATT B	3794
R-008397981-000U	1144	942	AUUCUUGGCUAUUACGACA	UGUCGUAAUAGCCAAGAAUUU	3795
R-008397984-000V	2075	943	CUUUAUUCUCCCAUUGAAA	B CUUUAUUCUCCCAUUGAAATT B	3796
R-008397984-000V	2075	943	CUUUAUUCUCCCAUUGAAA	UUUCAAUGGGAGAAUAAAGUU	3797
R-008397987-000W	759	94	ACCAGGUGGUGGUUAAUAA	B ACCAGGUGGUGGUUAAUAATT B	3798
R-008397987-000W	759	94	ACCAGGUGGUGGUUAAUAA	UUAUUAACCACCACCUGGUUU	3799
R-008397990-000C	1545	44	ACCUCACUUGCAAUAAUUA	B ACCUCACUUGCAAUAAUUATT B	3800
R-008397990-000C	1545	44	ACCUCACUUGCAAUAAUUA	UAAUUAUUGCAAGUGAGGUUU	3801
R-008397993-000D	504	944	UAGCUGAUAUUGAUGGACA	UGUCCAUCAAUAUCAGCUAUU	3803
R-008397993-000D	504	944	UAGCUGAUAUUGAUGGACA	B UAGCUGAUAUUGAUGGACATT B	3802
R-008397996-000E	1405	945	GAACUGUCUUUGGACUCUC	B GAACUGUCUUUGGACUCUCTT B	3804
R-008397996-000E	1405	945	GAACUGUCUUUGGACUCUC	GAGAGUCCAAAGACAGUUCUU	3805
R-008397999-000F	333	946	UUAGUCACUGGCAGCAACA	UGUUGCUGCCAGUGACUAAUU	3807
R-008397999-000F	333	946	UUAGUCACUGGCAGCAACA	B UUAGUCACUGGCAGCAACATT B	3806
R-008398002-000V	1032	947	CCAUUACAACUCUCCACAA	B CCAUUACAACUCUCCACAATT B	3808
R-008398002-000V	1032	947	CCAUUACAACUCUCCACAA	UUGUGGAGAGUUGUAAUGGUU	3809
R-008398005-000W	1748	948	GUGGUUAAGCUCUUACACC	B GUGGUUAAGCUCUUACACCTT B	3810
R-008398005-000W	1748	948	GUGGUUAAGCUCUUACACC	GGUGUAAGAGCUUAACCACUU	3811
R-008398008-000X	283	949	UGAUUUGAUGGAGUUGGAC	GUCCAACUCCAUCAAAUCAUU	3813
R-008398008-000X	283	949	UGAUUUGAUGGAGUUGGAC	B UGAUUUGAUGGAGUUGGACTT B	3812
R-008398011-000D	1700	950	GCAGAGAUGGCCCAGAAUG	B GCAGAGAUGGCCCAGAAUGTT B	3814
R-008398011-000D	1700	950	GCAGAGAUGGCCCAGAAUG	CAUUCUGGGCCAUCUCUGCUU	3815
R-008398014-000E	1445	951	ACUAAACAGGAAGGGAUGG	B ACUAAACAGGAAGGGAUGGTT B	3816

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398014-000E	1445	951	ACUAAACAGGAAGGGAUGG	CCAUCCCUUCCUGUUUAGUUU	3817
R-008398017-000F	1133	952	ACAAAUGUUAAAUUCUUGG	CCAAGAAUUUAACAUUUGUUU	3819
R-008398017-000F	1133	952	ACAAAUGUUAAAUUCUUGG	B ACAAAUGUUAAAUUCUUGGTT B	3818
R-008398020-000M	527	953	GCAAUGACUCGAGCUCAGA	UCUGAGCUCGAGUCAUUGCUU	3821
R-008398020-000M	527	953	GCAAUGACUCGAGCUCAGA	B GCAAUGACUCGAGCUCAGATT B	3820
R-008398023-000N	2010	954	CUCGGGAUGUUCACAACCG	CGGUUGUGAACAUCCCGAGUU	3823
R-008398023-000N	2010	954	CUCGGGAUGUUCACAACCG	B CUCGGGAUGUUCACAACCGTT B	3822
R-008398026-000P	851	955	GUGUCUGCUAUUGUACGUA	UACGUACAAUAGCAGACACUU	3825
R-008398026-000P	851	955	GUGUCUGCUAUUGUACGUA	B GUGUCUGCUAUUGUACGUATT B	3824
R-008398029-000R	436	956	UGUGGAUACCUCCCAAGUC	B UGUGGAUACCUCCCAAGUCTT B	3826
R-008398029-000R	436	956	UGUGGAUACCUCCCAAGUC	GACUUGGGAGGUAUCCACAUU	3827
R-008398032-000X	1601	2	GAGGCUCUUGUGCGUACUG	B GAGGCUCUUGUGCGUACUGTT B	3828
R-008398032-000X	1601	2	GAGGCUCUUGUGCGUACUG	CAGUACGCACAAGAGCCUCUU	3829
R-008398035-000Y	2446	957	GGAUGCCUUGGGUAUGGAC	B GGAUGCCUUGGGUAUGGACTT B	3830
R-008398035-000Y	2446	957	GGAUGCCUUGGGUAUGGAC	GUCCAUACCCAAGGCAUCCUU	3831
R-008398038-000Z	1142	958	AAAUUCUUGGCUAUUACGA	B AAAUUCUUGGCUAUUACGATT B	3832
R-008398038-000Z	1142	958	AAAUUCUUGGCUAUUACGA	UCGUAAUAGCCAAGAAUUUUU	3833
R-008398041-000F	549	959	UACGAGCUGCUAUGUUCCC	B UACGAGCUGCUAUGUUCCCTT B	3834
R-008398041-000F	549	959	UACGAGCUGCUAUGUUCCC	GGGAACAUAGCAGCUCGUAUU	3835
R-008398044-000G	1083	960	CAGUGCGUUUAGCUGGUGG	CCACCAGCUAAACGCACUGUU	3837
R-008398044-000G	1083	960	CAGUGCGUUUAGCUGGUGG	B CAGUGCGUUUAGCUGGUGGTT B	3836
R-008398047-000H	695	961	CAAGAUGAUGCAGAACUUG	CAAGUUCUGCAUCAUCUUGUU	3839
R-008398047-000H	695	961	CAAGAUGAUGCAGAACUUG	B CAAGAUGAUGCAGAACUUGTT B	3838
R-008398050-000P	885	962	AUGAUGUAGAAACAGCUCG	B AUGAUGUAGAAACAGCUCGTT B	3840
R-008398050-000P	885	962	AUGAUGUAGAAACAGCUCG	CGAGCUGUUUCUACAUCAUUU	3841
R-008398056-000S	2067	963	UGCAGCUGCUUUAUUCUCC	B UGCAGCUGCUUUAUUCUCCTT B	3842
R-008398056-000S	2067	963	UGCAGCUGCUUUAUUCUCC	GGAGAAUAAAGCAGCUGCAUU	3843
R-008398059-000T	390	964	CCACAGCUCCUUCUCUGAG	CUCAGAGAAGGAGCUGUGGUU	3845
R-008398059-000T	390	964	CCACAGCUCCUUCUCUGAG	B CCACAGCUCCUUCUCUGAGTT B	3844
R-008398062-000Z	1719	965	CAGUUCGCCUUCACUAUGG	G CAGUUCGCCUUCACUAUGGTT B	3846
R-008398062-000Z	1719	965	CAGUUCGCCUUCACUAUGG	CCAUAGUGAAGGCGAACUGUU	3847
R-008398065-000A	813	966	AAGCUUCCAGACACGCUAU	AUAGCGUGUCUGGAAGCUUUU	3849
R-008398065-000A	813	966	AAGCUUCCAGACACGCUAU	B AAGCUUCCAGACACGCUAUTT B	3848
R-008398068-000B	2289	967	UUUCAGUUGAGCUGACCAG	B UUUCAGUUGAGCUGACCAGTT B	3850
R-008398068-000B	2289	967	UUUCAGUUGAGCUGACCAG	CUGGUCAGCUCAACUGAAAUU	3851
R-008398071-000H	377	968	UCUGGUGCCACUACCACAG	B UCUGGUGCCACUACCACAGTT B	3852
R-008398071-000H	377	968	UCUGGUGCCACUACCACAG	CUGUGGUAGUGGCACCAGAUU	3853

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398074-000J	826	969	CGCUAUCAUGCGUUCUCCU	AGGAGAACGCAUGAUAGCGUU	3855
R-008398074-000J	826	969	CGCUAUCAUGCGUUCUCCU	B CGCUAUCAUGCGUUCUCCUTT B	3854
R-008398077-000K	1634	970	GACAGGGAAGACAUCACUG	CAGUGAUGUCUUCCCUGUCUU	3857
R-008398077-000K	1634	970	GACAGGGAAGACAUCACUG	B GACAGGGAAGACAUCACUGTT B	3856
R-008398080-000S	1208	971	AUCAUACUGGCUAGUGGUG	B AUCAUACUGGCUAGUGGUGTT B	3858
R-008398080-000S	1208	971	AUCAUACUGGCUAGUGGUG	CACCACUAGCCAGUAUGAUUU	3859
R-008398083-000T	1628	972	GCUGGUGACAGGGAAGACA	UGUCUUCCCUGUCACCAGCUU	3861
R-008398083-000T	1628	972	GCUGGUGACAGGGAAGACA	B GCUGGUGACAGGGAAGACATT B	3860
R-008398086-000U	2003	973	AUCCUAGCUCGGGAUGUUC	GAACAUCCCGAGCUAGGAUUU	3863
R-008398086-000U	2003	973	AUCCUAGCUCGGGAUGUUC	B AUCCUAGCUCGGGAUGUUCTT B	3862
R-008398089-000V	452	974	GUCCUGUAUGAGUGGGAAC	B GUCCUGUAUGAGUGGGAACTT B	3864
R-008398089-000V	452	974	GUCCUGUAUGAGUGGGAAC	GUUCCCACUCAUACAGGACUU	3865
R-008398092-000B	2543	175	GCCCAGGACCUCAUGGAUG	CAUCCAUGAGGUCCUGGGCUU	3867
R-008398092-000B	2543	175	GCCCAGGACCUCAUGGAUG	B GCCCAGGACCUCAUGGAUGTT B	3866
R-008398095-000C	3081	975	UGGGAUAUGUAUGGGUAGG	CCUACCCAUACAUAUCCCAUU	3869
R-008398095-000C	3081	975	UGGGAUAUGUAUGGGUAGG	B UGGGAUAUGUAUGGGUAGGTT B	3868
R-008398098-000D	2354	976	CUUGGACUUGAUAUUGGUG	B CUUGGACUUGAUAUUGGUGTT B	3870
R-008398098-000D	2354	976	CUUGGACUUGAUAUUGGUG	CACCAAUAUCAAGUCCAAGUU	3871
R-008398101-000W	1822	977	CCUUUGUCCCGCAAAUCAU	B CCUUUGUCCCGCAAAUCAUTT B	3872
R-008398101-000W	1822	977	CCUUUGUCCCGCAAAUCAU	AUGAUUUGCGGGACAAAGGUU	3873
R-008398107-000Y	1299	978	UGAAGGUGCUAUCUGUCUG	CAGACAGAUAGCACCUUCAUU	3875
R-008398107-000Y	1299	978	UGAAGGUGCUAUCUGUCUG	B UGAAGGUGCUAUCUGUCUGTT B	3874
R-008398110-000E	486	979	CCUUCACUCAAGAACAAGU	B CCUUCACUCAAGAACAAGUTT B	3876
R-008398110-000E	486	979	CCUUCACUCAAGAACAAGU	ACUUGUUCUUGAGUGAAGGUU	3877
R-008398116-000G	1463	980	GAAGGUCUCCUUGGGACUC	B GAAGGUCUCCUUGGGACUCTT B	3878
R-008398116-000G	1463	980	GAAGGUCUCCUUGGGACUC	GAGUCCCAAGGAGACCUUCUU	3879
R-008398119-000H	2280	981	AGAAACGGCUUUCAGUUGA	B AGAAACGGCUUUCAGUUGATT B	3880
R-008398119-000H	2280	981	AGAAACGGCUUUCAGUUGA	UCAACUGAAAGCCGUUUCUUU	3881
R-008398122-000P	1907	982	ACCCAGCGCCGUACGUCCA	B ACCCAGCGCCGUACGUCCATT B	3882
R-008398122-000P	1907	982	ACCCAGCGCCGUACGUCCA	UGGACGUACGGCGCUGGGUUU	3883
R-008398125-000R	923	983	CAUAACCUUUCCCAUCAUC	B CAUAACCUUUCCCAUCAUCTT B	3884
R-008398125-000R	923	983	CAUAACCUUUCCCAUCAUC	GAUGAUGGGAAAGGUUAUGUU	3885
R-008398128-000S	1979	984	GAAGGUUGUACCGGAGCCC	B GAAGGUUGUACCGGAGCCCTT B	3886
R-008398128-000S	1979	984	GAAGGUUGUACCGGAGCCC	GGGCUCCGGUACAACCUUCUU	3887
R-008398131-000Y	1827	985	GUCCCGCAAAUCAUGCACC	B GUCCCGCAAAUCAUGCACCTT B	3888
R-008398131-000Y	1827	985	GUCCCGCAAAUCAUGCACC	GGUGCAUGAUUUGCGGGACUU	3889

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398134-000Z	1201	986	CAAGCUCAUCAUACUGGCU	AGCCAGUAUGAUGAGCUUGUU	3891
R-008398134-000Z	1201	986	CAAGCUCAUCAUACUGGCU	B CAACGUCAUCAUACUGGCUTT B	3890
R-008398137-000A	1913	987	CGCCGUACGUCCAUGGGUG	B CGCCGUACGUCCAUGGGUGTT B	3892
R-008398137-000A	1913	987	CGCCGUACGUCCAUGGGUG	CACCCAUGGACGUACGGCGUU	3893
R-008398140-000G	2191	988	AGAGUUACUUCACUCUAGG	CCUAGAGUGAAGUAACUCUUU	3895
R-008398140-000G	2191	988	AGAGUUACUUCACUCUAGG	B AGAGUUACUUCACUCUAGGTT B	3894
R-008398143-000H	295	989	GUUGGACAUGGCCAUGGAA	UUCCAUGGCCAUGUCCAACUU	3897
R-008398143-000H	295	989	GUUGGACAUGGCCAUGGAA	B GUUGGACAUGGCCAUGGAATT B	3896
R-008398146-000J	1149	990	UGGCUAUUACGACAGACUG	B UGGCUAUUACGACAGACUGTT B	3898
R-008398146-000J	1149	990	UGGCUAUUACGACAGACUG	CAGUCUGUCGUAAUAGCCAUU	3899
R-008398149-000K	533	991	ACUCGAGCUCAGAGGGUAC	B ACUCGAGCUCAGAGGGUACTT B	3900
R-008398149-000K	533	991	ACUCGAGCUCAGAGGGUAC	GUACCCUCUGAGCUCGAGUUU	3901
R-008398152-000S	604	992	ACAGUUUGAUGCUGCUCAU	B ACAGUUUGAUGCUGCUCAUTT B	3902
R-008398152-000S	604	992	ACAGUUUGAUGCUGCUCAU	AUGAGCAGCAUCAAACUGUUU	3903
R-008398155-000T	766	993	GGUGGUUAAUAAGGCUGCA	B GGUGGUUAAUAAGGCUGCATT B	3904
R-008398155-000T	766	993	GGUGGUUAAUAAGGCUGCA	UGCAGCCUUAUUAACCACCUU	3905
R-008398158-000U	1823	994	CUUUGUCCCGCAAAUCAUG	B CUUUGUCCCGCAAAUCAUGTT B	3906
R-008398158-000U	1823	994	CUUUGUCCCGCAAAUCAUG	CAUGAUUUGCGGGACAAAGUU	3907
R-008398161-000A	2048	995	AAUACCAUUCCAUUGUUUG	CAAACAAUGGAAUGGUAUUUU	3909
R-008398161-000A	2048	995	AAUACCAUUCCAUUGUUUG	B AAUACCAUUCCAUUGUUUGTT B	3908
R-008398164-000B	714	996	CCACACGUGCAAUCCCUGA	G CCACACGUGCAAUCCCUGATT B	3910
R-008398164-000B	714	996	CCACACGUGCAAUCCCUGA	UCAGGGAUUGCACGUGUGGUU	3911
R-008398167-000C	2439	997	AUGGCCAGGAUGCCUUGGG	CCCAAGGCAUCCUGGCCAUUU	3913
R-008398167-000C	2439	997	AUGGCCAGGAUGCCUUGGG	B AUGGCCAGGAUGCCUUGGGTT B	3912
R-008398170-000J	1903	998	GGAUACCCAGCGCCGUACG	B GGAUACCCAGCGCCGUACGTT B	3914
R-008398170-000J	1903	998	GGAUACCCAGCGCCGUACG	CGUACGGCGCUGGGUAUCCUU	3915
R-008398173-000K	2395	999	UCGCCAGGAUGAUCCUAGC	GCUAGGAUCAUCCUGGCGAUU	3917
R-008398173-000K	2395	999	UCGCCAGGAUGAUCCUAGC	B UCGCCAGGAUGAUCCUAGCTT B	3916
R-008398175-000L	789	1000	UGGUCCAUCAGCUUUCUAA	UUAGAAAGCUGAUGGACCAUU	3919
R-008398175-000L	789	1000	UGGUCCAUCAGCUUUCUAA	B UGGUCCAUCAGCUUUCUAATT B	3918
R-008398179-000M	3085	1001	AUAUGUAUGGGUAGGGUAA	UUACCCUACCCAUACAUAUUU	3921
R-008398179-000M	3085	1001	AUAUGUAUGGGUAGGGUAA	B AUAUGUAUGGGUAGGGUAATT B	3920
R-008398182-000U	1710	1002	CCCAGAAUGCAGUUCGCCU	B CCCAGAAUGCAGUUCGCCUTT B	3922
R-008398182-000U	1710	1002	CCCAGAAUGCAGUUCGCCU	AGGCGAACUGCAUUCUGGGUU	3923
R-008398185-000V	1336	1003	UAUUGUAGAAGCUGGUGGA	B UAUUGUAGAAGCUGGUGGATT B	3924
R-008398185-000V	1336	1003	UAUUGUAGAAGCUGGUGGA	UCCACCAGCUUCUACAAUAUU	3925
R-008398188-000W	3089	1004	GUAUGGGUAGGGUAAAUCA	UGAUUUACCCUACCCAUACUU	3927

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398188-000W	3089	1004	GUAUGGGUAGGGUAAAUCA	B GUAUGGGUAGGGUAAAUCATT B	3926
R-008398191-000C	2351	1005	GAUCUUGGACUUGAUAUUG	B GAUCUUGGACUUGAUAUUGTT B	3928
R-008398191-000C	2351	1005	GAUCUUGGACUUGAUAUUG	CAAUAUCAAGUCCAAGAUCUU	3929
R-008398194-000D	716	1006	ACACGUGCAAUCCCUGAAC	B ACACGUGCAAUCCCUGAACTT B	3930
R-008398194-000D	716	1006	ACACGUGCAAUCCCUGAAC	GUUCAGGGAUUGCACGUGUUU	3931
R-008398197-000E	1911	1007	AGCGCCGUACGUCCAUGGG	B AGCGCCGUACGUCCAUGGGTT B	3932
R-008398197-000E	1911	1007	AGCGCCGUACGUCCAUGGG	CCCAUGGACGUACGGCGCUUU	3933
R-008398200-000X	1985	1008	UGUACCGGAGCCCUUCACA	UGUGAAGGGCUCCGGUACAUU	3935
R-008398200-000X	1985	1008	UGUACCGGAGCCCUUCACA	B UGUACCGGAGCCCUUCACATT B	3934
R-008398203-000Y	2516	1009	GUUGAUGGGCUGCCAGAUC	B GUUGAUGGGCUGCCAGAUCTT B	3936
R-008398203-000Y	2516	1009	GUUGAUGGGCUGCCAGAUC	GAUCUGGCAGCCCAUCAACUU	3937
R-008398206-000A	1762	1010	ACACCCACCAUCCCACUGG	CCAGUGGGAUGGUGGGUGUUU	3939
R-008398206-000A	1762	1010	ACACCCACCAUCCCACUGG	B ACACCCACCAUCCCACUGGTT B	3938
R-008398209-000A	1156	1011	UACGACAGACUGCCUUCAA	B UACGACAGACUGCCUUCAATT B	3940
R-008398209-000A	1156	1011	UACGACAGACUGCCUUCAA	UUGAAGGCAGUCUGUCGUAUU	3941
R-008398212-000G	1887	1012	UUGUUCGUGCACAUCAGGA	B UUGUUCGUGCACAUCAGGATT B	3942
R-008398212-000G	1887	1012	UUGUUCGUGCACAUCAGGA	UCCUGAUGUGCACGAACAAUU	3943
R-008398215-000H	1833	1013	CAAAUCAUGCACCUUUGCG	CGCAAAGGUGCAUGAUUUGUU	3945
R-008398215-000H	1833	1013	CAAAUCAUGCACCUUUGCG	B CAAAUCAUGCACCUUUGCGTT B	3944
R-008398218-000J	967	1014	GUCUGGAGGCAUUCCUGCC	GGCAGGAAUGCCUCCAGACUU	3947
R-008398218-000J	967	1014	GUCUGGAGGCAUUCCUGCC	B GUCUGGAGGCAUUCCUGCCTT B	3946
R-008398221-000R	1730	1015	CACUAUGGACUACCAGUUG	CAACUGGUAGUCCAUAGUGUU	3949
R-008398221-000R	1730	1015	CACUAUGGACUACCAGUUG	B CACUAUGGACUACCAGUUGTT B	3948
R-008398224-000S	829	1016	UAUCAUGCGUUCUCCUCAG	CUGAGGAGAACGCAUGAUAUU	3951
R-008398224-000S	829	1016	UAUCAUGCGUUCUCCUCAG	B UAUCAUGCGUUCUCCUCAGTT B	3950
R-008398227-000T	890	1017	GUAGAAACAGCUCGUUGUA	B GUAGAAACAGCUCGUUGUATT B	3952
R-008398227-000T	890	1017	GUAGAAACAGCUCGUUGUA	UACAACGAGCUGUUUCUACUU	3953
R-008398230-000Z	2181	1018	CUCCUCUGACAGAGUUACU	AGUAACUCUGUCAGAGGAGUU	3955
R-008398230-000Z	2181	1018	CUCCUCUGACAGAGUUACU	B CUCCUCUGACAGAGUUACUTT B	3954
R-008398233-000A	2131	1019	UGCUCAGGACAAGGAAGCU	B UGCUCAGGACAAGGAAGCUTT B	3956
R-008398233-000A	2131	1019	UGCUCAGGACAAGGAAGCU	AGCUUCCUUGUCCUGAGCAUU	3957
R-008398236-000B	1586	1020	CAAGUGGGUGGUAUAGAGG	B CAAGUGGGUGGUAUAGAGGTT B	3958
R-008398236-000B	1586	1020	CAAGUGGGUGGUAUAGAGG	CCUCUAUACCACCCACUUGUU	3959
R-008398239-000C	765	1021	UGGUGGUUAAUAAGGCUGC	B UGGUGGUUAAUAAGGCUGCTT B	3960
R-008398239-000C	765	1021	UGGUGGUUAAUAAGGCUGC	GCAGCCUUAUUAACCACCAUU	3961
R-003298242-000J	1369	1022	ACUUCACCUGACAGAUCCA	B ACUUCACCUGACAGAUCCATT B	3962

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-003298242-000J	1369	1022	ACUUCACCUGACAGAUCCA	UGGAUCUGUCAGGUGAAGUUU	3963
R-008398245-000K	1724	1023	CGCCUUCACUAUGGACUAC	GUAGUCCAUAGUGAAGGCGUU	3965
R-008398245-000K	1724	1023	CGCCUUCACUAUGGACUAC	B CGCCUUCACUAUGGACUACTT B	3964
R-008398248-000L	834	1024	UGCGUUCUCCUCAGAUGGU	ACCAUCUGAGGAGAACGCAUU	3967
R-008398248-000L	834	1024	UGCGUUCUCCUCAGAUGGU	B UGCGUUCUCCUCAGAUGGUTT B	3966
R-008398251-000T	1983	1025	GUUGUACCGGAGCCCUUCA	B GUUGUACCGGAGCCCUUCATT B	3968
R-008398251-000T	1983	1025	GUUGUACCGGAGCCCUUCA	UGAAGGGCUCCGGUACAACUU	3969
R-008398254-000U	1688	1026	CGACACCAAGAAGCAGAGA	B CGACACCAAGAAGCAGAGATT B	3970
R-008398254-000U	1688	1026	CGACACCAAGAAGCAGAGA	UCUCUGCUUCUUGGUGUCGUU	3971
R-008398257-000V	1004	1027	UCACCAGUGGAUUCUGUGU	B UCACCAGUGGAUUCUGUGUTT B	3972
R-008398257-000V	1004	1027	UCACCAGUGGAUUCUGUGU	ACACAGAAUCCACUGGUGAUU	3973
R-008398260-000B	1631	1028	GGUGACAGGGAAGACAUCA	UGAUGUCUUCCCUGUCACCUU	3975
R-008398260-000B	1631	1028	GGUGACAGGGAAGACAUCA	B GGUGACAGGGAAGACAUCATT B	3974
R-008398263-000C	1319	1029	UCUAGUAAUAAGCCGGCUA	UAGCCGGCUUAUUACUAGAUU	3977
R-008398263-000C	1319	1029	UCUAGUAAUAAGCCGGCUA	B UCUAGUAAUAAGCCGGCUATT B	3976
R-008398266-000D	767	1030	GUGGUUAAUAAGGCUGCAG	B GUGGUUAAUAAGGCUGCAGTT B	3978
R-008398266-000D	767	1030	GUGGUUAAUAAGGCUGCAG	CUGCAGCCUUAUUAACCACUU	3979
R-008398269-000E	841	1031	UCCUCAGAUGGUGUCUGCU	AGCAGACACCAUCUGAGGAUU	3981
R-008398269-000E	841	1031	UCCUCAGAUGGUGUCUGCU	B UCCUCAGAUGGUGUCUGCUTT B	3980
R-008398272-000L	516	1032	AUGGACAGUAUGCAAUGAC	B AUGGACAGUAUGCAAUGACTT B	3982
R-008398272-000L	516	1032	AUGGACAGUAUGCAAUGAC	GUCAUUGCAUACUGUCCAUUU	3983
R-008398275-000M	1848	1033	UGCGUGAGCAGGGUGCCAU	AUGGCACCCUGCUCACGCAUU	3985
R-008398275-000M	1848	1033	UGCGUGAGCAGGGUGCCAU	B UGCGUGAGCAGGGUGCCAUTT B	3984
R-008398278-000N	2202	1034	ACUCUAGGAAUGAAGGUGU	B ACUCUAGGAAUGAAGGUGUTT B	3986
R-008398278-000N	2202	1034	ACUCUAGGAAUGAAGGUGU	ACACCUUCAUUCCUAGAGUUU	3987
R-008398281-000V	571	1035	GACAUUAGAUGAGGGCAUG	B GACAUUAGAUGAGGGCAUGTT B	3988
R-008398281-000V	571	1035	GACAUUAGAUGAGGGCAUG	CAUGCCCUCAUCUAAUGUCUU	3989
R-008398284-000W	1629	1036	CUGGUGACAGGGAAGACAU	B CUGGUGACAGGGAAGACAUTT B	3990
R-008398284-000W	1629	1036	CUGGUGACAGGGAAGACAU	AUGUCUUCCCUGUCACCAGUU	3991
R-008398287-000X	1806	1037	UGAUUCGAAAUCUUGCCCU	B UGAUUCGAAAUCUUGCCCUTT B	3992
R-008398287-000X	1806	1037	UGAUUCGAAAUCUUGCCCU	AGGGCAAGAUUUCGAAUCAUU	3993
R-008398290-000D	1756	1038	GCUCUUACACCCACCAUCC	B GCUCUUACACCCACCAUCCTT B	3994
R-008398290-000D	1756	1038	GCUCUUACACCCACCAUCC	GGAUGGUGGGUGUAAGAGCUU	3995
R-008398293-000E	1619	1039	GUCCUUCGGGCUGGUGACA	UGUCACCAGCCCGAAGGACUU	3997
R-008398293-000E	1619	1039	GUCCUUCGGGCUGGUGACA	B GUCCUUCGGGCUGGUGACATT B	3996
R-008398296-000F	1610	1040	GUGCGUACUGUCCUUCGGG	B GUGCGUACUGUCCUUCGGGTT B	3998
R-008398296-000F	1610	1040	GUGCGUACUGUCCUUCGGG	CCCGAAGGACAGUACGCACUU	3999

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398299-000G	2500	1041	UGGUGCUGACUAUCCAGUU	B UGGUGCUGACUAUCCAGUUTT B	4000
R-008398299-000G	2500	1041	UGGUGCUGACUAUCCAGUU	AACUGGAUAGUCAGCACCAUU	4001
R-008398302-000Z	2156	1042	GCUAUUGAAGCUGAGGGAG	B GCUAUUGAAGCUGAGGGAGTT B	4002
R-008398302-000Z	2156	1042	GCUAUUGAAGCUGAGGGAG	CUCCCUCAGCUUCAAUAGCUU	4003
R-008398305-000A	1189	1043	CAACCAAGAAAGCAAGCUC	GAGCUUGCUUUCUUGGUUGUU	4005
R-008398305-000A	1189	1043	CAACCAAGAAAGCAAGCUC	B CAACCAAGAAAGCAAGCUCTT B	4004
R-008398308-000B	2066	1044	GUGCAGCUGCUUUAUUCUC	GAGAAUAAAGCAGCUGCACUU	4007
R-008398308-000B	2066	1044	GUGCAGCUGCUUUAUUCUC	B GUGCAGCUGCUUUAUUCUCTT B	4006
R-008398311-000H	1307	1045	CUAUCUGUCUGCUCUAGUA	UACUAGAGCAGACAGAUAGUU	4009
R-008398311-000H	1307	1045	CUAUCUGUCUGCUCUAGUA	B CUAUCUGUCUGCUCUAGUATT B	4008
R-008398314-000J	1448	1046	AAACAGGAAGGGAUGGAAG	CUUCCAUCCCUUCCUGUUUUU	4011
R-008398314-000J	1448	1046	AAACAGGAAGGGAUGGAAG	B AAACAGGAAGGGAUGGAAGTT B	4010
R-008398317-000K	1213	1047	ACUGGCUAGUGGUGGACCC	B ACUGGCUAGUGGUGGACCCTT B	4012
R-008398317-000K	1213	1047	ACUGGCUAGUGGUGGACCC	GGGUCCACCACUAGCCAGUUU	4013
R-008398320-000S	2119	1048	CCUCUGUGAACUUGCUCAG	B CCUCUGUGAACUUGCUCAGTT B	4014
R-008398320-000S	2119	1048	CCUCUGUGAACUUGCUCAG	CUGAGCAAGUUCACAGAGGUU	4015
R-008398323-000T	2546	72	CAGGACCUCAUGGAUGGGC	B CAGGACCUCAUGGAUGGGCTT B	4016
R-008398323-000T	2546	72	CAGGACCUCAUGGAUGGGC	GCCCAUCCAUGAGGUCCUGUU	4017
R-008398326-000U	889	1049	UGUAGAAACAGCUCGUUGU	B UGUAGAAACAGCUCGUUGUTT B	4018
R-008398326-000U	889	1049	UGUAGAAACAGCUCGUUGU	ACAACGAGCUGUUUCUACAUU	4019
R-008398327-000V	1376	1050	CUGACAGAUCCAAGUCAAC	B CUGACAGAUCCAAGUCAACTT B	4020
R-008398327-000V	1376	1050	CUGACAGAUCCAAGUCAAC	GUUGACUUGGAUCUGUCAGUU	4021
R-008398332-000B	427	1051	GGAAGAGGAUGUGGAUACC	GGUAUCCACAUCCUCUUCCUU	4023
R-008398332-000B	427	1051	GGAAGAGGAUGUGGAUACC	B GGAAGAGGAUGUGGAUACCTT B	4022
R-008398335-000C	649	1052	ACCAUCACAGAUGCUGAAA	B ACCAUCACAGAUGCUGAAATT B	4024
R-008398335-000C	649	1052	ACCAUCACAGAUGCUGAAA	UUUCAGCAUCUGUGAUGGUUU	4025
R-008398338-000D	1915	1053	CCGUACGUCCAUGGGUGGG	B CCGUACGUCCAUGGGUGGGTT B	4026
R-008398338-000D	1915	1053	CCGUACGUCCAUGGGUGGG	CCCACCCAUGGACGUACGGUU	4027
R-008398341-000K	2053	1054	CAUUCCAUUGUUUGUGCAG	B CAUUCCAUUGUUUGUGCAGTT B	4028
R-008398341-000K	2053	1054	CAUUCCAUUGUUUGUGCAG	CUGCACAAACAAUGGAAUGUU	4029
R-008398344-000L	2000	24	CACAUCCUAGCUCGGGAUG	CAUCCCGAGCUAGGAUGUGUU	4031
R-008398344-000L	2000	24	CACAUCCUAGCUCGGGAUG	B CACAUCCUAGCUCGGGAUGTT B	4030
R-008398347-000M	2568	1055	CUCCAGGUGACAGCAAUCA	B CUCCAGGUGACAGCAAUCATT B	4032
R-008398347-000M	2568	1055	CUCCAGGUGACAGCAAUCA	UGAUUGCUGUCACCUGGAGUU	4033
R-008398350-000U	1739	1056	CUACCAGUUGUGGUUAAGC	GCUUAACCACAACUGGUAGUU	4035
R-008398350-000U	1739	1056	CUACCAGUUGUGGUUAAGC	B CUACCAGUUGUGGUUAAGCTT B	4034

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398353-000V	1746	1057	UUGUGGUUAAGCUCUUACA	B UUGUGGUUAAGCUCUUACA*TT* B	4036
R-008398353-000V	1746	1057	UUGUGGUUAAGCUCUUACA	UGUAAGAGCUUAACCACAA<u>UU</u>	4037
R-008398356-000W	1321	1058	UAGUAAUAAGCCGGCUAUU	AAUAGCCGGCUUAUUACUA<u>UU</u>	4039
R-008398356-000W	1321	1058	UAGUAAUAAGCCGGCUAUU	B UAGUAAUAAGCCGGCUAU*UTT* B	4038
R-008398359-000X	482	1059	CAGUCCUUCACUCAAGAAC	GUUCUUGAGUGAAGGACUG<u>UU</u>	4041
R-008398359-000X	482	1059	CAGUCCUUCACUCAAGAAC	B CAGUCCUUCACUCAAGAAC*TT* B	4040
R-008398362-000D	280	1060	AGCUGAUUUGAUGGAGUUG	CAACUCCAUCAAAUCAGCU<u>UU</u>	4043
R-008398362-000D	280	1060	AGCUGAUUUGAUGGAGUUG	B AGCUGAUUUGAUGGAGUUG*TT* B	4042
R-008398365-000E	1465	1061	AGGUCUCCUUGGGACUCUU	B AGGUCUCCUUGGGACUCUU*TT* B	4044
R-008398365-000E	1465	1061	AGGUCUCCUUGGGACUCUU	AAGAGUCCCAAGGAGACCU<u>UU</u>	4045
R-008398368-000F	1731	1062	ACUAUGGACUACCAGUUGU	ACAACUGGUAGUCCAUAGU<u>UU</u>	4047
R-008398368-000F	1731	1062	ACUAUGGACUACCAGUUGU	B ACUAUGGACUACCAGUUGU*TT* B	4046
R-008398371-000M	1937	1063	CAGCAGCAAUUUGUGGAGG	B CAGCAGCAAUUUGUGGAGG*TT* B	4048
R-008398371-000M	1937	1063	CAGCAGCAAUUUGUGGAGG	CCUCCACAAAUUGCUGCUG<u>UU</u>	4049
R-008398374-000N	1892	1064	CGUGCACAUCAGGAUACCC	B CGUGCACAUCAGGAUACCC*TT* B	4050
R-008398374-000N	1892	1064	CGUGCACAUCAGGAUACCC	GGGUAUCCUGAUGUGCACG<u>UU</u>	4051
R-008398377-000P	836	1065	CGUUCUCCUCAGAUGGUGU	B CGUUCUCCUCAGAUGGUGU*TT* B	4052
R-008398377-000P	836	1065	CGUUCUCCUCAGAUGGUGU	ACACCAUCUGAGGAGAACG<u>UU</u>	4053
R-008398380-000W	521	1066	CAGUAUGCAAUGACUCGAG	CUCGAGUCAUUGCAUACUG<u>UU</u>	4055
R-008398380-000W	521	1066	CAGUAUGCAAUGACUCGAG	B CAGUAUGCAAUGACUCGAG*TT* B	4054
R-008398383-000X	1595	1067	GGUAUAGAGGCUCUUGUGC	GCACAAGAGCCUCUAUACC<u>UU</u>	4057
R-008398383-000X	1595	1067	GGUAUAGAGGCUCUUGUGC	B GGUAUAGAGGCUCUUGUGC*TT* B	4056
R-008398386-000Y	2511	1068	AUCCAGUUGAUGGGCUGCC	GGCAGCCCAUCAACUGGAU<u>UU</u>	4059
R-008398386-000Y	2511	1068	AUCCAGUUGAUGGGCUGCC	B AUCCAGUUGAUGGGCUGCC*TT* B	4058
R-008398389-000Z	1583	1069	UGCCAAGUGGGUGGUAUAG	B UGCCAAGUGGGUGGUAUAG*TT* B	4060
R-008398389-000Z	1583	1069	UGCCAAGUGGGUGGUAUAG	CUAUACCACCCACUUGGCA<u>UU</u>	4061
R-008398392-000F	1897	1070	ACAUCAGGAUACCCAGCGC	GCGCUGGGUAUCCUGAUGU<u>UU</u>	4063
R-008398392-000F	1897	1070	ACAUCAGGAUACCCAGCGC	B ACAUCAGGAUACCCAGCGC*TT* B	4062
R-008398395-000G	956	1071	GCCAUCUUUAAGUCUGGAG	CUCCAGACUUAAAGAUGGC<u>UU</u>	4065
R-008398395-000G	956	1071	GCCAUCUUUAAGUCUGGAG	B GCCAUCUUUAAGUCUGGAG*TT* B	4064
R-008398398-000H	926	1072	AACCUUUCCCAUCAUCGUG	B AACCUUUCCCAUCAUCGUG*TT* B	4066
R-008398398-000H	926	1072	AACCUUUCCCAUCAUCGUG	CACGAUGAUGGGAAAGGUU<u>UU</u>	4067
R-008398401-000A	1874	1073	CUAGUUCAGUUGCUUGUUC	GAACAAGCAACUGAACUAG<u>UU</u>	4069
R-008398401-000A	1874	1073	CUAGUUCAGUUGCUUGUUC	B CUAGUUCAGUUGCUUGUUC*TT* B	4068
R-008398404-000B	488	1074	UUCACUCAAGAACAAGUAG	B UUCACUCAAGAACAAGUAG*TT* B	4070
R-008398404-000B	488	1074	UUCACUCAAGAACAAGUAG	CUACUUGUUCUUGAGUGAA<u>UU</u>	4071
R-008398407-000C	1602	21	AGGCUCUUGUGCGUACUGU	B AGGCUCUUGUGCGUACUGU*TT* B	4072

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398407-000C	1602	21	AGGCUCUUGUGCGUACUGU	ACAGUACGCACAAGAGCCUUU	4073
R-008398410-000J	1695	1075	AAGAAGCAGAGAUGGCCCA	UGGGCCAUCUCUGCUUCUUUU	4075
R-008398410-000J	1695	1075	AAGAAGCAGAGAUGGCCCA	B AAGAAGCAGAGAUGGCCCATT B	4074
R-008398413-000K	2182	1076	UCCUCUGACAGAGUUACUU	B UCCUCUGACAGAGUUACUUTT B	4076
R-008398413-000K	2182	1076	UCCUCUGACAGAGUUACUU	AAGUAACUCUGUCAGAGGAUU	4077
R-008398415-000L	2029	1077	AAUUGUUAUCAGAGGACUA	UAGUCCUCUGAUAACAAUUUU	4079
R-008398415-000L	2029	1077	AAUUGUUAUCAGAGGACUA	B AAUUGUUAUCAGAGGACUATT B	4078
R-008398419-000M	479	1078	UCUCAGUCCUUCACUCAAG	B UCUCAGUCCUUCACUCAAGTT B	4080
R-008398419-000M	479	1078	UCUCAGUCCUUCACUCAAG	CUUGAGUGAAGGACUGAGAUU	4081
R-008398422-000U	818	1079	UCCAGACACGCUAUCAUGC	GCAUGAUAGCGUGUCUGGAUU	4083
R-008398422-000U	818	1079	UCCAGACACGCUAUCAUGC	B UCCAGACACGCUAUCAUGCTT B	4082
R-008398425-000V	625	1080	CACUAAUGUCCAGCGUUUG	B CACUAAUGUCCAGCGUUUGTT B	4084
R-008398425-000V	625	1080	CACUAAUGUCCAGCGUUUG	CAAACGCUGGACAUUAGUGUU	4085
R-008398428-000W	3172	1081	UUGUAACCUGCUGUGAUAC	B UUGUAACCUGCUGUGAUACTT B	4086
R-008398428-000W	3172	1081	UUGUAACCUGCUGUGAUAC	GUAUCACAGCAGGUUACAAUU	4087
R-008398431-000C	1490	1082	CUUCUGGGUUCAGAUGAUA	B CUUCUGGGUUCAGAUGAUATT B	4088
R-008398431-000C	1490	1082	CUUCUGGGUUCAGAUGAUA	UAUCAUCUGAACCCAGAAGUU	4089
R-008398434-000D	1914	1083	GCCGUACGUCCAUGGGUGG	B GCCGUACGUCCAUGGGUGGTT B	4090
R-008398434-000D	1914	1083	GCCGUACGUCCAUGGGUGG	CCACCCAUGGACGUACGGCUU	4091
R-008398437-000E	882	100	CAAAUGAUGUAGAAACAGC	GCUGUUUCUACAUCAUUUGUU	4093
R-008398437-000E	882	100	CAAAUGAUGUAGAAACAGC	B CAAAUGAUGUAGAAACAGCTT B	4092
R-008398440-000L	1974	1084	UAGUUGAAGGUUGUACCGG	CCGGUACAACCUUCAACUAUU	4095
R-008398440-000L	1974	1084	UAGUUGAAGGUUGUACCGG	B UAGUUGAAGGUUGUACCGGTT B	4094
R-008398443-000M	2258	1085	GAGGACAAGCCACAAGAUU	B GAGGACAAGCCACAAGAUUTT B	4096
R-008398443-000M	2258	1085	GAGGACAAGCCACAAGAUU	AAUCUUGUGGCUUGUCCUCUU	4097
R-008398446-000N	2170	1086	GGGAGCCACAGCUCCUCUG	CAGAGGAGCUGUGGCUCCCUU	4099
R-008398446-000N	2170	1086	GGGAGCCACAGCUCCUCUG	B GGGAGCCACAGCUCCUCUGTT B	4098
R-008398449-000P	1370	1087	CUUCACCUGACAGAUCCAA	B CUUCACCUGACAGAUCCAATT B	4100
R-008398449-000P	1370	1087	CUUCACCUGACAGAUCCAA	UUGGAUCUGUCAGGUGAAGUU	4101
R-008398453-000W	1429	1088	UCUUUCAGAUGCUGCAACU	B UCUUUCAGAUGCUGCAACUTT B	4102
R-008398453-000W	1429	1088	UCUUUCAGAUGCUGCAACU	AGUUGCAGCAUCUGAAAGAUU	4103
R-008398455-000X	3173	1089	UGUAACCUGCUGUGAUACG	B UGUAACCUGCUGUGAUACGTT B	4104
R-008398455-000X	3173	1089	UGUAACCUGCUGUGAUACG	CGUAUCACAGCAGGUUACAUU	4105
R-008398458-000Y	444	1090	CCUCCCAAGUCCUGUAUGA	B CCUCCCAAGUCCUGUAUGATT B	4106
R-008398458-000Y	444	1090	CCUCCCAAGUCCUGUAUGA	UCAUACAGGACUUGGGAGGUU	4107
R-008398461-000E	1081	1091	GGCAGUGCGUUUAGCUGGU	B GGCAGUGCGUUUAGCUGGUTT B	4108

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398461-000E	1081	1091	GGCAGUGCGUUUAGCUGGU	ACCAGCUAAACGCACUGCCUU	4109
R-008398464-000F	1318	1092	CUCUAGUAAUAAGCCGGCU	AGCCGGCUUAUUACUAGAGUU	4111
R-008398464-000F	1318	1092	CUCUAGUAAUAAGCCGGCU	B CUCUAGUAAUAAGCCGGCUTT B	4110
R-008398467-000G	329	1093	GCUGUUAGUCACUGGCAGC	B GCUGUUAGUCACUGGCAGCTT B	4112
R-008398467-000G	329	1093	GCUGUUAGUCACUGGCAGC	GCUGCCAGUGACUAACAGCUU	4113
R-008398470-000N	1389	1094	GUCAACGUCUUGUUCAGAA	UUCUGAACAAGACGUUGACUU	4115
R-008398470-000N	1389	1094	GUCAACGUCUUGUUCAGAA	B GUCAACGUCUUGUUCAGAATT B	4114
R-008398473-000P	428	1095	GAAGAGGAUGUGGAUACCU	AGGUAUCCACAUCCUCUUCUU	4117
R-008398473-000P	428	1095	GAAGAGGAUGUGGAUACCU	B GAAGAGGAUGUGGAUACCUTT B	4116
R-008398476-000R	3175	1096	UAACCUGCUGUGAUACGAU	AUCGUAUCACAGCAGGUUAUU	4119
R-008398476-000R	3175	1096	UAACCUGCUGUGAUACGAU	B UAACCUGCUGUGAUACGAUTT B	4118
R-008398479-000S	1422	114	UCAGGAAUCUUUCAGAUGC	B UCAGGAAUCUUUCAGAUGCTT B	4120
R-008398479-000S	1422	114	UCAGGAAUCUUUCAGAUGC	GCAUCUGAAAGAUUCCUGAUU	4121
R-008398482-000Y	1500	97	CAGUAGAUAUAAAUGUGGU	ACCACAUUUAUAUCAUCUGUU	4123
R-008398482-000Y	1500	97	CAGUAGAUAUAAAUGUGGU	B CAGAUGAUAUAAAUGUGGUTT B	4122
R-008398485-000Z	3117	1097	GUUAUUUGGAACCUUGUUU	B GUUAUUUGGAACCUUGUUUTT B	4124
R-008398485-000Z	3117	1097	GUUAUUUGGAACCUUGUUU	AAACAAGGUUCCAAAUAACUU	4125
R-008398488-000A	2020	1098	UCACAACCGAAUUGUUAUC	B UCACAACCGAAUUGUUAUCTT B	4126
R-008398488-000A	2020	1098	UCACAACCGAAUUGUUAUC	GAUAACAAUUCGGUUGUGAUU	4127
R-008398491-000G	1625	1099	CGGGCUGGUGACAGGGAAG	B CGGGCUGGUGACAGGGAAGTT B	4128
R-008398491-000G	1625	1099	CGGGCUGGUGACAGGGAAG	CUUCCCUGUCACCAGCCCGUU	4129
R-008398494-000H	2022	1100	ACAACCGAAUUGUUAUCAG	B ACAACCGAAUUGUUAUCAGTT B	4130
R-008398494-000H	2022	1100	ACAACCGAAUUGUUAUCAG	CUGAUAACAAUUCGGUUGUUU	4131
R-008398497-000J	624	1101	CCACUAAUGUCCAGCGUUU	B CCACUAAUGUCCAGCGUUUTT B	4132
R-008398497-000J	624	1101	CCACUAAUGUCCAGCGUUU	AAACGCUGGACAUUAGUGGUU	4133
R-008398500-000B	1648	1102	CACUGAGCCUGCCAUCUGU	ACAGAUGGCAGGCUCAGUGUU	4135
R-008398500-000B	1648	1102	CACUGAGCCUGCCAUCUGU	B CACUGAGCCUGCCAUCUGUTT B	4134
R-008398503-000C	790	1103	GGUCCAUCAGCUUUCUAAA	B GGUCCAUCAGCUUUCUAAATT B	4136
R-008398503-000C	790	1103	GGUCCAUCAGCUUUCUAAA	UUUAGAAAGCUGAUGGACCUU	4137
R-008398506-000D	2122	59	CUGUGAACUUGCUCAGGAC	B CUGUGAACUUGCUCAGGACTT B	4138
R-008398506-000D	2122	59	CUGUGAACUUGCUCAGGAC	GUCCUGAGCAAGUUCACAGUU	4139
R-008398509-000E	3160	1104	AUCCCAAAGUUGUUGUAAC	B AUCCCAAAGUUGUUGUAACTT B	4140
R-008398509-000E	3160	1104	AUCCCAAAGUUGUUGUAAC	GUUACAACAACUUUGGGAUUU	4141
R-008398512-000L	1251	1105	UGAGGACCUAUACUUACGA	B UGAGGACCUAUACUUACGATT B	4142
R-008398512-000L	1251	1105	UGAGGACCUAUACUUACGA	UCGUAAGUAUAGGUCCUCAUU	4143
R-008398518-000N	2253	1106	UGUCUGAGGACAAGCCACA	UGUGGCUUGUCCUCAGACAUU	4145
R-008398518-000N	2253	1106	UGUCUGAGGACAAGCCACA	B UGUCUGAGGACAAGCCACATT B	4144

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398521-000V	2515	1107	AGUUGAUGGGCUGCCAGAU	B AGUUGAUGGGCUGCCAGAUTT B	4146
R-008398521-000V	2515	1107	AGUUGAUGGGCUGCCAGAU	AUCUGGCAGCCCAUCAACUUU	4147
R-008398524-000W	1680	1108	UGACCAGCCGACACCAAGA	B UGACCAGCCGACACCAAGATT B	4148
R-008398524-000W	1680	1108	UGACCAGCCGACACCAAGA	UCUUGGUGUCGGCUGGUCAUU	4149
R-008398527-000X	2169	1109	AGGGAGCCACAGCUCCUCU	B AGGGAGCCACAGCUCCUCUTT B	4150
R-008398527-000X	2169	1109	AGGGAGCCACAGCUCCUCU	AGAGGAGCUGUGGCUCCCUUU	4151
R-008398530-000D	3165	1110	AAAGUUGUUGUAACCUGCU	AGCAGGUUACAACAACUUUUU	4153
R-008398530-000D	3165	1110	AAAGUUGUUGUAACCUGCU	B AAAGUUGUUGUAACCUGCUTT B	4152
R-008398533-000E	780	1111	CUGCAGUUAUGGUCCAUCA	UGAUGGACCAUAACUGCAGUU	4155
R-008398533-000E	780	1111	CUGCAGUUAUGGUCCAUCA	B CUGCAGUUAUGGUCCAUCATT B	4154
R-008398536-000F	1978	1112	UGAAGGUUGUACCGGAGCC	B UGAAGGUUGUACCGGAGCCTT B	4156
R-008398536-000F	1978	1112	UGAAGGUUGUACCGGAGCC	GGCUCCGGUACAACCUUCAUU	4157
R-008398539-000G	661	122	GCUGAAACAUGCAGUUGUA	B GCUGAAACAUGCAGUUGUATT B	4158
R-008398539-000G	661	122	GCUGAAACAUGCAGUUGUA	UACAACUGCAUGUUUCAGCUU	4159
R-008398542-000N	1354	181	AAUGCAAGCUUUAGGACUU	B AAUGCAAGCUUUAGGACUUTT B	4160
R-008398542-000N	1354	181	AAUGCAAGCUUUAGGACUU	AAGUCCUAAAGCUUGCAUUUU	4161
R-008398545-000P	563	1113	UUCCCUGAGACAUUAGAUG	B UUCCCUGAGACAUUAGAUGTT B	4162
R-008398545-000P	563	1113	UUCCCUGAGACAUUAGAUG	CAUCUAAUGUCUCAGGGAAUU	4163
R-008398548-000R	1622	1114	CUUCGGGCUGGUGACAGGG	B CUUCGGGCUGGUGACAGGGTT B	4164
R-008398548-000R	1622	1114	CUUCGGGCUGGUGACAGGG	CCCUGUCACCAGCCCGAAGUU	4165
R-008398551-000X	2295	1115	UUGAGCUGACCAGCUCUCU	AGAGAGCUGGUCAGCUCAAUU	4167
R-008398551-000X	2295	1115	UUGAGCUGACCAGCUCUCU	B UUGAGCUGACCAGCUCUCUTT B	4166
R-008398554-000Y	2126	1116	GAACUUGCUCAGGACAAGG	CCUUGUCCUGAGCAAGUUCUU	4169
R-008398554-000Y	2126	1116	GAACUUGCUCAGGACAAGG	B GAACUUGCUCAGGACAAGGTT B	4168
R-008398557-000Z	1683	1117	CCAGCCGACACCAAGAAGC	GCUUCUUGGUGUCGGCUGGUU	4171
R-008398557-000Z	1683	1117	CCAGCCGACACCAAGAAGC	B CCAGCCGACACCAAGAAGCTT B	4170
R-008398560-000F	1857	1118	AGGGUGCCAUUCCACGACU	AGUCGUGGAAUGGCACCCUUU	4173
R-008398560-000F	1857	1118	AGGGUGCCAUUCCACGACU	B AGGGUGCCAUUCCACGACUTT B	4172
R-008398563-000G	2064	1119	UUGUGCAGCUGCUUUAUUC	GAAUAAAGCAGCUGCACAAUU	4175
R-008398563-000G	2064	1119	UUGUGCAGCUGCUUUAUUC	B UUGUGCAGCUGCUUUAUUCTT B	4174
R-008398566-000H	1245	31	AUAUAAUGAGGACCUAUAC	GUAUAGGUCCUCAUUAUAUUU	4177
R-008398566-000H	1245	31	AUAUAAUGAGGACCUAUAC	B AUAUAAUGAGGACCUAUACTT B	4176
R-008398569-000J	489	1120	UCACUCAAGAACAAGUAGC	B UCACUCAAGAACAAGUAGCTT B	4178
R-008398569-000J	489	1120	UCACUCAAGAACAAGUAGC	GCUACUUGUUCUUGAGUGAUU	4179
R-008398572-000R	1346	1121	GCUGGUGGAAUGCAAGCUU	B GCUGGUGGAAUGCAAGCUUTT B	4180
R-008398572-000R	1346	1121	GCUGGUGGAAUGCAAGCUU	AAGCUUGCAUUCCACCAGCUU	4181

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398575-000S	1442	1122	GCAACUAAACAGGAAGGGA	UCCCUUCCUGUUUAGUUGCUU	4183
R-008398575-000S	1442	1122	GCAACUAAACAGGAAGGGA	B GCAACUAAACAGGAAGGGATT B	4182
R-008398578-000T	1981	1123	AGGUUGUACCGGAGCCCUU	B AGGUUGUACCGGAGCCCUUTT B	4184
R-008398578-000T	1981	1123	AGGUUGUACCGGAGCCCUU	AAGGGCUCCGGUACAACCUUU	4185
R-008398581-000Z	777	1124	AGGCUGCAGUUAUGGUCCA	UGGACCAUAACUGCAGCCUUU	4187
R-008398581-000Z	777	1124	AGGCUGCAGUUAUGGUCCA	B AGGCUGCAGUUAUGGUCCATT B	4186
R-008398584-000A	589	1125	GCAGAUCCCAUCUACACAG	CUGUGUAGAUGGGAUCUGCUU	4189
R-008398584-000A	589	1125	GCAGAUCCCAUCUACACAG	B GCAGAUCCCAUCUACACAGTT B	4188
R-008398587-000B	2205	1126	CUAGGAAUGAAGGUGUGGC	GCCACACCUUCAUUCCUAGUU	4191
R-008398587-000B	2205	1126	CUAGGAAUGAAGGUGUGGC	B CUAGGAAUGAAGGUGUGGCTT B	4190
R-008398590-000H	394	1127	AGCUCCUUCUCUGAGUGGU	B AGCUCCUUCUCUGAGUGGUTT B	4192
R-008398590-000H	394	1127	AGCUCCUUCUCUGAGUGGU	ACCACUCAGAGAAGGAGCUUU	4193
R-008398593-000J	1035	1128	UUACAACUCUCCACAACCU	B UUACAACUCUCCACAACCUTT B	4194
R-008398593-000J	1035	1128	UUACAACUCUCCACAACCU	AGGUUGUGGAGAGUUGUAAUU	4195
R-008398605-000E	410	1129	GGUAAAGGCAAUCCUGAGG	B GGUAAAGGCAAUCCUGAGGTT B	4196
R-008398605-000E	410	1129	GGUAAAGGCAAUCCUGAGG	CCUCAGGAUUGCCUUUACCUU	4197
R-008398608-000F	1721	1130	GUUCGCCUUCACUAUGGAC	GUCCAUAGUGAAGGCGAACUU	4199
R-008398608-000F	1721	1130	GUUCGCCUUCACUAUGGAC	B GUUCGCCUUCACUAUGGACTT B	4198
R-008398611-000M	1134	1131	CAAAUGUUAAAUUCUUGGC	GCCAAGAAUUUAACAUUUGUU	4201
R-008398611-000M	1134	1131	CAAAUGUUAAAUUCUUGGC	B CAAAUGUUAAAUUCUUGGCTT B	4200
R-008398614-000N	3182	1132	CUGUGAUACGAUGCUUCAA	B CUGUGAUACGAUGCUUCAATT B	4202
R-008398614-000N	3182	1132	CUGUGAUACGAUGCUUCAA	UUGAAGCAUCGUAUCACAGUU	4203
R-008398617-000P	881	1133	ACAAAUGAUGUAGAAACAG	B ACAAAUGAUGUAGAAACAGTT B	4204
R-008398617-000P	881	1133	ACAAAUGAUGUAGAAACAG	CUGUUUCUACAUCAUUUGUUU	4205
R-008398620-000W	547	1134	GGUACGAGCUGCUAUGUUC	GAACAUAGCAGCUCGUACCUU	4207
R-008398620-000W	547	1134	GGUACGAGCUGCUAUGUUC	B GGUACGAGCUGCUAUGUUCTT B	4206
R-008398623-000X	2028	1135	GAAUUGUUAUCAGAGGACU	AGUCCUCUGAUAACAAUUCUU	4209
R-008398623-000X	2028	1135	GAAUUGUUAUCAGAGGACU	B GAAUUGUUAUCAGAGGACUTT B	4208
R-008398629-000Z	2023	1136	CAACCGAAUUGUUAUCAGA	B CAACCGAAUUGUUAUCAGATT B	4210
R-008398629-000Z	2023	1136	CAACCGAAUUGUUAUCAGA	UCUGAUAACAAUUCGGUUGUU	4211
R-008398632-000F	3184	1137	GUGAUACGAUGCUUCAAGA	B GUGAUACGAUGCUUCAAGATT B	4212
R-008398632-000F	3184	1137	GUGAUACGAUGCUUCAAGA	UCUUGAAGCAUCGUAUCACUU	4213
R-008398635-000G	413	1138	AAAGGCAAUCCUGAGGAAG	CUUCCUCAGGAUUGCCUUUUU	4215
R-008398635-000G	413	1138	AAAGGCAAUCCUGAGGAAG	B AAAGGCAAUCCUGAGGAAGTT B	4214
R-008398638-000H	2178	1139	CAGCUCCUCUGACAGAGUU	B CAGCUCCUCUGACAGAGUUTT B	4216
R-008398638-000H	2178	1139	CAGCUCCUCUGACAGAGUU	AACUCUGUCAGAGGAGCUGUU	4217
R-008398641-000P	618	143	CUCAUCCCACUAAUGUCCA	B CUCAUCCCACUAAUGUCCATT B	4218

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398641-000P	618	143	CUCAUCCCACUAAUGUCCA	UGGACAUUAGUGGGAUGAGUU	4219
R-008398644-000R	1577	1140	AUGGUCUGCCAAGUGGGUG	B AUGGUCUGCCAAGUGGGUGTT B	4220
R-008398644-000R	1577	1140	AUGGUCUGCCAAGUGGGUG	CACCCACUUGGCAGACCAUUU	4221
R-008398647-000S	1793	1141	GCUACUGUUGGAUUGAUUC	GAAUCAAUCCAACAGUAGCUU	4223
R-008398647-000S	1793	1141	GCUACUGUUGGAUUGAUUC	B GCUACUGUUGGAUUGAUUCTT B	4222
R-008398650-000Y	526	1142	UGCAAUGACUCGAGCUCAG	B UGCAAUGACUCGAGCUCAGTT B	4224
R-008398650-000Y	526	1142	UGCAAUGACUCGAGCUCAG	CUGAGCUCGAGUCAUUGCAUU	4225
R-008398653-000Z	2358	1143	GACUUGAUAUUGGUGCCCA	UGGGCACCAAUAUCAAGUCUU	4227
R-008398653-000Z	2358	1143	GACUUGAUAUUGGUGCCCA	B GACUUGAUAUUGGUGCCCATT B	4226
R-008398656-000A	852	11	UGUCUGCUAUUGUACGUAC	B UGUCUGCUAUUGUACGUACTT B	4228
R-008398656-000A	852	11	UGUCUGCUAUUGUACGUAC	GUACGUACAAUAGCAGACAUU	4229
R-008398659-000B	1403	1144	CAGAACUGUCUUUGGACUC	GAGUCCAAAGACAGUUCUGUU	4231
R-008398659-000B	1403	1144	CAGAACUGUCUUUGGACUC	B CAGAACUGUCUUUGGACUCTT B	4230
R-008398662-000H	1875	1145	UAGUUCAGUUGCUUGUUCG	CGAACAAGCAACUGAACUAUU	4233
R-008398662-000H	1875	1145	UAGUUCAGUUGCUUGUUCG	B UAGUUCAGUUGCUUGUUCGTT B	4232
R-008398665-000J	1160	1146	ACAGACUGCCUUCAAAUUU	B ACAGACUGCCUUCAAAUUUTT B	4234
R-008398665-000J	1160	1146	ACAGACUGCCUUCAAAUUU	AAAUUUGAAGGCAGUCUGUUU	4235
R-008398668-000K	1591	1147	GGGUGGUAUAGAGGCUCUU	AAGAGCCUCUAUACCACCCUU	4237
R-008398668-000K	1591	1147	GGGUGGUAUAGAGGCUCUU	B GGGUGGUAUAGAGGCUCUUTT B	4236
R-008398671-000S	1734	1148	AUGGACUACCAGUUGUGGU	B AUGGACUACCAGUUGUGGUTT B	4238
R-008398671-000S	1734	1148	AUGGACUACCAGUUGUGGU	ACCACAACUGGUAGUCCAUUU	4239
R-008398674-000T	2030	1149	AUUGUUAUCAGAGGACUAA	UUAGUCCUCUGAUAACAAUUU	4241
R-008398674-000T	2030	1149	AUUGUUAUCAGAGGACUAA	B AUUGUUAUCAGAGGACUAATT B	4240
R-008398677-000U	775	1150	UAAGGCUGCAGUUAUGGUC	GACCAUAACUGCAGCCUUAUU	4243
R-008398677-000U	775	1150	UAAGGCUGCAGUUAUGGUC	B UAAGGCUGCAGUUAUGGUCTT B	4242
R-008398680-000A	1813	1151	AAAUCUUGCCCUUUGUCCC	GGGACAAAGGGCAAGAUUUUU	4245
R-008398680-000A	1813	1151	AAAUCUUGCCCUUUGUCCC	B AAAUCUUGCCCUUUGUCCCTT B	4244
R-008398683-000B	1938	1152	AGCAGCAAUUUGUGGAGGG	B AGCAGCAAUUUGUGGAGGGTT B	4246
R-008398683-000B	1938	1152	AGCAGCAAUUUGUGGAGGG	CCCUCCACAAAUUGCUGCUUU	4247
R-008398686-000C	2039	1153	AGAGGACUAAAUACCAUUC	B AGAGGACUAAAUACCAUUCTT B	4248
R-008398686-000C	2039	1153	AGAGGACUAAAUACCAUUC	GAAUGGUAUUUAGUCCUCUUU	4249
R-008398689-000D	1297	1154	GCUGAAGGUGCUAUCUGUC	B GCUGAAGGUGCUAUCUGUCTT B	4250
R-008398689-000D	1297	1154	GCUGAAGGUGCUAUCUGUC	GACAGAUAGCACCUUCAGCUU	4251
R-008398692-000K	456	1155	UGUAUGAGUGGGAACAGGG	CCCUGUUCCCACUCAUACAUU	4253
R-008398692-000K	456	1155	UGUAUGAGUGGGAACAGGG	B UGUAUGAGUGGGAACAGGGTT B	4252
R-008398695-000L	869	51	ACCAUGCAGAAUACAAAUG	B ACCAUGCAGAAUACAAAUGTT B	4254

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398695-000L	869	51	ACCAUGCAGAAUACAAAUG	CAUUUGUAUUCUGCAUGGUUU	4255
R-008398698-000M	590	1156	CAGAUCCCAUCUACACAGU	B CAGAUCCCAUCUACACAGUTT B	4256
R-008398698-000M	590	1156	CAGAUCCCAUCUACACAGU	ACUGUGUAGAUGGGAUCUGUU	4257
R-008398701-000E	1933	1157	GACACAGCAGCAAUUUGUG	B GACACAGCAGCAAUUUGUGTT B	4258
R-008398701-000E	1933	1157	GACACAGCAGCAAUUUGUG	CACAAAUUGCUGCUGUGUCUU	4259
R-008398704-000F	583	1158	GGGCAUGCAGAUCCCAUCU	AGAUGGGAUCUGCAUGCCCUU	4261
R-008398704-000F	583	1158	GGGCAUGCAGAUCCCAUCU	B GGGCAUGCAGAUCCCAUCUTT B	4260
R-008398707-000G	2540	1159	CAUGCCCAGGACCUCAUGG	B CAUGCCCAGGACCUCAUGGTT B	4262
R-008398707-000G	2540	1159	CAUGCCCAGGACCUCAUGG	CCAUGAGGUCCUGGGCAUGUU	4263
R-008398710-000N	2162	1160	GAAGCUGAGGGAGCCACAG	B GAAGCUGAGGGAGCCACAGTT B	4264
R-008398710-000N	2162	1160	GAAGCUGAGGGAGCCACAG	CUGUGGCUCCCUCAGCUUCUU	4265
R-008398713-000P	330	1161	CUGUUAGUCACUGGCAGCA	B CUGUUAGUCACUGGCAGCATT B	4266
R-008398713-000P	330	1161	CUGUUAGUCACUGGCAGCA	UGCUGCCAGUGACUAACAGUU	4267
R-008398716-000R	1481	1162	CUUGUUCAGCUUCUGGGUU	B CUUGUUCAGCUUCUGGGUUTT B	4268
R-008398716-000R	1481	1162	CUUGUUCAGCUUCUGGGUU	AACCCAGAAGCUGAACAAGUU	4269
R-008398719-000S	1612	22	GCGUACUGUCCUUCGGGCU	AGCCCGAAGGACAGUACGCUU	4271
R-008398719-000S	1612	22	GCGUACUGUCCUUCGGGCU	B GCGUACUGUCCUUCGGGCUTT B	4270
R-008398722-000Y	1709	3	GCCCAGAAUGCAGUUCGCC	GGCGAACUGCAUUCUGGGCUU	4273
R-008398722-000Y	1709	3	GCCCAGAAUGCAGUUCGCC	B GCCCAGAAUGCAGUUCGCCTT B	4272
R-008398725-000Z	1344	1163	AAGCUGGUGGAAUGCAAGC	GCUUGCAUUCCACCAGCUUUU	4275
R-008398725-000Z	1344	1163	AAGCUGGUGGAAUGCAAGC	B AAGCUGGUGGAAUGCAAGCTT B	4274
R-008398728-000Z	431	1164	GAGGAUGUGGAUACCUCCC	GGGAGGUAUCCACAUCCUCUU	4277
R-008398728-000Z	431	1164	GAGGAUGUGGAUACCUCCC	B GAGGAUGUGGAUACCUCCCTT B	4276
R-008398731-000G	1508	1165	AUAAAUGUGGUCACCUGUG	CACAGGUGACCACAUUUAUUU	4279
R-008398731-000G	1508	1165	AUAAAUGUGGUCACCUGUG	B AUAAAUGUGGUCACCUGUGTT B	4278
R-008398734-000H	1918	1166	UACGUCCAUGGGUGGGACA	B UACGUCCAUGGGUGGGACATT B	4280
R-008398734-000H	1918	1166	UACGUCCAUGGGUGGGACA	UGUCCCACCCAUGGACGUAUU	4281
R-008398737-000J	289	1167	GAUGGAGUUGGACAUGGCC	GGCCAUGUCCAACUCCAUCUU	4283
R-008398737-000J	289	1167	GAUGGAGUUGGACAUGGCC	B GAUGGAGUUGGACAUGGCCTT B	4282
R-008398740-000R	631	1168	UGUCCAGCGUUUGGCUGAA	B UGUCCAGCGUUUGGCUGAATT B	4284
R-008398740-000R	631	1168	UGUCCAGCGUUUGGCUGAA	UUCAGCCAAACGCUGGACAUU	4285
R-008398743-000S	1642	60	AGACAUCACUGAGCCUGCC	B AGACAUCACUGAGCCUGCCTT B	4286
R-008398743-000S	1642	60	AGACAUCACUGAGCCUGCC	GGCAGGCUCAGUGAUGUCUUU	4287
R-008398746-000T	1853	1169	GAGCAGGGUGCCAUUCCAC	B GAGCAGGGUGCCAUUCCACTT B	4288
R-008398746-000T	1853	1169	GAGCAGGGUGCCAUUCCAC	GUGGAAUGGCACCCUGCUCUU	4289
R-008398749-000U	1243	1170	AAAUAUAAUGAGGACCUAU	AUAGGUCCUCAUUAUAUUUUU	4291
R-008398749-000U	1243	1170	AAAUAUAAUGAGGACCUAU	B AAAUAUAAUGAGGACCUAUTT B	4290

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398752-000A	1212	1171	UACUGGCUAGUGGUGGACC	GGUCCACCACUAGCCAGUAUU	4293
R-008398752-000A	1212	1171	UACUGGCUAGUGGUGGACC	B UACUGGCUAGUGGUGGACCTT B	4292
R-008398755-000B	996	1172	UGCUUGGUUCACCAGUGGA	UCCACUGGUGAACCAAGCAUU	4295
R-008398755-000B	996	1172	UGCUUGGUUCACCAGUGGA	B UGCUUGGUUCACCAGUGGATT B	4294
R-008398758-000C	2256	1173	CUGAGGACAAGCCACAAGA	B CUGAGGACAAGCCACAAGATT B	4296
R-008398758-000C	2256	1173	CUGAGGACAAGCCACAAGA	UCUUGUGGCUUGUCCUCAGUU	4297
R-008398761-000J	1607	1174	CUUGUGCGUACUGUCCUUC	GAAGGACAGUACGCACAAGUU	4299
R-008398761-000J	1607	1174	CUUGUGCGUACUGUCCUUC	B CUUGUGCGUACUGUCCUUCTT B	4298
R-008398764-000K	3116	1175	UGUUAUUUGGAACCUUGUU	B UGUUAUUUGGAACCUUGUUTT B	4300
R-008398764-000K	3116	1175	UGUUAUUUGGAACCUUGUU	AACAAGGUUCCAAAUAACAUU	4301
R-008398767-000L	1179	1176	UAGCUUAUGGCAACCAAGA	UCUUGGUUGCCAUAAGCUAUU	4303
R-008398767-000L	1179	1176	UAGCUUAUGGCAACCAAGA	B UAGCUUAUGGCAACCAAGATT B	4302
R-008398770-000T	3185	1177	UGAUACGAUGCUUCAAGAG	CUCUUGAAGCAUCGUAUCAUU	4305
R-008398770-000T	3185	1177	UGAUACGAUGCUUCAAGAG	B UGAUACGAUGCUUCAAGAGTT B	4304
R-008398773-000U	1594	1178	UGGUAUAGAGGCUCUUGUG	CACAAGAGCCUCUAUACCAUU	4307
R-008398773-000U	1594	1178	UGGUAUAGAGGCUCUUGUG	B UGGUAUAGAGGCUCUUGUGTT B	4306
R-008398776-000V	887	1179	GAUGUAGAAACAGCUCGUU	B GAUGUAGAAACAGCUCGUUTT B	4308
R-008398776-000V	887	1179	GAUGUAGAAACAGCUCGUU	AACGAGCUGUUUCUACAUCUU	4309
R-008398779-000W	928	1180	CCUUUCCCAUCAUCGUGAG	B CCUUUCCCAUCAUCGUGAGTT B	4310
R-008398779-000W	928	1180	CCUUUCCCAUCAUCGUGAG	CUCACGAUGAUGGGAAAGGUU	4311
R-008398782-000C	835	1181	GCGUUCUCCUCAGAUGGUG	CACCAUCUGAGGAGAACGCUU	4313
R-008398782-000C	835	1181	GCGUUCUCCUCAGAUGGUG	B GCGUUCUCCUCAGAUGGUGTT B	4312
R-008398785-000D	1900	1182	UCAGGAUACCCAGCGCCGU	B UCAGGAUACCCAGCGCCGUTT B	4314
R-008398785-000D	1900	1182	UCAGGAUACCCAGCGCCGU	ACGGCGCUGGGUAUCCUGAUU	4315
R-008398788-000E	2284	1183	ACGGCUUUCAGUUGAGCUG	B ACGGCUUUCAGUUGAGCUGTT B	4316
R-008398788-000E	2284	1183	ACGGCUUUCAGUUGAGCUG	CAGCUCAACUGAAAGCCGUUU	4317
R-008398791-000L	1976	1184	GUUGAAGGUUGUACCGGAG	CUCCGGUACAACCUUCAACUU	4319
R-008398791-000L	1976	1184	GUUGAAGGUUGUACCGGAG	B GUUGAAGGUUGUACCGGAGTT B	4318
R-008398794-000M	2393	1185	UAUCGCCAGGAUGAUCCUA	B UAUCGCCAGGAUGAUCCUATT B	4320
R-008398794-000M	2393	1185	UAUCGCCAGGAUGAUCCUA	UAGGAUCAUCCUGGCGAUAUU	4321
R-008398797-000N	1295	1186	GUGCUGAAGGUGCUAUCUG	B GUGCUGAAGGUGCUAUCUGTT B	4322
R-008398797-000N	1295	1186	GUGCUGAAGGUGCUAUCUG	CAGAUAGCACCUUCAGCACUU	4323
R-008398800-000F	1410	1187	GUCUUUGGACUCUCAGGAA	UUCCUGAGAGUCCAAAGACUU	4325
R-008398800-000F	1410	1187	GUCUUUGGACUCUCAGGAA	B GUCUUUGGACUCUCAGGAATT B	4324
R-008398803-000G	1457	1188	GGGAUGGAAGGUCUCCUUG	B GGGAUGGAAGGUCUCCUUGTT B	4326
R-008398803-000G	1457	1188	GGGAUGGAAGGUCUCCUUG	CAAGGAGACCUUCCAUCCCUU	4327

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398806-000H	2296	1189	UGAGCUGACCAGCUCUCUC	B UGAGCUGACCAGCUCUCUC*TT* B	4328
R-008398806-000H	2296	1189	UGAGCUGACCAGCUCUCUC	GAGAGAGCUGGUCAGCUCA<u>UU</u>	4329
R-008398809-000J	929	1190	CUUUCCCAUCAUCGUGAGG	CCUCACGAUGAUGGGAAAG<u>UU</u>	4331
R-008398809-000J	929	1190	CUUUCCCAUCAUCGUGAGG	B CUUUCCCAUCAUCGUGAGG*TT* B	4330
R-008398812-000R	1359	1191	AAGCUUUAGGACUUCACCU	B AAGCUUUAGGACUUCACC*UTT* B	4332
R-008398812-000R	1359	1191	AAGCUUUAGGACUUCACCU	AGGUGAAGUCCUAAAGCUU<u>UU</u>	4333
R-008398815-000S	1357	1192	UGGAAUGCAAGCUUUAGGA	B UGGAAUGCAAGCUUUAGG*ATT* B	4334
R-008398815-000S	1357	1192	UGGAAUGCAAGCUUUAGGA	UCCUAAAGCUUGCAUUCCA<u>UU</u>	4335
R-008398818-000T	969	1193	CUGGAGGCAUUCCUGCCCU	B CUGGAGGCAUUCCUGCCC*UTT* B	4336
R-008398818-000T	969	1193	CUGGAGGCAUUCCUGCCCU	AGGGCAGGAAUGCCUCCAG<u>UU</u>	4337
R-008398821-000Z	1876	1194	AGUUCAGUUGCUUGUUCGU	ACGAACAAGCAACUGAACU<u>UU</u>	4339
R-008398821-000Z	1876	1194	AGUUCAGUUGCUUGUUCGU	B AGUUCAGUUGCUUGUUCGU*TT* B	4338
R-008398824-000A	552	1195	GAGCUGCUAUGUUCCCUGA	B GAGCUGCUAUGUUCCCUGA*TT* B	4340
R-008398824-000A	552	1195	GAGCUGCUAUGUUCCCUGA	UCAGGGAACAUAGCAGCUC<u>UU</u>	4341
R-008398827-000B	2441	1196	GGCCAGGAUGCCUUGGGUA	B GGCCAGGAUGCCUUGGGUA*TT* B	4342
R-008398827-000B	2441	1196	GGCCAGGAUGCCUUGGGUA	UACCCAAGGCAUCCUGGCC<u>UU</u>	4343
R-008398830-000H	2402	1197	GAUGAUCCUAGCUAUCGUU	B GAUGAUCCUAGCUAUCGUU*TT* B	4344
R-008398830-000H	2402	1197	GAUGAUCCUAGCUAUCGUU	AACGAUAGCUAGGAUCAUC<u>UU</u>	4345
R-008398833-000J	1803	1198	GAUUGAUUCGAAAUCUUGC	GCAAGAUUUCGAAUCAAUC<u>UU</u>	4347
R-008398833-000J	1803	1198	GAUUGAUUCGAAAUCUUGC	B GAUUGAUUCGAAAUCUUGC*TT* B	4346
R-008398836-000K	1701	1199	CAGAGAUGGCCCAGAAUGC	B CAGAGAUGGCCCAGAAUGC*TT* B	4348
R-008398836-000K	1701	1199	CAGAGAUGGCCCAGAAUGC	GCAUUCUGGGCCAUCUCUG<u>UU</u>	4349
R-008398839-000L	1910	1200	CAGCGCCGUACGUCCAUGG	CCAUGGACGUACGGCGCUG<u>UU</u>	4351
R-008398839-000L	1910	1200	CAGCGCCGUACGUCCAUGG	B CAGCGCCGUACGUCCAUGG*TT* B	4350
R-008398842-000T	888	1201	AUGUAGAAACAGCUCGUUG	CAACGAGCUGUUUCUACAU<u>UU</u>	4353
R-008398842-000T	888	1201	AUGUAGAAACAGCUCGUUG	B AUGUAGAAACAGCUCGUUG*TT* B	4352
R-008398845-000U	1294	1202	AGUGCUGAAGGUGCUAUCU	AGAUAGCACCUUCAGCACU<u>UU</u>	4355
R-008398845-000U	1294	1202	AGUGCUGAAGGUGCUAUCU	B AGUGCUGAAGGUGCUAUCU*TT* B	4354
R-008398848-000V	1737	1203	GACUACCAGUUGUGGUUAA	UUAACCACAACUGGUAGUC<u>UU</u>	4357
R-008398848-000V	1737	1203	GACUACCAGUUGUGGUUAA	B GACUACCAGUUGUGGUUAA*TT* B	4356
R-008398851-000B	1450	1204	ACAGGAAGGGAUGGAAGGU	B ACAGGAAGGGAUGGAAGG*UTT* B	4358
R-008398851-000B	1450	1204	ACAGGAAGGGAUGGAAGGU	ACCUUCCAUCCCUUCCUGU<u>UU</u>	4359
R-008398854-000C	761	1205	CAGGUGGUGGUUAAUAAGG	CCUUAUUAACCACCACCUG<u>UU</u>	4361
R-008398854-000C	761	1205	CAGGUGGUGGUUAAUAAGG	B CAGGUGGUGGUUAAUAAGG*TT* B	4360
R-008398857-000D	776	1206	AAGGCUGCAGUUAUGGUCC	B AAGGCUGCAGUUAUGGUCC*TT* B	4362
R-008398857-000D	776	1206	AAGGCUGCAGUUAUGGUCC	GGACCAUAACUGCAGCCUU<u>UU</u>	4363
R-008398860-000K	1509	1207	UAAAUGUGGUCACCUGUGC	GCACAGGUGACCACAUUUA<u>UU</u>	4365

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398860-000K	1509	1207	UAAAUGUGGUCACCUGUGC	B UAAAUGUGGUCACCUGUGCTT B	4364
R-008398863-000L	1788	1208	UAAAGGCUACUGUUGGAUU	B UAAAGGCUACUGUUGGAUUTT B	4366
R-008398863-000L	1788	1208	UAAAGGCUACUGUUGGAUU	AAUCCAACAGUAGCCUUUAUU	4367
R-008398866-000M	515	1209	GAUGGACAGUAUGCAAUGA	UCAUUGCAUACUGUCCAUCUU	4369
R-008398866-000M	515	1209	GAUGGACAGUAUGCAAUGA	B GAUGGACAGUAUGCAAUGATT B	4368
R-008398869-000N	1491	1210	UUCUGGGUUCAGAUGAUAU	B UUCUGGGUUCAGAUGAUAUTT B	4370
R-008398869-000N	1491	1210	UUCUGGGUUCAGAUGAUAU	AUAUCAUCUGAACCCAGAAUU	4371
R-008398872-000V	1614	1211	GUACUGUCCUUCGGGCUGG	B GUACUGUCCUUCGGGCUGGTT B	4372
R-008398872-000V	1614	1211	GUACUGUCCUUCGGGCUGG	CCAGCCCGAAGGACAGUACUU	4373
R-008398875-000W	998	1212	CUUGGUUCACCAGUGGAUU	B CUUGGUUCACCAGUGGAUUTT B	4374
R-008398875-000W	998	1212	CUUGGUUCACCAGUGGAUU	AAUCCACUGGUGAACCAAGUU	4375
R-008398878-000X	2158	1213	UAUUGAAGCUGAGGGAGCC	B UAUUGAAGCUGAGGGAGCCTT B	4376
R-008398878-000X	2158	1213	UAUUGAAGCUGAGGGAGCC	GGCUCCCUCAGCUUCAAUAUU	4377
R-008398881-000D	3168	1214	GUUGUUGUAACCUGCUGUG	B GUUGUUGUAACCUGCUGUGTT B	4378
R-008398881-000D	3168	1214	GUUGUUGUAACCUGCUGUG	CACAGCAGGUUACAACAACUU	4378
R-008398884-000E	1854	1215	AGCAGGGUGCCAUUCCACG	B AGCAGGGUGCCAUUCCACGTT B	4380
R-008398884-000E	1854	1215	AGCAGGGUGCCAUUCCACG	CGUGGAAUGGCACCCUGCUUU	4381
R-008398887-000F	2117	1216	GUCCUCUGUGAACUUGCUC	GAGCAAGUUCACAGAGGACUU	4383
R-008398887-000F	2117	1216	GUCCUCUGUGAACUUGCUC	B GUCCUCUGUGAACUUGCUCTT B	4382
R-008398890-000M	1678	1217	UCUGACCAGCCGACACCAA	UUGGUGUCGGCUGGUCAGAUU	4385
R-008398890-000M	1678	1217	UCUGACCAGCCGACACCAA	B UCUGACCAGCCGACACCAATT B	4384
R-008398893-000N	2159	63	AUUGAAGCUGAGGGAGCCA	B AUUGAAGCUGAGGGAGCCATT B	4386
R-008398893-000N	2159	63	AUUGAAGCUGAGGGAGCCA	UGGCUCCCUCAGCUUCAAUUU	4387
R-008398896-000P	305	1218	GCCAUGGAACCAGACAGAA	UUCUGUCUGGUUCCAUGGCUU	4389
R-008398896-000P	305	1218	GCCAUGGAACCAGACAGAA	B GCCAUGGAACCAGACAGAATT B	4388
R-008398899-000R	2154	1219	AAGCUAUUGAAGCUGAGGG	B AAGCUAUUGAAGCUGAGGGTT B	4390
R-008398899-000R	2154	1219	AAGCUAUUGAAGCUGAGGG	CCCUCAGCUUCAAUAGCUUUU	4391
R-008398902-000H	1807	1220	GAUUCGAAAUCUUGCCCUU	B GAUUCGAAAUCUUGCCCUUTT B	4392
R-008398902-000H	1807	1220	GAUUCGAAAUCUUGCCCUU	AAGGGCAAGAUUUCGAAUCUU	4393
R-008398905-000J	1881	1221	AGUUGCUUGUUCGUGCACA	B AGUUGCUUGUUCGUGCACATT B	4394
R-008398905-000J	1881	1221	AGUUGCUUGUUCGUGCACA	UGUGCACGAACAAGCAACUUU	4395
R-008398908-000K	1565	1222	AAGAACAAGAUGAUGGUCU	B AAGAACAAGAUGAUGGUCUTT B	4396
R-008398908-000K	1565	1222	AAGAACAAGAUGAUGGUCU	AGACCAUCAUCUUGUUCUUUU	4397
R-008398911-000S	407	1223	AGUGGUAAAGGCAAUCCUG	B AGUGGUAAAGGCAAUCCUGTT B	4398
R-008398911-000S	407	1223	AGUGGUAAAGGCAAUCCUG	CAGGAUUGCCUUUACCACUUU	4399
R-008398914-000T	1434	1224	CAGAUGCUGCAACUAAACA	UGUUUAGUUGCAGCAUCUGUU	4401

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398914-000T	1434	1224	CAGAUGCUGCAACUAAACA	B CAGAUGCUGCAACUAAACA*TT* B	4400
R-008398917-000U	566	1225	CCUGAGACAUUAGAUGAGG	B CCUGAGACAUUAGAUGAGG*TT* B	4402
R-008398917-000U	566	1225	CCUGAGACAUUAGAUGAGG	CCUCAUCUAAUGUCUCAGG<u>UU</u>	4403
R-008398920-000A	3161	1226	UCCCAAAGUUGUUGUAACC	GGUUACAACAACUUUGGGA<u>UU</u>	4405
R-008398920-000A	3161	1226	UCCCAAAGUUGUUGUAACC	B UCCCAAAGUUGUUGUAACC*TT* B	4404
R-008398923-000B	666	117	AACAUGCAGUUGUAAACUU	AAGUUUACAACUGCAUGUU<u>UU</u>	4407
R-008398923-000B	666	117	AACAUGCAGUUGUAAACUU	B AACAUGCAGUUGUAAACUU*TT* B	4406
R-008398926-000C	848	98	AUGGUGUCUGCUAUUGUAC	GUACAAUAGCAGACACCAU<u>UU</u>	4409
R-008398926-000C	848	98	AUGGUGUCUGCUAUUGUAC	B AUGGUGUCUGCUAUUGUAC*TT* B	4408
R-008398929-000D	1679	1227	CUGACCAGCCGACACCAAG	B CUGACCAGCCGACACCAAG*TT* B	4410
R-008398929-000D	1679	1227	CUGACCAGCCGACACCAAG	CUUGGUGUCGGCUGGUCAG<u>UU</u>	4411
R-008398932-000K	2096	1228	AUCCAAAGAGUAGCUGCAG	B AUCCAAAGAGUAGCUGCAG*TT* B	4412
R-008398932-000K	2096	1228	AUCCAAAGAGUAGCUGCAG	CUGCAGCUACUCUUUGGAU<u>UU</u>	4413
R-008398935-000L	630	1229	AUGUCCAGCGUUUGGCUGA	B AUGUCCAGCGUUUGGCUGA*TT* B	4414
R-008398935-000L	630	1229	AUGUCCAGCGUUUGGCUGA	UCAGCCAAACGCUGGACAU<u>UU</u>	4415
R-008398938-000M	1606	1230	UCUUGUGCGUACUGUCCUU	AAGGACAGUACGCACAAGA<u>UU</u>	4417
R-008398938-000M	1606	1230	UCUUGUGCGUACUGUCCUU	B UCUUGUGCGUACUGUCCUU*TT* B	4416
R-008398941-000U	432	1231	AGGAUGUGGAUACCUCCCA	UGGGAGGUAUCCACAUCCU<u>UU</u>	4419
R-008398941-000U	432	1231	AGGAUGUGGAUACCUCCCA	B AGGAUGUGGAUACCUCCCA*TT* B	4418
R-008398944-000V	778	1232	GGCUGCAGUUAUGGUCCAU	B GGCUGCAGUUAUGGUCCAU*TT* B	4420
R-008398944-000V	778	1232	GGCUGCAGUUAUGGUCCAU	AUGGACCAUAACUGCAGCC<u>UU</u>	4421
R-00839894700000W	1999	1233	UCACAUCCUAGCUCGGGAU	B UCACAUCCUAGCUCGGGAU*TT* B	4422
R-00839894700000W	1999	1233	UCACAUCCUAGCUCGGGAU	AUCCCGAGCUAGGAUGUGA<u>UU</u>	4423
R-008398950-000C	1692	1234	ACCAAGAAGCAGAGAUGGC	GCCAUCUCUGCUUCUUGGU<u>UU</u>	4425
R-008398950-000C	1692	1234	ACCAAGAAGCAGAGAUGGC	B ACCAAGAAGCAGAGAUGGC*TT* B	4424
R-008398953-000D	2490	1235	GCCACCACCCUGGUGCUGA	B GCCACCACCCUGGUGCUGA*TT* B	4426
R-008398953-000D	2490	1235	GCCACCACCCUGGUGCUGA	UCAGCACCAGGGUGGUGGC<u>UU</u>	4427
R-008398956-000E	623	1236	CCCACUAAUGUCCAGCGUU	AACGCUGGACAUUAGUGGG<u>UU</u>	4429
R-008398956-000E	623	1236	CCCACUAAUGUCCAGCGUU	B CCCACUAAUGUCCAGCGUU*TT* B	4428
R-008398959-000F	339	1237	ACUGGCAGCAACAGUCUUA	B ACUGGCAGCAACAGUCUUA*TT* B	4430
R-008398959-000F	339	1237	ACUGGCAGCAACAGUCUUA	UAAGACUGUUGCUGCCAGU<u>UU</u>	4431
R-008398962-000M	2471	166	AUGGAACAUGAGAUGGGUG	CACCCAUCUCAUGUUCCAU<u>UU</u>	4433
R-008398962-000M	2471	166	AUGGAACAUGAGAUGGGUG	B AUGGAACAUGAGAUGGGUG*TT* B	4432
R-008398965-000N	2037	164	UCAGAGGACUAAAUACCAU	AUGGUAUUUAGUCCUCUGA<u>UU</u>	4435
R-008398965-000N	2037	164	UCAGAGGACUAAAUACCAU	B UCAGAGGACUAAAUACCAU*TT* B	4434
R-008398968-000P	912	179	CUGGGACCUUGCAUAACCU	AGGUUAUGCAAGGUCCCAG<u>UU</u>	4437
R-008398968-000P	912	179	CUGGGACCUUGCAUAACCU	B CUGGGACCUUGCAUAACCU*TT* B	4436

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008398971-000W	2946	1238	AUCUGAAUAAAGUGUAACA	B AUCUGAAUAAAGUGUAACATT B	4438
R-008398971-000W	2946	1238	AUCUGAAUAAAGUGUAACA	UGUUACACUUUAUUCAGAUUU	4439
R-008398974-000X	1654	1239	GCCUGCCAUCUGUGCUCUU	AAGAGCACAGAUGGCAGGCUU	4441
R-008398974-000X	1654	1239	GCCUGCCAUCUGUGCUCUU	B GCCUGCCAUCUGUGCUCUUTT B	4440
R-008398977-000Y	1033	1240	CAUUACAACUCUCCACAAC	B CAUUACAACUCUCCACAACTT B	4442
R-008398977-000Y	1033	1240	CAUUACAACUCUCCACAAC	GUUGUGGAGAGUUGUAAUGUU	4443
R-008398980-000E	840	1241	CUCCUCAGAUGGUGUCUGC	GCAGACACCAUCUGAGGAGUU	4445
R-008398980-000E	840	1241	CUCCUCAGAUGGUGUCUGC	B CUCCUCAGAUGGUGUCUGCTT B	4444
R-008398983-000F	1880	1242	CAGUUGCUUGUUCGUGCAC	GUGCACGAACAAGCAACUGUU	4447
R-008398983-000F	1880	1242	CAGUUGCUUGUUCGUGCAC	B CAGUUGCUUGUUCGUGCACTT B	4446
R-008398986-000G	420	1243	AUCCUGAGGAAGAGGAUGU	B AUCCUGAGGAAGAGGAUGUTT B	4448
R-008398986-000G	420	1243	AUCCUGAGGAAGAGGAUGU	ACAUCCUCUUCCUCAGGAUUU	4449
R-008398989-000H	1005	1244	CACCAGUGGAUUCUGUGUU	B CACCAGUGGAUUCUGUGUUTT B	4450
R-008398989-000H	1005	1244	CACCAGUGGAUUCUGUGUU	AACACAGAAUCCACUGGUGUU	4451
R-008398992-000P	1193	1245	CAAGAAAGCAAGCUCAUCA	B CAAGAAAGCAAGCUCAUCATT B	4452
R-008398992-000P	1193	1245	CAAGAAAGCAAGCUCAUCA	UGAUGAGCUUGCUUUCUUGUU	4453
R-008398995-000R	919	1246	CUUGCAUAACCUUUCCCAU	AUGGGAAAGGUUAUGCAAGUU	4455
R-008398995-000R	919	1246	CUUGCAUAACCUUUCCCAU	B CUUGCAUAACCUUUCCCAUTT B	4454
R-008399001-000F	1727	1247	CUUCACUAUGGACUACCAG	CUGGUAGUCCAUAGUGAAGUU	4457
R-008399001-000F	1727	1247	CUUCACUAUGGACUACCAG	B CUUCACUAUGGACUACCAGTT B	4456
R-008399004-000G	1883	1248	UUGCUUGUUCGUGCACAUC	B UUGCUUGUUCGUGCACAUCTT B	4458
R-008399004-000G	1883	1248	UUGCUUGUUCGUGCACAUC	GAUGUGCACGAACAAGCAAUU	4459
R-008399007-000H	859	1249	UAUUGUACGUACCAUGCAG	B UAUUGUACGUACCAUGCAGTT B	4460
R-008399007-000H	859	1249	UAUUGUACGUACCAUGCAG	CUGCAUGGUACGUACAAUAUU	4461
R-008399010-000P	870	57	CCAUGCAGAAUACAAAUGA	B CCAUGCAGAAUACAAAUGATT B	4462
R-008399010-000P	870	57	CCAUGCAGAAUACAAAUGA	UCAUUUGUAUUCUGCAUGGUU	4463
R-008399013-000R	1812	1250	GAAAUCUUGCCCUUUGUCC	GGACAAAGGGCAAGAUUUCUU	4465
R-008399013-000R	1812	1250	GAAAUCUUGCCCUUUGUCC	B GAAAUCUUGCCCUUUGUCCTT B	4464
R-008399016-000S	1605	1251	CUCUUGUGCGUACUGUCCU	AGGACAGUACGCACAAGAGUU	4467
R-008399016-000S	1605	1251	CUCUUGUGCGUACUGUCCU	B CUCUUGUGCGUACUGUCCUTT B	4466
R-008399019-000T	2021	1252	CACAACCGAAUUGUUAUCA	UGAUAACAAUUCGGUUGUGUU	4469
R-008399019-000T	2021	1252	CACAACCGAAUUGUUAUCA	B CACAACCGAAUUGUUAUCATT B	4468
R-008399022-000Z	2180	1253	GCUCCUCUGACAGAGUUAC	GUAACUCUGUCAGAGGAGCUU	4471
R-008399022-000Z	2180	1253	GCUCCUCUGACAGAGUUAC	B GCUCCUCUGACAGAGUUACTT B	4470
R-008399025-000A	636	1254	AGCGUUUGGCUGAACCAUC	B AGCGUUUGGCUGAACCAUCTT B	4472
R-008399025-000A	636	1254	AGCGUUUGGCUGAACCAUC	GAUGGUUCAGCCAAACGCUUU	4473

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399031-000H	871	48	CAUGCAGAAUACAAAUGAU	B CAUGCAGAAUACAAAUGAUTT B	4474
R-008399031-000H	871	48	CAUGCAGAAUACAAAUGAU	AUCAUUUGUAUUCUGCAUGUU	4475
R-008399034-000J	1801	96	UGGAUUGAUUCGAAAUCUU	B UGGAUUGAUUCGAAAUCUUTT B	4476
R-008399034-000J	1801	96	UGGAUUGAUUCGAAAUCUU	AAGAUUUCGAAUCAAUCCAUU	4477
R-008399037-000K	2282	1255	AAACGGCUUUCAGUUGAGC	GCUCAACUGAAAGCCGUUUUU	4479
R-008399037-000K	2282	1255	AAACGGCUUUCAGUUGAGC	B AAACGGCUUUCAGUUGAGCTT B	4478
R-008399040-000S	1824	1256	UUUGUCCCGCAAAUCAUGC	GCAUGAUUUGCGGGACAAAUU	4481
R-008399040-000S	1824	1256	UUUGUCCCGCAAAUCAUGC	B UUUGUCCCGCAAAUCAUGCTT B	4480
R-008399043-000T	2204	1257	UCUAGGAAUGAAGGUGUGG	CCACACCUUCAUUCCUAGAUU	4483
R-008399043-000T	2204	1257	UCUAGGAAUGAAGGUGUGG	B UCUAGGAAUGAAGGUGUGGTT B	4482
R-008399046-000U	450	1258	AAGUCCUGUAUGAGUGGGA	B AAGUCCUGUAUGAGUGGGATT B	4484
R-008399046-000U	450	1258	AAGUCCUGUAUGAGUGGGA	UCCCACUCAUACAGGACUUUU	4485
R-008399049-000V	1001	1259	GGUUCACCAGUGGAUUCUG	B GGUUCACCAGUGGAUUCUGTT B	4486
R-008399049-000V	1001	1259	GGUUCACCAGUGGAUUCUG	CAGAAUCCACUGGUGAACCUU	4487
R-008399052-000B	1579	1260	GGUCUGCCAAGUGGGUGGU	ACCACCCACUUGGCAGACCUU	4489
R-008399052-000B	1579	1260	GGUCUGCCAAGUGGGUGGU	B GGUCUGCCAAGUGGGUGGUTT B	4488
R-008399055-000C	2179	1261	AGCUCCUCUGACAGAGUUA	UAACUCUGUCAGAGGAGCUUU	4491
R-008399055-000C	2179	1261	AGCUCCUCUGACAGAGUUA	B AGCUCCUCUGACAGAGUUATT B	4490
R-008399058-000D	376	1262	UUCUGGUGCCACUACCACA	B UUCUGGUGCCACUACCACATT B	4492
R-008399058-000D	376	1262	UUCUGGUGCCACUACCACA	UGUGGUAGUGGCACCAGAAUU	4492
R-008399061-000K	556	1263	UGCUAUGUUCCCUGAGACA	B UGCUAUGUUCCCUGAGACATT B	4494
R-008399061-000K	556	1263	UGCUAUGUUCCCUGAGACA	UGUCUCAGGGAACAUAGCAUU	4495
R-008399064-000L	1804	1264	AUUGAUUCGAAAUCUUGCC	B AUUGAUUCGAAAUCUUGCCTT B	4496
R-008399064-000L	1804	1264	AUUGAUUCGAAAUCUUGCC	GGCAAGAUUUCGAAUCAAUUU	4497
R-008399067-000M	2552	1265	CUCAUGGAUGGGCUGCCUC	B CUCAUGGAUGGGCUGCCUCTT B	4498
R-008399067-000M	2552	1265	CUCAUGGAUGGGCUGCCUC	GAGGCAGCCCAUCCAUGAGUU	4499
R-008399070-000U	2071	1266	GCUGCUUUAUUCUCCCAUU	B GCUGCUUUAUUCUCCCAUUTT B	4500
R-008399070-000U	2071	1266	GCUGCUUUAUUCUCCCAUU	AAUGGGAGAAUAAAGCAGCUU	4501
R-008399073-000V	1145	16	UUCUUGGCUAUUACGACAG	B UUCUUGGCUAUUACGACAGTT B	4502
R-008399073-000V	1145	16	UUCUUGGCUAUUACGACAG	CUGUCGUAAUAGCCAAGAAUU	4503
R-008399076-000W	1836	1267	AUCAUGCACCUUUGCGUGA	UCACGCAAAGGUGCAUGAUUU	4505
R-008399076-000W	1836	1267	AUCAUGCACCUUUGCGUGA	B AUCAUGCACCUUUGCGUGATT B	4504
R-008399079-000X	336	1268	GUCACUGGCAGCAACAGUC	B GUCACUGGCAGCAACAGUCTT B	4506
R-008399079-000X	336	1268	GUCACUGGCAGCAACAGUC	GACUGUUGCUGCCAGUGACUU	4507
R-008399082-000D	460	1269	UGAGUGGGAACAGGGAUUU	AAAUCCCUGUUCCCACUCAUU	4509
R-008399082-000D	460	1269	UGAGUGGGAACAGGGAUUU	B UGAGUGGGAACAGGGAUUUTT B	4508
R-008399085-000E	1559	1270	AAUUAUAAGAACAAGAUGA	B AAUUAUAAGAACAAGAUGATT B	4510

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399085-000E	1559	1270	AAUUAUAAGAACAAGAUGA	UCAUCUUGUUCUUAUAAUUUU	4511
R-008399091-000M	3136	1271	UGGACAGUUUACCAGUUGC	B UGGACAGUUUACCAGUUGCTT B	4512
R-008399091-000M	3136	1271	UGGACAGUUUACCAGUUGC	GCAACUGGUAAACUGUCCAUU	4513
R-008399097-000P	1250	1272	AUGAGGACCUAUACUUACG	B AUGAGGACCUAUACUUACGTT B	4514
R-008399097-000P	1250	1272	AUGAGGACCUAUACUUACG	CGUAAGUAUAGGUCCUCAUUU	4515
R-008399100-000G	1462	1273	GGAAGGUCUCCUUGGGACU	B GGAAGGUCUCCUUGGGACUTT B	4516
R-008399100-000G	1462	1273	GGAAGGUCUCCUUGGGACU	AGUCCCAAGGAGACCUUCCUU	4517
R-008399103-000H	1965	1274	UGGAAGAAAUAGUUGAAGG	B UGGAAGAAAUAGUUGAAGGTT B	4518
R-008399103-000H	1965	1274	UGGAAGAAAUAGUUGAAGG	CCUUCAACUAUUUCUUCCAUU	4519
R-008399109-000K	3114	1275	GGUGUUAUUUGGAACCUUG	CAAGGUUCCAAUAACACCUU	4521
R-008399109-000K	3114	1275	GGUGUUAUUUGGAACCUUG	B GGUGUUAUUUGGAACCUUGTT B	4520
R-008399112-000S	1665	1276	GUGCUCUUCGUCAUCUGAC	B GUGCUCUUCGUCAUCUGACTT B	4522
R-008399112-000S	1665	1276	GUGCUCUUCGUCAUCUGAC	GUCAGAUGACGAAGAGCACUU	4523
R-008399115-000T	304	1277	GGCCAUGGAACCAGACAGA	UCUGUCUGGUUCCAUGGCCUU	4525
R-008399115-000T	304	1277	GGCCAUGGAACCAGACAGA	B GGCCAUGGAACCAGACAGATT B	4524
R-008399118-000U	327	1278	CGGCUGUUAGUCACUGGCA	UGCCAGUGACUAACAGCCGUU	4527
R-008399118-000U	327	1278	CGGCUGUUAGUCACUGGCA	B CGGCUGUUAGUCACUGGCATT B	4526
R-008399121-000A	1866	1279	UUCCACGACUAGUUCAGUU	B UUCCACGACUAGUUCAGUUTT B	4528
R-008399121-000A	1866	1279	UUCCACGACUAGUUCAGUU	AACUGAACUAGUCGUGGAAUU	4529
R-008399124-000B	1699	1280	AGCAGAGAUGGCCCAGAAU	AUUCUGGGCCAUCUCUGCUUU	4531
R-008399124-000B	1699	1280	AGCAGAGAUGGCCCAGAAU	B AGCAGAGAUGGCCCAGAAUTT B	4530
R-008399127-000C	2397	1281	GCCAGGAUGAUCCUAGCUA	UAGCUAGGAUCAUCCUGGCUU	4533
R-008399127-000C	2397	1281	GCCAGGAUGAUCCUAGCUA	B GCCAGGAUGAUCCUAGCUATT B	4532
R-008399130-000J	1658	1282	GCCAUCUGUGCUCUUCGUC	B GCCAUCUGUGCUCUUCGUCTT B	4534
R-008399130-000J	1658	1282	GCCAUCUGUGCUCUUCGUC	GACGAAGAGCACAGAUGGCUU	4535
R-008399133-000K	891	1283	UAGAAACAGCUCGUUGUAC	GUACAACGAGCUGUUUCUAUU	4537
R-008399133-000K	891	1283	UAGAAACAGCUCGUUGUAC	B UAGAAACAGCUCGUUGUACTT B	4536
R-008399136-000K	1572	1284	AGAUGAUGGUCUGCCAAGU	B AGAUGAUGGUCUGCCAAGUTT B	4538
R-008399136-000K	1572	1284	AGAUGAUGGUCUGCCAAGU	ACUUGGCAGACCAUCAUCUUU	4539
R-008399139-000M	927	1285	ACCUUUCCCAUCAUCGUGA	B ACCUUUCCCAUCAUCGUGATT B	4540
R-008399139-000M	927	1285	ACCUUUCCCAUCAUCGUGA	UCACGAUGAUGGGAAAGGUUU	4541
R-008399142-000U	290	1286	AUGGAGUUGGACAUGGCCA	UGGCCAUGUCCAACUCCAUUU	4543
R-008399142-000U	290	1286	AUGGAGUUGGACAUGGCCA	B AUGGAGUUGGACAUGGCCATT B	4542
R-008399145-000V	1663	1287	CUGUGCUCUUCGUCAUCUG	CAGAUGACGAAGAGCACAGUU	4545
R-008399145-000V	1663	1287	CUGUGCUCUUCGUCAUCUG	B CUGUGCUCUUCGUCAUCUGTT B	4544
R-008399148-000W	1562	1288	UAUAAGAACAAGAUGAUGG	B UAUAAGAACAAGAUGAUGGTT B	4546

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399148-000W	1562	1288	UAUAAGAACAAGAUGAUGG	CCAUCAUCUUGUUCUUAUAUU	4547
R-008399154-000D	2947	1289	UCUGAAUAAAGUGUAACAA	UUGUUACACUUUAUUCAGAUU	4549
R-008399154-000D	2947	1289	UCUGAAUAAAGUGUAACAA	B UCUGAAUAAAGUGUAACAATT B	4548
R-008399157-000E	1711	1290	CCAGAAUGCAGUUCGCCUU	AAGGCGAACUGCAUUCUGGUU	4551
R-008399157-000E	1711	1290	CCAGAAUGCAGUUCGCCUU	B CCAGAAUGCAGUUCGCCUUTT B	4550
R-008399160-000L	1566	1291	AGAACAAGAUGAUGGUCUG	B AGAACAAGAUGAUGGUCUGTT B	4552
R-008399160-000L	1566	1291	AGAACAAGAUGAUGGUCUG	CAGACCAUCAUCUUGUUCUUU	4553
R-008399163-000M	1815	1292	AUCUUGCCCUUUGUCCCGC	GCGGGACAAAGGGCAAGAUUU	4555
R-008399163-000M	1815	1292	AUCUUGCCCUUUGUCCCGC	B AUCUUGCCCUUUGUCCCGCTT B	4554
R-008399166-000N	1087	1293	GCGUUUAGCUGGUGGGCUG	CAGCCCACCAGCUAAACGCUU	4557
R-008399166-000N	1087	1293	GCGUUUAGCUGGUGGGCUG	B GCGUUUAGCUGGUGGGCUGTT B	4556
R-008399169-000P	1495	1294	GGGUUCAGAUGAUAUAAAU	B GGGUUCAGAUGAUAUAAAUTT B	4558
R-008399169-000P	1495	1294	GGGUUCAGAUGAUAUAAAU	AUUUAUAUCAUCUGAACCCUU	4559
R-008399172-000W	1363	1295	UUUAGGACUUCACCUGACA	B UUUAGGACUUCACCUGACATT B	4560
R-008399172-000W	1363	1295	UUUAGGACUUCACCUGACA	UGUCAGGUGAAGUCCUAAAUU	4561
R-008399175-000X	391	1296	CACAGCUCCUUCUCUGAGU	ACUCAGAGAAGGAGCUGUGUU	4563
R-008399175-000X	391	1296	CACAGCUCCUUCUCUGAGU	B CACAGCUCCUUCUCUGAGUTT B	4562
R-008399178-000Y	1392	1297	AACGUCUUGUUCAGAACUG	CAGUUCUGAACAAGACGUUUU	4565
R-008399178-000Y	1392	1297	AACGUCUUGUUCAGAACUG	B AACGUCUUGUUCAGAACUGTT B	4564
R-008399181-000E	1935	1298	CACAGCAGCAAUUUGUGGA	B CACAGCAGCAAUUUGUGGATT B	4566
R-008399181-000E	1935	1298	CACAGCAGCAAUUUGUGGA	UCCACAAAUUGCUGCUGUGUU	4567
R-008399184-000F	1872	1299	GACUAGUUCAGUUGCUUGU	B GACUAGUUCAGUUGCUUGUTT B	4568
R-008399184-000F	1872	1299	GACUAGUUCAGUUGCUUGU	ACAAGCAACUGAACUAGUCUU	4569
R-008399187-000G	1159	1300	GACAGACUGCCUUCAAAUU	AAUUUGAAGGCAGUCUGUCUU	4571
R-008399187-000G	1159	1300	GACAGACUGCCUUCAAAUU	B GACAGACUGCCUUCAAAUUTT B	4570
R-008399190-000N	2308	1301	CUCUCUCUUCAGAACAGAG	CUCUGUUCUGAAGAGAGAGUU	4573
R-008399190-000N	2308	1301	CUCUCUCUUCAGAACAGAG	B CUCUCUCUUCAGAACAGAGTT B	4572
R-008399193-000P	632	1302	GUCCAGCGUUUGGCUGAAC	GUUCAGCCAAACGCUGGACUU	4575
R-008399193-000P	632	1302	GUCCAGCGUUUGGCUGAAC	B GUCCAGCGUUUGGCUGAACTT B	4574
R-008399196-000R	580	173	UGAGGGCAUGCAGAUCCCA	B UGAGGGCAUGCAGAUCCCATT B	4576
R-008399196-000R	580	173	UGAGGGCAUGCAGAUCCCA	UGGGAUCUGCAUGCCCUCAUU	4577
R-008399199-000S	1564	1303	UAAGAACAAGAUGAUGGUC	B UAAGAACAAGAUGAUGGUCTT B	4578
R-008399199-000S	1564	1303	UAAGAACAAGAUGAUGGUC	GACCAUCAUCUUGUUCUUAUU	4579
R-008399202-000J	1384	1304	UCCAAGUCAACGUCUUGUU	B UCCAAGUCAACGUCUUGUUTT B	4580
R-008399202-000J	1384	1304	UCCAAGUCAACGUCUUGUU	AACAAGACGUUGACUUGGAUU	4581
R-008399205-000K	1690	1305	ACACCAAGAAGCAGAGAUG	B ACACCAAGAAGCAGAGAUGTT B	4582
R-008399205-000K	1690	1305	ACACCAAGAAGCAGAGAUG	CAUCUCUGCUUCUUGGUGUUU	4583

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399208-000L	1421	1306	CUCAGGAAUCUUUCAGAUG	B CUCAGGAAUCUUUCAGAUGTT B	4584
R-008399208-000L	1421	1306	CUCAGGAAUCUUUCAGAUG	CAUCUGAAAGAUUCCUGAGUU	4585
R-008399211-000T	1141	1307	UAAAUUCUUGGCUAUUACG	B UAAAUUCUUGGCUAUUACGTT B	4586
R-008399211-000T	1141	1307	UAAAUUCUUGGCUAUUACG	CGUAAUAGCCAAGAAUUUAUU	4587
R-008399214-000U	1732	1308	CUAUGGACUACCAGUUGUG	B CUAUGGACUACCAGUUGUGTT B	4588
R-008399214-000U	1732	1308	CUAUGGACUACCAGUUGUG	CACAACUGGUAGUCCAUAGUU	4589
R-008399217-000V	634	1309	CCAGCGUUUGGCUGAACCA	B CCAGCGUUUGGCUGAACCATT B	4590
R-008399217-000V	634	1309	CCAGCGUUUGGCUGAACCA	UGGUUCAGCCAAACGCUGGUU	4591
R-008399220-000B	932	1310	UCCCAUCAUCGUGAGGGCU	B UCCCAUCAUCGUGAGGGCUTT B	4592
R-008399220-000B	932	1310	UCCCAUCAUCGUGAGGGCU	AGCCCUCACGAUGAUGGGAUU	4593
R-008399223-000C	579	171	AUGAGGGCAUGCAGAUCCC	GGGAUCUGCAUGCCCUCAUUU	4595
R-008399223-000C	579	171	AUGAGGGCAUGCAGAUCCC	B AUGAGGGCAUGCAGAUCCCTT B	4594
R-008399226-000D	1366	1311	AGGACUUCACCUGACAGAU	AUCUGUCAGGUGAAGUCCUUU	4597
R-008399226-000D	1366	1311	AGGACUUCACCUGACAGAU	B AGGACUUCACCUGACAGAUTT B	4596
R-008399229-000E	1608	1312	UUGUGCGUACUGUCCUUCG	B UUGUGCGUACUGUCCUUCGTT B	4598
R-008399229-000E	1608	1312	UUGUGCGUACUGUCCUUCG	CGAAGGACAGUACGCACAAUU	4599
R-008399232-000L	814	10	AGCUUCCAGACACGCUAUC	GAUAGCGUGUCUGGAAGCUUU	4601
R-008399232-000L	814	10	AGCUUCCAGACACGCUAUC	B AGCUUCCAGACACGCUAUCTT B	4600
R-008399235-000M	1923	1313	CCAUGGGUGGGACACAGCA	B CCAUGGGUGGGACACAGCATT B	4602
R-008399235-000M	1923	1313	CCAUGGGUGGGACACAGCA	UGCUGUGUCCCACCCAUGGUU	4603
R-008399238-000N	1458	1314	GGAUGGAAGGUCUCCUUGG	CCAAGGAGACCUUCCAUCCUU	4605
R-008399238-000N	1458	1314	GGAUGGAAGGUCUCCUUGG	B GGAUGGAAGGUCUCCUUGGTT B	4604
R-008399241-000V	1908	1315	CCCAGCGCCGUACGUCCAU	G CCCAGCGCCGUACGUCCATT B	4606
R-008399241-000V	1908	1315	CCCAGCGCCGUACGUCCAU	AUGGACGUACGGCGCUGGGUU	4607
R-008399244-000W	539	1316	GCUCAGAGGGUACGAGCUG	CAGCUCGUACCCUCUGAGCUU	4609
R-008399244-000W	539	1316	GCUCAGAGGGUACGAGCUG	B GCUCAGAGGGUACGAGCUGTT B	4608
R-008399247-000X	2016	1317	AUGUUCACAACCGAAUUGU	ACAAUUCGGUUGUGAACAUUU	4611
R-008399247-000X	2016	1317	AUGUUCACAACCGAAUUGU	B AUGUUCACAACCGAAUUGUTT B	4610
R-008399250-000D	1884	1318	UGCUUGUUCGUGCACAUCA	B UGCUUGUUCGUGCACAUCATT B	4612
R-008399250-000D	1884	1318	UGCUUGUUCGUGCACAUCA	UGAUGUGCACGAACAAGCAUU	4613
R-008399253-000E	560	1319	AUGUUCCCUGAGACAUUAG	B AUGUUCCCUGAGACAUUAGTT B	4614
R-008399253-000E	560	1319	AUGUUCCCUGAGACAUUAG	CUAAUGUCUCAGGGAACAUUU	4615
R-008399256-000F	411	1320	GUAAAGGCAAUCCUGAGGA	UCCUCAGGAUUGCCUUUACUU	4617
R-008399256-000F	411	1320	GUAAAGGCAAUCCUGAGGA	B GUAAAGGCAAUCCUGAGGATT B	4616
R-008399259-000G	338	1321	CACUGGCAGCAACAGUCUU	AAGACUGUUGCUGCCAGUGUU	4619
R-008399259-000G	338	1321	CACUGGCAGCAACAGUCUU	B CACUGGCAGCAACAGUCUUTT B	4618

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399262-000N	830	1322	AUCAUGCGUUCUCCUCAGA	UCUGAGGAGAACGCAUGAUUU	4621
R-008399262-000N	830	1322	AUCAUGCGUUCUCCUCAGA	B AUCAUGCGUUCUCCUCAGATT B	4620
R-008399265-000P	3086	1323	UAUGUAUGGGUAGGGUAAA	B UAUGUAUGGGUAGGGUAAATT B	4622
R-008399265-000P	3086	1323	UAUGUAUGGGUAGGGUAAA	UUUACCCUACCCAUACAUAUU	4623
R-008399258-000R	3115	1324	GUGUUAUUUGGAACCUUGU	ACAAGGUUCCAAAUAACACUU	4625
R-008399258-000R	3115	1324	GUGUUAUUUGGAACCUUGU	B GUGUUAUUUGGAACCUUGUTT B	4624
R-008399271-000X	2177	1325	ACAGCUCCUCUGACAGAGU	B ACAGCUCCUCUGACAGAGUTT B	4626
R-008399271-000X	2177	1325	ACAGCUCCUCUGACAGAGU	ACUCUGUCAGAGGAGCUGUUU	4627
R-008399274-000Y	1733	1326	UAUGGACUACCAGUUGUGG	B UAUGGACUACCAGUUGUGGTT B	4628
R-008399274-000Y	1733	1326	UAUGGACUACCAGUUGUGG	CCACAACUGGUAGUCCAUAUU	4629
R-008399277-000Z	375	1327	AUUCUGGUGCCACUACCAC	GUGGUAGUGGCACCAGAAUUU	4631
R-008399277-000Z	375	1327	AUUCUGGUGCCACUACCAC	B AUUCUGGUGCCACUACCACTT B	4630
R-008399280-000F	2565	1328	UGCCUCCAGGUGACAGCAA	B UGCCUCCAGGUGACAGCAATT B	4632
R-008399280-000F	2565	1328	UGCCUCCAGGUGACAGCAA	UUGCUGUCACCUGGAGGCAUU	4633
R-008399283-000G	442	1329	UACCUCCCAAGUCCUGUAU	AUACAGGACUUGGGAGGUAUU	4635
R-008399283-000G	442	1329	UACCUCCCAAGUCCUGUAU	B UACCUCCCAAGUCCUGUAUTT B	4634
R-008399286-000H	819	1330	CCAGACACGCUAUCAUGCG	CGCAUGAUAGCGUGUCUGGUU	4637
R-008399286-000H	819	1330	CCAGACACGCUAUCAUGCG	B CCAGACACGCUAUCAUGCGTT B	4636
R-008399289-000J	700	1331	UGAUGCAGAACUUGCCACA	B UGAUGCAGAACUUGCCACATT B	4638
R-008399289-000J	700	1331	UGAUGCAGAACUUGCCACA	UGUGGCAAGUUCUGCAUCAUU	4639
R-008399292-000R	1089	1332	GUUUAGCUGGUGGGCUGCA	B GUUUAGCUGGUGGGCUGCATT B	4640
R-008399292-000R	1089	1332	GUUUAGCUGGUGGGCUGCA	UGCAGCCCACCAGCUAAACUU	4641
R-008399295-000S	1580	1333	GUCUGCCAAGUGGGUGGUA	UACCACCCACUUGGCAGACUU	4643
R-008399295-000S	1580	1333	GUCUGCCAAGUGGGUGGUA	B GUCUGCCAAGUGGGUGGUATT B	4642
R-008399298-000T	1982	1334	GGUUGUACCGGAGCCCUUC	GAAGGGCUCCGGUACAACCUU	4645
R-008399298-000T	1982	1334	GGUUGUACCGGAGCCCUUC	B GGUUGUACCGGAGCCCUUCTT B	4644
R-008399301-000K	1986	1335	GUACCGGAGCCCUUCACAU	B GUACCGGAGCCCUUCACAUTT B	4646
R-008399301-000K	1986	1335	GUACCGGAGCCCUUCACAU	AUGUGAAGGGCUCCGGUACUU	4647
R-008399304-000L	418	1336	CAAUCCUGAGGAAGAGGAU	AUCCUCUUCCUCAGGAUUGUU	4649
R-008399304-000L	418	1336	CAAUCCUGAGGAAGAGGAU	B CAAUCCUGAGGAAGAGGAUTT B	4648
R-008399307-000M	1306	1337	GCUAUCUGUCUGCUCUAGU	ACUAGAGCAGACAGAUAGCUU	4651
R-008399307-000M	1306	1337	GCUAUCUGUCUGCUCUAGU	B GCUAUCUGUCUGCUCUAGUTT B	4650
R-008399310-000U	1377	1338	UGACAGAUCCAAGUCAACG	CGUUGACUUGGAUCUGUCAUU	4653
R-008399310-000U	1377	1338	UGACAGAUCCAAGUCAACG	B UGACAGAUCCAAGUCAACGTT B	4652
R-008399313-000V	2467	1339	CAUGAUGGAACAUGAGAUG	CAUCUCAUGUUCCAUCAUGUU	4655
R-008399313-000V	2467	1339	CAUGAUGGAACAUGAGAUG	B CAUGAUGGAACAUGAGAUGTT B	4654
R-008399316-000W	1414	1340	UUGGACUCUCAGGAAUCUU	B UUGGACUCUCAGGAAUCUUTT B	4656

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399316-000W	1414	1340	UUGGACUCUCAGGAAUCUU	AAGAUUCCUGAGAGUCCAAUU	4657
R-008399319-000X	1668	1341	CUCUUCGUCAUCUGACCAG	B CUCUUCGUCAUCUGACCAGTT B	4658
R-008399319-000X	1668	1341	CUCUUCGUCAUCUGACCAG	CUGGUCAGAUGACGAAGAGUU	4659
R-008399322-000D	1818	1342	UUGCCCUUUGUCCCGCAAA	B UUGCCCUUUGUCCCGCAAATT B	4660
R-008399322-000D	1818	1342	UUGCCCUUUGUCCCGCAAA	UUUGCGGGACAAAGGGCAAUU	4661
R-008399325-000E	1697	1343	GAAGCAGAGAUGGCCCAGA	B GAAGCAGAGAUGGCCCAGATT B	4662
R-008399325-000E	1697	1343	GAAGCAGAGAUGGCCCAGA	UCUGGGCCAUCUCUGCUUCUU	4663
R-008399328-000F	918	1344	CCUUGCAUAACCUUUCCCA	B CCUUGCAUAACCUUUCCCATT B	4664
R-008399328-000F	918	1344	CCUUGCAUAACCUUUCCCA	UGGGAAAGGUUAUGCAAGGUU	4665
R-008399331-000M	605	1345	CAGUUUGAUGCUGCUCAUC	GAUGAGCAGCAUCAAACUGUU	4667
R-008399331-000M	605	1345	CAGUUUGAUGCUGCUCAUC	B CAGUUUGAUGCUGCUCAUCTT B	4666
R-008399334-000N	1374	1346	ACCUGACAGAUCCAAGUCA	B ACCUGACAGAUCCAAGUCATT B	4668
R-008399334-000N	1374	1346	ACCUGACAGAUCCAAGUCA	UGACUUGGAUCUGUCAGGUUU	4669
R-008399337-000P	1430	1347	CUUUCAGAUGCUGCAACUA	UAGUUGCAGCAUCUGAAAGUU	4671
R-008399337-000P	1430	1347	CUUUCAGAUGCUGCAACUA	B CUUUCAGAUGCUGCAACUATT B	4670
R-008399340-000W	3186	1348	GAUACGAUGCUUCAAGAGA	UCUCUUGAAGCAUCGUAUCUU	4673
R-008399340-000W	3186	1348	GAUACGAUGCUUCAAGAGA	B GAUACGAUGCUUCAAGAGATT B	4672
R-008399343-000X	1355	1348	AUGCAAGCUUUAGGACUUC	B AUGCAAGCUUUAGGACUUCTT B	4674
R-008399343-000X	1355	1348	AUGCAAGCUUUAGGACUUC	GAAGUCCUAAAGCUUGCAUUU	4675
R-008399346-000Y	433	1350	GGAUGUGGAUACCUCCCAA	UUGGGAGGUAUCCACAUCCUU	4677
R-008399346-000Y	433	1350	GGAUGUGGAUACCUCCCAA	B GGAUGUGGAUACCUCCCAATT B	4676
R-008399349-000Z	1901	13	CAGGAUACCCAGCGCCGUA	B CAGGAUACCCAGCGCCGUATT B	4678
R-008399349-000Z	1901	13	CAGGAUACCCAGCGCCGUA	UACGGCGCUGGGUAUCCUGUU	4679
R-008399352-000F	1713	1351	AGAAUGCAGUUCGCCUUCA	UGAAGGCGAACUGCAUUCUUU	4681
R-008399352-000F	1713	1351	AGAAUGCAGUUCGCCUUCA	B AGAAUGCAGUUCGCCUUCATT B	4680
R-008399355-000G	823	17	ACACGCUAUCAUGCGUUCU	AGAACGCAUGAUAGCGUGUUU	4683
R-008399355-000G	823	17	ACACGCUAUCAUGCGUUCU	B ACACGCUAUCAUGCGUUCUTT B	4683
R-008399358-000H	1811	1352	CGAAAUCUUGCCCUUUGUC	B CGAAAUCUUGCCCUUUGUCTT B	4684
R-008399358-000H	1811	1352	CGAAAUCUUGCCCUUUGUC	GACAAAGGGCAAGAUUUCGUU	4685
R-008399361-000P	491	1353	ACUCAAGAACAAGUAGCUG	B ACUCAAGAACAAGUAGCUGTT B	4686
R-008399361-000P	491	1353	ACUCAAGAACAAGUAGCUG	CAGCUACUUGUUCUUGAGUUU	4687
R-008399364-000R	2209	1354	GAAUGAAGGUGUGGCGACA	UGUCGCCACACCUUCAUUCUU	4689
R-008399364-000R	2209	1354	GAAUGAAGGUGUGGCGACA	B GAAUGAAGGUGUGGCGACATT B	4688
R-008399367-000S	1840	1355	UGCACCUUUGCGUGAGCAG	B UGCACCUUUGCGUGAGCAGTT B	4690
R-008399367-000S	1840	1355	UGCACCUUUGCGUGAGCAG	CUGCUCACGCAAAGGUGCAUU	4691
R-008399370-000Y	550	1356	ACGAGCUGCUAUGUUCCCU	AGGGAACAUAGCAGCUCGUUU	4693

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399370-000Y	550	1356	ACGAGCUGCUAUGUUCCCU	B ACGAGCUGCUAUGUUCCCUTT B	4692
R-008399373-000Z	429	1357	AAGAGGAUGUGGAUACCUC	GAGGUAUCCACAUCCUCUUU	4695
R-008399373-000Z	429	1357	AAGAGGAUGUGGAUACCUC	B AAGAGGAUGUGGAUACCUCTT B	4694
R-008399376-000A	2436	1358	GAUAUGGCCAGGAUGCCUU	AAGGCAUCCUGGCCAUAUCUU	4697
R-008399376-000A	2436	1358	GAUAUGGCCAGGAUGCCUU	B GAUAUGGCCAGGAUGCCUUTT B	4696
R-008399379-000B	1597	1359	UAUAGAGGCUCUUGUGCGU	B UAUAGAGGCUCUUGUGCGUTT B	4698
R-008399379-000B	1597	1359	UAUAGAGGCUCUUGUGCGU	ACGCACAAGAGCCUCUAUAUU	4699
R-008399382-000H	1496	1360	GGUUCAGAUGAUAUAAAUG	B GGUUCAGAUGAUAUAAAUGTT B	4700
R-008399382-000H	1496	1360	GGUUCAGAUGAUAUAAAUG	CAUUUAUAUCAUCUGAACCUU	4701
R-008399385-000J	1456	1361	AGGGAUGGAAGGUCUCCUU	AAGGAGACCUUCCAUCCCUUU	4703
R-008399385-000J	1456	1361	AGGGAUGGAAGGUCUCCUU	B AGGGAUGGAAGGUCUCCUUTT B	4702
R-008399388-000K	3159	1362	UAUCCCAAAGUUGUUGUAA	UUACAACAACUUUGGGAUAUU	4705
R-008399388-000K	3159	1362	UAUCCCAAAGUUGUUGUAA	B UAUCCCAAAGUUGUUGUAATT B	4704
R-008399391-000S	2309	1363	UCUCUCUUCAGAACAGAGC	B UCUCUCUUCAGAACAGAGCTT B	4706
R-008399391-000S	2309	1363	UCUCUCUUCAGAACAGAGC	GCUCUGUUCUGAAGAGAGAUU	4707
R-008399394-000T	2300	1364	CUGACCAGCUCUCUCUUCA	B CUGACCAGCUCUCUCUUCATT B	4708
R-008399394-000T	2300	1364	CUGACCAGCUCUCUCUUCA	UGAAGAGAGAGCUGGUCAGUU	4709
R-008399397-000U	3177	1365	ACCUGCUGUGAUACGAUGC	B ACCUGCUGUGAUACGAUGCTT B	4710
R-008399397-000U	3177	1365	ACCUGCUGUGAUACGAUGC	GCAUCGUAUCACAGCAGGUUU	4711
R-008399400-000L	1079	1366	AUGGCAGUGCGUUUAGCUG	B AUGGCAGUGCGUUUAGCUGTT B	4712
R-008399400-000L	1079	1366	AUGGCAGUGCGUUUAGCUG	CAGCUAAACGCACUGCCAUUU	4713
R-008399403-000M	1383	1367	AUCCAAGUCAACGUCUUGU	ACAAGACGUUGACUUGGAUUU	4715
R-008399403-000M	1383	1367	AUCCAAGUCAACGUCUUGU	B AUCCAAGUCAACGUCUUGUTT B	4714
R-008399406-000N	2563	1368	GCUGCCUCCAGGUGACAGC	GCUGUCACCUGGAGGCAGCUU	4717
R-008399406-000N	2563	1368	GCUGCCUCCAGGUGACAGC	B GCUGCCUCCAGGUGACAGCTT B	4716
R-008399409-000P	1084	1369	AGUGCGUUUAGCUGGUGGG	B AGUGCGUUUAGCUGGUGGGTT B	4718
R-008399409-000P	1084	1369	AGUGCGUUUAGCUGGUGGG	CCCACCAGCUAAACGCACUUU	4719
R-008399412-000W	1329	1370	AGCCGGCUAUUGUAGAAGC	B AGCCGGCUAUUGUAGAAGCTT B	4720
R-008399412-000W	1329	1370	AGCCGGCUAUUGUAGAAGC	GCUUCUACAAUAGCCGGCUUU	4721
R-008399415-000X	1662	169	UCUGUGCUCUUCGUCAUCU	AGAUGACGAAGAGCACAGAUU	4723
R-008399415-000X	1662	169	UCUGUGCUCUUCGUCAUCU	B UCUGUGCUCUUCGUCAUCUTT B	4722
R-008399418-000Y	2268	99	CACAAGAUUACAAGAAACG	CGUUUCUUGUAAUCUUGUGUU	4725
R-008399418-000Y	2268	99	CACAAGAUUACAAGAAACG	B CACAAGAUUACAAGAAACGTT B	4724
R-008399421-000E	2470	108	GAUGGAACAUGAGAUGGGU	B GAUGGAACAUGAGAUGGGUTT B	4726
R-008399421-000E	2470	108	GAUGGAACAUGAGAUGGGU	ACCCAUCUCAUGUUCCAUCUU	4727
R-008399424-000F	573	1371	CAUUAGAUGAGGGCAUGCA	B CAUUAGAUGAGGGCAUGCATT B	4728
R-008399424-000F	573	1371	CAUUAGAUGAGGGCAUGCA	UGCAUGCCCUCAUCUAAUGUU	4729

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399427-000G	2213	1372	GAAGGUGUGGCGACAUAUG	B GAAGGUGUGGCGACAUAUGTT B	4730
R-008399427-000G	2213	1372	GAAGGUGUGGCGACAUAUG	CAUAUGUCGCCACACCUUCUU	4731
R-008399430-000N	1587	1373	AAGUGGGUGGUAUAGAGGC	B AAGUGGGUGGUAUAGAGGCTT B	4732
R-008399430-000N	1587	1373	AAGUGGGUGGUAUAGAGGC	GCCUCUAUACCACCCACUUUU	4733
R-008399433-000P	2166	1374	CUGAGGGAGCCACAGCUCC	B CUGAGGGAGCCACAGCUCCTT B	4734
R-008399433-000P	2166	1374	CUGAGGGAGCCACAGCUCC	GGAGCUGUGGCUCCCUCAGUU	4735
R-008399436-000R	637	1375	GCGUUUGGCUGAACCAUCA	UGAUGGUUCAGCCAAACGCUU	4737
R-008399436-000R	637	1375	GCGUUUGGCUGAACCAUCA	B GCGUUUGGCUGAACCAUCATT B	4736
R-008399439-000S	397	1376	UCCUUCUCUGAGUGGUAAA	B UCCUUCUCUGAGUGGUAAATT B	4738
R-008399439-000S	397	1376	UCCUUCUCUGAGUGGUAAA	UUUACCACUCAGAGAAGGAUU	4739
R-008399442-000Y	1718	1377	GCAGUUCGCCUUCACUAUG	B GCAGUUCGCCUUCACUAUGTT B	4740
R-008399442-000Y	1718	1377	GCAGUUCGCCUUCACUAUG	CAUAGUGAAGGCGAACUGCUU	4741
R-008399445-000Z	1415	111	UGGACUCUCAGGAAUCUUU	B UGGACUCUCAGGAAUCUUUTT B	4742
R-008399445-000Z	1415	111	UGGACUCUCAGGAAUCUUU	AAAGAUUCCUGAGAGUCCAUU	4743
R-008399448-000Z	1413	162	UUUGGACUCUCAGGAAUCU	B UUUGGACUCUCAGGAAUCUTT B	4744
R-008399448-000Z	1413	162	UUUGGACUCUCAGGAAUCU	AGAUUCCUGAGAGUCCAAAUU	4745
R-008399451-000G	2445	160	AGGAUGCCUUGGGUAUGGA	B AGGAUGCCUUGGGUAUGGATT B	4746
R-008399451-000G	2445	160	AGGAUGCCUUGGGUAUGGA	UCCAUACCCAAGGCAUCCUUU	4747
R-008399454-000H	567	157	CUGAGACAUUAGAUGAGGG	B CUGAGACAUUAGAUGAGGGTT B	4748
R-008399454-000H	567	157	CUGAGACAUUAGAUGAGGG	CCCUCAUCUAAUGUCUCAGUU	4749
R-008399457-000J	1498	86	UUCAGAUGAUAUAAAUGUG	CACAUUUAUAUCAUCUGAAUU	4751
R-008399457-000J	1498	86	UUCAGAUGAUAUAAAUGUG	B UUCAGAUGAUAUAAAUGUGTT B	4750
R-008399460-000R	2357	1378	GGACUUGAUAUUGGUGCCC	B GGACUUGAUAUUGGUGCCCTT B	4752
R-008399460-000R	2357	1378	GGACUUGAUAUUGGUGCCC	GGGCACCAAUAUCAAGUCCUU	4753
R-008399463-000S	639	1379	GUUUGGCUGAACCAUCACA	UGUGAUGGUUCAGCCAAACUU	4755
R-008399463-000S	639	1379	GUUUGGCUGAACCAUCACA	B GUUUGGCUGAACCAUCACATT B	4754
R-008399466-000T	585	1380	GCAUGCAGAUCCCAUCUAC	GUAGAUGGGAUCUGCAUGCUU	4757
R-008399466-000T	585	1380	GCAUGCAGAUCCCAUCUAC	B GCAUGCAGAUCCCAUCUACTT B	4756
R-008399469-000U	2519	1381	GAUGGGCUGCCAGAUCUGG	B GAUGGGCUGCCAGAUCUGGTT B	4758
R-008399469-000U	2519	1381	GAUGGGCUGCCAGAUCUGG	CCAGAUCUGGCAGCCCAUCUU	4759
R-008399472-000A	1367	1382	GGACUUCACCUGACAGAUC	B GGACUUCACCUGACAGAUCTT B	4760
R-008399472-000A	1367	1382	GGACUUCACCUGACAGAUC	GAUCUGUCAGGUGAAGUCCUU	4761
R-008399475-000B	1391	1383	CAACGUCUUGUUCAGAACU	B CAACGUCUUGUUCAGAACUTT B	4762
R-008399475-000B	1391	1383	CAACGUCUUGUUCAGAACU	AGUUCUGAACAAGACGUUGUU	4763
R-008399478-000C	509	1384	GAUAUUGAUGGACAGUAUG	B GAUAUUGAUGGACAGUAUGTT B	4764
R-008399478-000C	509	1384	GAUAUUGAUGGACAGUAUG	CAUACUGUCCAUCAAUAUCUU	4765

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399481-000J	303	1385	UGGCCAUGGAACCAGACAG	B UGGCCAUGGAACCAGACAGTT B	4766
R-008399481-000J	303	1385	UGGCCAUGGAACCAGACAG	CUGUCUGGUUCCAUGGCCAUU	4767
R-008399484-000K	494	1386	CAAGAACAAGUAGCUGAUA	UAUCAGCUACUUGUUCUUGUU	4769
R-008399484-000K	494	1386	CAAGAACAAGUAGCUGAUA	B CAAGAACAAGUAGCUGAUATT B	4768
R-008399487-000L	328	1387	GGCUGUUAGUCACUGGCAG	CUGCCAGUGACUAACAGCCUU	4771
R-008399487-000L	328	1387	GGCUGUUAGUCACUGGCAG	B GGCUGUUAGUCACUGGCAGTT B	4770
R-008399490-000T	2058	1388	CAUUGUUUGUGCAGCUGCU	AGCAGCUGCACAAACAAUGUU	4773
R-008399490-000T	2058	1388	CAUUGUUUGUGCAGCUGCU	B CAUUGUUUGUGCAGCUGCUTT B	4772
R-008399493-000U	1447	1389	UAAACAGGAAGGGAUGGAA	B UAAACAGGAAGGGAUGGAATT B	4774
R-008399493-000U	1447	1389	UAAACAGGAAGGGAUGGAA	UUCCAUCCCUUCCUGUUUAUU	4775
R-008399496-000V	1563	1390	AUAAGAACAAGAUGAUGGU	ACCAUCAUCUUGUUCUUAUUU	4777
R-008399496-000V	1563	1390	AUAAGAACAAGAUGAUGGU	B AUAAGAACAAGAUGAUGGUTT B	4776
R-008399499-000W	1350	1391	GUGGAAUGCAAGCUUUAGG	CCUAAAGCUUGCAUUCCACUU	4779
R-008399499-000W	1350	1391	GUGGAAUGCAAGCUUUAGG	B GUGGAAUGCAAGCUUUAGGTT B	4778
R-008399503-000N	2208	1392	GGAAUGAAGGUGUGGCGAC	GUCGCCACACCUUCAUUCCUU	4781
R-008399503-000N	2208	1392	GGAAUGAAGGUGUGGCGAC	B GGAAUGAAGGUGUGGCGACTT B	4780
R-008399505-000P	1689	1393	GACACCAAGAAGCAGAGAU	AUCUCUGCUUCUUGGUGUCUU	4783
R-008399505-000P	1689	1393	GACACCAAGAAGCAGAGAU	B GACACCAAGAAGCAGAGAUTT B	4782
R-008399508-000R	1407	1394	ACUGUCUUUGGACUCUCAG	B ACUGUCUUUGGACUCUCAGTT B	4784
R-008399508-000R	1407	1394	ACUGUCUUUGGACUCUCAG	CUGAGAGUCCAAAGACAGUUU	4785
R-008399511-000X	2137	1395	GGACAAGGAAGCUGCAGAA	B GGACAAGGAAGCUGCAGAATT B	4786
R-008399511-000X	2137	1395	GGACAAGGAAGCUGCAGAA	UUCUGCAGCUUCCUUGUCCUU	4787
R-008399514-000Y	854	1396	UCUGCUAUUGUACGUACCA	B UCUGCUAUUGUACGUACCATT B	4788
R-008399514-000Y	854	1396	UCUGCUAUUGUACGUACCA	UGGUACGUACAAUAGCAGAUU	4789
R-008399517-000Z	2070	1397	AGCUGCUUUAUUCUCCCAU	AUGGGAGAAUAAAGCAGCUUU	4791
R-008399517-000Z	2070	1397	AGCUGCUUUAUUCUCCCAU	B AGCUGCUUUAUUCUCCCAUTT B	4790
R-008399520-000F	545	1398	AGGGUACGAGCUGCUAUGU	ACAUAGCAGCUCGUACCCUUU	4793
R-008399520-000F	545	1398	AGGGUACGAGCUGCUAUGU	B AGGGUACGAGCUGCUAUGUTT B	4792
R-008399523-000G	1640	1399	GAAGACAUCACUGAGCCUG	B GAAGACAUCACUGAGCCUGTT B	4794
R-008399523-000G	1640	1399	GAAGACAUCACUGAGCCUG	CAGGCUCAGUGAUGUCUUCUU	4795
R-008399526-000H	2012	1400	CGGGAUGUUCACAACCGAA	UUCGGUUGUGAACAUCCCGUU	4797
R-008399526-000H	2012	1400	CGGGAUGUUCACAACCGAA	B CGGGAUGUUCACAACCGAATT B	4796
R-008399529-000J	1684	1401	CAGCCGACACCAAGAAGCA	B CAGCCGACACCAAGAAGCATT B	4798
R-008399529-000J	1684	1401	CAGCCGACACCAAGAAGCA	UGCUUCUUGGUGUCGGCUGUU	4799
R-008399535-000S	520	9	ACAGUAUGCAAUGACUCGA	UCGAGUCAUUGCAUACUGUUU	4801
R-008399535-000S	520	9	ACAGUAUGCAAUGACUCGA	B ACAGUAUGCAAUGACUCGATT B	4800
R-008399538-000T	1969	182	AGAAAUAGUUGAAGGUUGU	B AGAAAUAGUUGAAGGUUGUTT B	4802

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399538-000T	1969	182	AGAAAUAGUUGAAGGUUGU	ACAACCUUCAACUAUUUCUUU	4803
R-008399541-000Z	2017	1402	UGUUCACAACCGAAUUGUU	B UGUUCACAACCGAAUUGUUTT B	4804
R-008399541-000Z	2017	1402	UGUUCACAACCGAAUUGUU	AACAAUUCGGUUGUGAACAUU	4805
R-008399544-000Z	2307	1403	GCUCUCUCUUCAGAACAGA	B GCUCUCUCUUCAGAACAGATT B	4806
R-008399544-000Z	2307	1403	GCUCUCUCUUCAGAACAGA	UCUGUUCUGAAGAGAGAGCUU	4807
R-008399547-000B	844	1404	UCAGAUGGUGUCUGCUAUU	B UCAGAUGGUGUCUGCUAUUTT B	4808
R-008399547-000B	844	1404	UCAGAUGGUGUCUGCUAUU	AAUAGCAGACACCAUCUGAUU	4809
R-008399550-000H	405	1405	UGAGUGGUAAAGGCAAUCC	GGAUUGCCUUUACCACUCAUU	4811
R-008399550-000H	405	1405	UGAGUGGUAAAGGCAAUCC	B UGAGUGGUAAAGGCAAUCCTT B	4810
R-008399553-000J	379	1406	UGGUGCCACUACCACAGCU	B UGGUGCCACUACCACAGCUTT B	4812
R-008399553-000J	379	1406	UGGUGCCACUACCACAGCU	AGCUGUGGUAGUGGCACCAUU	4813
R-008399556-000K	1825	1407	UUGUCCCGCAAAUCAUGCA	B UUGUCCCGCAAAUCAUGCATT B	4814
R-008399556-000K	1825	1407	UUGUCCCGCAAAUCAUGCA	UGCAUGAUUUGCGGGACAAUU	4815
R-008399559-000L	2495	1408	CACCCUGGUGCUGACUAUC	GAUAGUCAGCACCAGGGUGUU	4817
R-008399559-000L	2495	1408	CACCCUGGUGCUGACUAUC	B CACCCUGGUGCUGACUAUCTT B	4816
R-008399563-000T	629	1409	AAUGUCCAGCGUUUGGCUG	B AAUGUCCAGCGUUUGGCUGTT B	4818
R-008399563-000T	629	1409	AAUGUCCAGCGUUUGGCUG	CAGCCAAACGCUGGACAUUUU	4819
R-008399565-000U	2561	1410	GGGCUGCCUCCAGGUGACA	UGUCACCUGGAGGCAGCCCUU	4821
R-008399565-000U	2561	1410	GGGCUGCCUCCAGGUGACA	B GGGCUGCCUCCAGGUGACATT B	4820
R-008399568-000V	2192	1411	GAGUUACUUCACUCUAGGA	B GAGUUACUUCACUCUAGGATT B	4822
R-008399568-000V	2192	1411	GAGUUACUUCACUCUAGGA	UCCUAGAGUGAAGUAACUCUU	4823
R-008399571-000B	1809	1412	UUCGAAAUCUUGCCCUUUG	B UUCGAAAUCUUGCCCUUUGTT B	4824
R-008399571-000B	1809	1412	UUCGAAAUCUUGCCCUUUG	CAAAGGGCAAGAUUUCGAAUU	4825
R-008399574-000C	1596	1413	GUAUAGAGGCUCUUGUGCG	B GUAUAGAGGCUCUUGUGCGTT B	4826
R-008399574-000C	1596	1413	GUAUAGAGGCUCUUGUGCG	CGCACAAGAGCCUCUAUACUU	4827
R-008399577-000D	2298	1414	AGCUGACCAGCUCUCUCUU	AAGAGAGAGCUGGUCAGCUUU	4829
R-008399577-000D	2298	1414	AGCUGACCAGCUCUCUCUU	B AGCUGACCAGCUCUCUCUUTT B	4828
R-008399580-000K	858	1415	CUAUUGUACGUACCAUGCA	UGCAUGGUACGUACAAUAGUU	4831
R-008399580-000K	858	1415	CUAUUGUACGUACCAUGCA	B CUAUUGUACGUACCAUGCATT B	4830
R-008399583-000L	524	1416	UAUGCAAUGACUCGAGCUC	B UAUGCAAUGACUCGAGCUCTT B	4832
R-008399583-000L	524	1416	UAUGCAAUGACUCGAGCUC	GAGCUCGAGUCAUUGCAUAUU	4833
R-008399586-000M	2542	1417	UGCCCAGGACCUCAUGGAU	B UGCCCAGGACCUCAUGGAUTT B	4834
R-008399586-000M	2542	1417	UGCCCAGGACCUCAUGGAU	AUCCAUGAGGUCCUGGGCAUU	4835
R-008399589-000N	498	1418	AACAAGUAGCUGAUAUUGA	B AACAAGUAGCUGAUAUUGATT B	4836
R-008399589-000N	498	1418	AACAAGUAGCUGAUAUUGA	UCAAUAUCAGCUACUUGUUUU	4837
R-008399592-000V	414	1419	AAGGCAAUCCUGAGGAAGA	UCUUCCUCAGGAUUGCCUUUU	4839

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399592-000V	414	1419	AAGGCAAUCCUGAGGAAGA	B AAGGCAAUCCUGAGGAAGA*TT* B	4838
R-008399595-000W	1570	1420	CAAGAUGAUGGUCUGCCAA	B CAAGAUGAUGGUCUGCCAA*TT* B	4840
R-008399595-000W	1570	1420	CAAGAUGAUGGUCUGCCAA	UUGGCAGACCAUCAUCUUGUU	4841
R-008399598-000X	1030	1421	UGCCAUUACAACUCUCCAC	GUGGAGAGUUGUAAUGGCAUU	4843
R-008399598-000X	1030	1421	UGCCAUUACAACUCUCCAC	B UGCCAUUACAACUCUCCAC*TT* B	4842
R-008399601-000P	1380	20	CAGAUCCAAGUCAACGUCU	AGACGUUGACUUGGAUCUGUU	4845
R-008399601-000P	1380	20	CAGAUCCAAGUCAACGUCU	B CAGAUCCAAGUCAACGUCU*TT* B	4844
R-008399604-000R	3087	1422	AUGUAUGGGUAGGGUAAAU	B AUGUAUGGGUAGGGUAAAU*TT* B	4846
R-008399604-000R	3087	1422	AUGUAUGGGUAGGGUAAAU	AUUUACCCUACCCAUACAUUU	4847
R-008399607-000S	1664	1423	UGUGCUCUUCGUCAUCUGA	B UGUGCUCUUCGUCAUCUGA*TT* B	4848
R-008399607-000S	1664	1423	UGUGCUCUUCGUCAUCUGA	UCAGAUGACGAAGAGCACAUU	4849
R-008399610-000Y	1790	1424	AAGGCUACUGUUGGAUUGA	B AAGGCUACUGUUGGAUUGA*TT* B	4850
R-008399610-000Y	1790	1424	AAGGCUACUGUUGGAUUGA	UCAAUCCAACAGUAGCCUUUU	4851
R-008399613-000Z	1615	1425	UACUGUCCUUCGGGCUGGU	ACCAGCCCGAAGGACAGUAUU	4853
R-008399613-000Z	1615	1425	UACUGUCCUUCGGGCUGGU	B UACUGUCCUUCGGGCUGGU*TT* B	4852
R-008399616-000A	774	1426	AUAAGGCUGCAGUUAUGGU	ACCAUAACUGCAGCCUUAUUU	4855
R-008399616-000A	774	1426	AUAAGGCUGCAGUUAUGGU	B AUAAGGCUGCAGUUAUGGU*TT* B	4854
R-008399619-000B	1672	1427	UCGUCAUCUGACCAGCCGA	UCGGCUGGUCAGAUGACGAUU	4857
R-008399619-000B	1672	1427	UCGUCAUCUGACCAGCCGA	B UCGUCAUCUGACCAGCCGA*TT* B	4856
R-008399625-000J	3171	1428	GUUGUAACCUGCUGUGAUA	UAUCACAGCAGGUUACAACUU	4859
R-008399625-000J	3171	1428	GUUGUAACCUGCUGUGAUA	B GUUGUAACCUGCUGUGAUA*TT* B	4858
R-008399628-000K	2271	1429	AAGAUUACAAGAAACGGCU	B AAGAUUACAAGAAACGGCU*TT* B	4860
R-008399628-000K	2271	1429	AAGAUUACAAGAAACGGCU	AGCCGUUUCUUGUAAUCUUUU	4861
R-008399631-000S	1183	1430	UUAUGGCAACCAAGAAAGC	B UUAUGGCAACCAAGAAAGC*TT* B	4862
R-008399631-000S	1183	1430	UUAUGGCAACCAAGAAAGC	GCUUUCUUGGUUGCCAUAAUU	4863
R-008399634-000T	2512	1431	UCCAGUUGAUGGGCUGCCA	B UCCAGUUGAUGGGCUGCCA*TT* B	4864
R-008399634-000T	2512	1431	UCCAGUUGAUGGGCUGCCA	UGGCAGCCCAUCAACUGGAUU	4865
R-008399637-000U	1521	132	CCUGUGCAGCUGGAAUUCU	AGAAUUCCAGCUGCACAGGUU	4867
R-008399637-000U	1521	132	CCUGUGCAGCUGGAAUUCU	B CCUGUGCAGCUGGAAUUCU*TT* B	4866
R-008399640-000A	1931	1432	GGGACACAGCAGCAAUUUG	CAAAUUGCUGCUGUGUCCCUU	4869
R-008399640-000A	1931	1432	GGGACACAGCAGCAAUUUG	B GGGACACAGCAGCAAUUUG*TT* B	4868
R-008399643-000B	2468	1433	AUGAUGGAACAUGAGAUGG	B AUGAUGGAACAUGAGAUGG*TT* B	4870
R-008399643-000B	2468	1433	AUGAUGGAACAUGAGAUGG	CCAUCUCAUGUUCCAUCAUUU	4871
R-008399646-000C	3077	1434	UAUUUGGGAUAUGUAUGGG	B UAUUUGGGAUAUGUAUGGG*TT* B	4872
R-008399646-000C	3077	1434	UAUUUGGGAUAUGUAUGGG	CCCAUACAUAUCCCAAAUAUU	4873
R-008399649-000D	2069	1435	CAGCUGCUUUAUUCUCCCA	UGGGAGAAUAAAGCAGCUGUU	4875
R-008399649-000D	2069	1435	CAGCUGCUUUAUUCUCCCA	B CAGCUGCUUUAUUCUCCCA*TT* B	4874

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399652-000K	272	1436	GCUACUCAAGCUGAUUUGA	B GCUACUCAAGCUGAUUUGATT B	4876
R-008399652-000K	272	1436	GCUACUCAAGCUGAUUUGA	UCAUCUAAGCUUGAGUAGCUU	4877
R-008399655-000L	564	1437	UCCCUGAGACAUUAGAUGA	UCAUCUAAUGUCUCAGGGAUU	4879
R-008399655-000L	564	1437	UCCCUGAGACAUUAGAUGA	B UCCCUGAGACAUUAGAUGATT B	4878
R-008399658-000M	437	1438	GUGGAUACCUCCCAAGUCC	GGACUUGGGAGGUAUUCCACUU	4881
R-008399658-000M	437	1438	GUGGAUACCUCCCAAGUCC	B GUGGAUACCUCCCAAGUCCTT B	4880
R-008399661-000U	2206	1439	UAGGAAUGAAGGUGUGGCG	B UAGGAAUGAAGGUGUGGCGTT B	4882
R-008399661-000U	2206	1439	UAGGAAUGAAGGUGUGGCG	CGCCACACCUUCAUUCCUAUU	4883
R-008399664-000V	2187	1440	UGACAGAGUUACUUCACUC	GAGUGAAGUAACUCUGUCAUU	4885
R-008399664-000V	2187	1440	UGACAGAGUUACUUCACUC	B UGACAGAGUUACUUCACUCTT B	4884
R-008399667-000W	325	1441	AGCGGCUGUUAGUCACUGG	CCAGUGACUAACAGCCGCUUU	4887
R-008399667-000W	325	1441	AGCGGCUGUUAGUCACUGG	B AGCGGCUGUUAGUCACUGGTT B	4885
R-008399670-000C	3222	1442	AUGGUUCAGAAUUAAACUU	B AUGGUUCAGAAUUAAACUUTT B	4888
R-008399670-000C	3222	1442	AUGGUUCAGAAUUAAACUU	AAGUUUAAUUCUGAACCAUUU	4889
R-008399673-000D	2024	1443	AACCGAAUUGUUAUCAGAG	B AACCGAAUUGUUAUCAGAGTT B	4890
R-008399673-000D	2024	1443	AACCGAAUUGUUAUCAGAG	CUCUGAUAACAAUUCGGUUUU	4891
R-008399676-000E	1858	1444	GGGUGCCAUUCCACGACUA	B GGGUGCCAUUCCACGACUATT B	4892
R-008399676-000E	1858	1444	GGGUGCCAUUCCACGACUA	UAGUCGUGGAAUGGCACCCUU	4893
R-008399679-000F	1574	1445	AUGAUGGUCUGCCAAGUGG	B AUGAUGGUCUGCCAAGUGGTT B	4894
R-008399679-000F	1574	1445	AUGAUGGUCUGCCAAGUGG	CCACUUGGCAGACCAUCAUUU	4895
R-008399682-000M	1638	78	GGGAAGACAUCACUGAGCC	B GGGAAGACAUCACUGAGCCTT B	4896
R-008399682-000M	1638	78	GGGAAGACAUCACUGAGCC	GGCUCAGUGAUGUCUUCCCUU	4897
R-008399685-000N	1896	1446	CACAUCAGGAUACCCAGCG	B CACAUCAGGAUACCCAGCGTT B	4898
R-008399685-000N	1896	1446	CACAUCAGGAUACCCAGCG	CGCUGGGUAUCCUGAUGUGUU	4899
R-008399688-000P	2207	1447	AGGAAUGAAGGUGUGGCGA	B AGGAAUGAAGGUGUGGCGATT B	4900
R-008399688-000P	2207	1447	AGGAAUGAAGGUGUGGCGA	UCGCCACACCUUCAUUCCUUU	4901
R-008399691-000W	1300	1448	GAAGGUGCUAUCUGUCUGC	B GAAGGUGCUAUCUGUCUGCTT B	4902
R-008399691-000W	1300	1448	GAAGGUGCUAUCUGUCUGC	GCAGACAGAUAGCACCUUCUU	4903
R-008399694-000X	1192	1449	CCAAGAAAGCAAGCUCAUC	GAUGAGCUUGCUUUCUUGGUU	4905
R-008399694-000X	1192	1449	CCAAGAAAGCAAGCUCAUC	B CCAAGAAAGCAAGCUCAUCTT B	4904
R-008399697-000Y	551	1450	CGAGCUGCUAUGUUCCCUG	B CGAGCUGCUAUGUUCCCUGTT B	4906
R-008399697-000Y	551	1450	CGAGCUGCUAUGUUCCCUG	CAGGGAACAUAGCAGCUCGUU	4907
R-008399700-000R	2498	1451	CCUGGUGCUGACUAUCCAG	B CCUGGUGCUGACUAUCCAGTT B	4908
R-008399700-000R	2498	1451	CCUGGUGCUGACUAUCCAG	CUGGAUAGUCAGCACCAGGUU	4909
R-008399703-000S	1305	1452	UGCUAUCUGUCUGCUCUAG	B UGCUAUCUGUCUGCUCUAGTT B	4910
R-008399703-000S	1305	1452	UGCUAUCUGUCUGCUCUAG	CUAGAGCAGACAGAUAGCAUU	4911

TABLE 1c -continued

CTNNB1 siNA Strands Synthesized Antisense sequences are readily identified as being complementary to the target sequence shown.

R Number	Target Site human	SEQ ID NO: 1	Target Sequence	Modified Sequence	SEQ ID NO: 2
R-008399706-000T	1337	1453	AUUGUAGAAGCUGGUGGAA	B AUUGUAGAAGCUGGUGGAA*TT* B	4912
R-008399706-000T	1337	1453	AUUGUAGAAGCUGGUGGAA	UUCCACCAGCUUCUACAAUUU	4913
R-008472717-000G	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaCUAguUCAGUUGCUUUsU B	2147
R-008472717-000G	1870	194	ACGACUAGUUCAGUUGCUU	aaGCAAcUgAAcuagUCGUUsU	6367
R-008472765-000B	1870	194	ACGACUAGUUCAGUUGCUU	aaGCaAcUGAAcuaGUCGUUsU	6368
R-008472765-000B	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaC*U*AguUC*AGUUGCUUU*sU B	2147
R-008488882-000B	1797	5	CUGUUGGAUUGAUUCGAAA	B CUGUUGGAUUGAUUCGAAAUU B	6370
R-008488882-000B	1797	5	CUGUUGGAUUGAUUCGAAA	uuucGAauCaAUCcAaCaGUU	6369
R-008488887-000V	1870	194	ACGACUAGUUCAGUUGCUU	aaGCAAcUgAaCuagUcGUUU	6371
R-008488887-000V	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaC*U*AguUC*AGUUGCUUUU* B	6372
R-008488885-000C	1870	194	ACGACUAGUUCAGUUGCUU	aaGCAAcUgAAcuagUCGUUU	6373
R-008488885-000C	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaC*U*AguUC*AGUUGCUUUU* B	6372
R-008488889-000M	1870	194	ACGACUAGUUCAGUUGCUU	B aCgaC*U*AguUC*AGUUGCUUUU* B	6372
R-008488889-000M	1870	194	ACGACUAGUUCAGUUGCUU	aaGCaAcUGAAcuaGUCGUUU	6374

wherein:
A, C, G, and U = ribose A, C, G or U
a, g, c and u = 2'-deoxy-2'-fluoro A, G, C or U
A, U, C and G = 2'-O-methyl 2'-OMe A, U, C, or G
A, U, C, and *G* = deoxy A, U, C, or G
B = inverted abasic
T = thymidine
I = inosine
s = phosphorothioate linkage

Further Synthesis Steps for Commercial Preparation

Once analysis indicates that the target product purity ahs been achieved after the annealing step, the material is transferred to the tangential flow filtration (TFF) system for concentration and desalting, as opposed to doing this prior to the annealing step.

Ultrafiltration: The annealed product solution is concentrated using a TFF system containing an appropriate molecular weight cut-off membrane. Following concentration, the product solution is desalted via diafiltration using Milli-Q water until the conductivity of the filtrate is that of water.

Lyophilization: The concentrated solution is transferred to a bottle, flash frozen and attached to a lyophilizer. The product is then freeze-dried to a powder. The bottle is removed from the lyophilizer and is now ready for use.

Initial Screening Protocol (96-Well Plate Transfections)

Cell Culture Preparation:

Human hepatoma cell line, HepG2, rhesus kidney epithelial cell line, LLC-MK2 Derivative, and the Huh7 cell line, were grown in modified Eagle's medium. All the culture media were supplemented with 10% fetal bovine serum, 100 μg/mL streptomycin, 100 U/mL penicillin, and 1% sodium bicarbonate.

Transfection and Screening

Cells were plated in all wells of tissue-culture treated, 96-well plates at a final count of 3500 (HepG2 and LLC-MK2 Derivative and Huh7) cells/well in 100 μL of the appropriate culture media. The cells were cultured for overnight after plating at 37° C. in the presence of 5% CO_2.

On the next day, complexes containing siNA and RNAiMax (Invitrogen) were created as follows. A solution of RNAiMax diluted 33-fold in OPTI-MEM was prepared. In parallel, solutions of the siNAs for testing were prepared to a final concentration of 120 mM in OPTI-MEM. After incubation of RNAiMax/OPTI-MEM solution at room temperature for 5 min, an equal volume of the siNA solution and the RNAiMax solution were added together for each of the siNAs.

Mixing resulted in a solution of siNA/RNAiMax where the concentration of siNA was 60 nM. This solution was incubated at room temperature for 20 minutes. After incubation, 20 μL of the solution was added to each of the relevant wells. The final concentration of siNA in each well was 10 nM and the final volume of RNAimax in each well was 0.3 ul.

For low concentration screens, siNAs were transfected at 200, 150, 100 or 75 pM per well. For 12-point dose response curve studies, the siNA series are 6-fold serial dilution starting at 30 nM or 4-fold serial dilution starting at 40 nM. All transfections were set up as multiple biological replicates.

The time of incubation with the RNAiMax-siNA complexes was 24 hours and there was no change in media

between transfection and harvesting for screening and dose response curve studies. For duration assays, the time of incubation with the RNAiMax-siNA complexes was 24, 72, and 120 hours. There was no change in media between transfection and harvesting for 24- and 72-hour time points. Media was replaced with fresh media 72 hours after transfection for 120-hour time point.

Cells-to-Ct and Reverse Transcription Reactions

The culture medium was aspirated and discarded from the wells of the culture plates at the desired time points. The transfected cells were washed once with 50 uL DPBS solution per well. Fifty microliters per well of the Lysis Solution from the TaqMan® Gene Expression Cells-to-CT™ Kit (Applied Biosystems, Cat#4399002) supplemented with DNase I was added directly to the plates to lyse the cells. Five microliters per well of Stop Solution from the same kit was added to the plates to inactivate DNase I 5 minutes later. The lysis plates were incubated for at least 2 minutes at room temperature. The plates can be stored for 2 hours at 4° C., or −80° C. for two months.

Each well of the reverse transcription plate required 10 uL of 2× reverse transcriptase buffer, 1 uL of 20× reverse transcription enzyme and 2 uL of nuclease-free water. The reverse transcription master mix was prepared by mixing 2× reverse transcription buffer, 20× reverse transcription enzyme mix, and nuclease-free water. 13 uL of the reverse transcription master mix was dispensed into each well of the reverse transcription plate (semi-skirted). A separate reverse transcription plate was prepared for each cell plate. A separate reverse transcription plate was prepared for each cell plate. Seven microliters per lysate from the cell lysis procedure described above was added into each well of the reverse transcription plate. The plate was sealed and spun on a centrifuge (1000 rpm for 30 seconds) to settle the contents to the bottom of the reverse transcription plate. The pate was placed in a thermocycler at 37° C. for 60 min, 95° C. for 5 min, and 4° C. until the plate is removed from the thermocycler. Upon removal, if not used immediately, the plate was frozen at −20° C.

For duration assays, a similar protocol was followed, however, the cells were lysed 1, 3, or 5 days after transfection. cDNA was generated using Cells-to-Ct™ Kit (Applied Biosystems).

Quantitative RT-PCR (Taqman)

A series of probes and primers were used to detect the various mRNA transcripts of the genes of CTNNB1 and GAPDH. All Taqman probes and primers for the experiments here-in described were supplied as pre-validated sets by Applied Biosystems, Inc. (see Table 2).

TABLE 2

Probes and primers used to carry out Real-Time RT/PCR (Taqman) for CTNNB1 mRNA analysis.

Species	Gene	ABI Cat. #
Human	CTNNB1	Hs00355045_m1
Human	GAPDH	4310884E
Rhesus	GAPDH	Rh02621745_g1
Mouse	CTNNB1	Mm00483033_m1
Mouse	GAPDH	4352339E

The assays were performed on an ABI 7900 instrument, according to the manufacturer's instructions. A TaqMan Gene Expression Master Mix (provided in the Cells-to-CT™ Kit, Applied Biosystems, Cat #4399002) was used. The PCR reactions were carried out at 50° C. for 2 min, 95° C. for 10 min followed by 40 cycles at 95° C. for 15 secs and 60° C. for 1 minute.

Within each experiment, the baseline was set in the exponential phase of the amplification curve, and based on the intersection point of the baselines with the amplification curve, a Ct value was assigned by the instrument.

Calculations

The expression level of the gene of interest and % inhibition of gene expression (% KD) was calculated using Comparative Ct method:

$$\Delta Ct = Ct_{Target} - Ct_{GAPDH}$$

$$\Delta\Delta Ct(\text{log 2(fold change)}) = \Delta Ct_{(Target\ siNA)} - \Delta Ct(\text{NTO})$$

$$\text{Relative expression level} = 2^{-\Delta\Delta Ct}$$

$$\%\ KD = 100\times(1-2^{-\Delta\Delta Ct})$$

The non-targeting control siNA was, unless otherwise indicated, chosen as the value against which to calculate the percent inhibition (knockdown) of gene expression, because it is the most relevant control.

Additionally, only normalized data, which reflects the general health of the cell and quality of the RNA extraction, was examined. This was done by looking at the level of two different mRNAs in the treated cells, the first being the target mRNA and the second being the normalizer RNA. This allowed for elimination of siNAs that might be potentially toxic to cells rather than solely knocking down the gene of interest. This was done by comparing the Ct for GAPDH in each well relative to the GAPDH Ct for the entire plate.

All calculations of IC_{50}s were performed using R.2.9.2 software. The data were analyzed using the sigmoidal dose-response (variable slope) equation for simple ligand binding. In all of the calculations of the percent inhibition (knockdown), the calculation was made relative to the normalized level of expression of the gene of interest in the samples treated with the non-targeting control (Ctrl siNA) unless otherwise indicated.

The level of protein was quantified using the Bio-Rad VersaDoc Imager according to the protocols of that piece of equipment. A pixel count was performed in each lane using an area of identical size. Each sample was then compared to the appropriate control treated sample and converted to a percent of protein remaining compared to control.

The effects of lead siNAs on CTNNB1 protein level were compared to the effects of the universal control using a two tail Student's T-test to obtain a P value. $P<0.05$ was considered significant.

Results:

The CTNNB1 siNAs were designed and synthesized as described previously. Various siNAs were screened in HepG2, MK2D and Huh7 cells. The log 2(fold change) in CTNNB1 gene expression data upon treatment with various modified CTNNB1 siNAs in human cells is shown in Table 3a. Each screen was performed at 24 hrs. Quantitative RT-PCR was used to assess the level of CTNNB1 mRNA and the data were normalized to the expression level of GAPDH (an ubiquitously expressed 'house-keeping' gene). Each treatment was then normalized against the non-CTNNB1 targeting control.

TABLE 3a

Primary screening data in HepG2 Cells, MK2D Cells and Huh7 Cells (n = 2), recorded as log 2(fold change) in CTNNB1 gene expression.

siNA Duplex ID	HEPG2 Mean ΔΔCt	HEPG2 SD ΔΔCt	MK2D Mean ΔΔCt	MK2D SD ΔΔCt	Huh7 Mean ΔΔCt	Huh7 SD ΔΔCt
R-008362875-000L	5.06	0.28	5.05	0.05	4.10	0.12
R-008362785-000U	4.92	0.24	4.98	0.05	4.05	0.14
R-008362959-000W	4.76	0.11	4.90	0.14	3.99	0.05
R-008363073-000K	4.54	0.16	5.15	0.14	3.98	0.60
R-008308997-000F	4.27	0.32	4.86	0.17	3.97	0.16
R-008362932-000A	4.57	0.50	5.13	0.13	3.97	0.11
R-008362713-000E	4.52	0.02	4.56	0.00	3.96	0.20
R-008362791-000B	5.14	0.21	5.96	0.04	3.94	0.06
R-008362689-000U	5.16	0.20	5.24	0.04	3.94	0.08
R-008362692-000A	0.84	0.06	4.30	0.09	3.94	0.00
R-008363055-000T	4.87	0.16	5.19	0.11	3.86	0.13
R-008309033-000Y	4.39	0.08	5.35	0.15	3.83	0.04
R-008363058-000U	4.20	0.23	4.68	0.22	3.83	0.43
R-008362755-000S	4.18	0.21	4.37	0.08	3.83	0.10
R-008362821-000P	4.29	0.53	4.95	0.11	3.83	0.09
R-008362722-000N	5.37	0.36	5.27	0.19	3.82	0.25
R-008362824-000R	4.36	0.23	4.92	0.06	3.80	0.05
R-008363070-000J	4.51	0.03	4.54	0.01	3.79	0.14
R-008362686-000T	4.84	0.26	5.03	0.08	3.79	0.34
R-008362947-000L	4.45	0.25	4.74	0.04	3.79	0.44
R-008362728-000R	4.66	0.15	4.47	0.12	3.77	0.15
R-008363019-000H	4.75	0.08	5.06	0.05	3.77	0.21
R-008362833-000Z	4.26	0.11	4.61	0.15	3.75	0.09
R-008362812-000F	4.79	0.14	4.93	0.17	3.75	0.37
R-008363064-000B	4.54	0.11	4.87	0.16	3.75	0.49
R-008362980-000V	1.07	0.02	4.48	0.13	3.73	0.09
R-008362992-000E	0.35	0.09	4.24	0.04	3.72	0.00
R-008362872-000K	4.28	0.26	4.77	0.11	3.70	0.02
R-008362677-000J	4.37	0.06	4.60	0.01	3.68	0.08
R-008362878-000M	3.85	0.09	4.54	0.06	3.67	0.01
R-008363031-000Y	4.82	0.26	5.19	0.14	3.65	0.00
R-008363043-000H	4.89	0.27	5.61	0.03	3.65	0.04
R-008362797-000D	4.77	0.03	4.31	0.09	3.63	0.09
R-008362842-000H	3.92	0.00	4.71	0.09	3.63	0.26
R-008362704-000W	4.11	0.16	4.38	0.12	3.60	0.17
R-008362740-000F	0.66	0.11	4.74	0.10	3.60	0.00
R-008362839-000B	4.10	0.22	4.43	0.16	3.57	0.40
R-008362950-000T	4.73	0.08	4.80	0.21	3.55	0.03
R-008363010-000E	4.28	0.12	4.44	0.09	3.51	0.40
R-008362752-000R	3.42	0.03	2.93	0.04	3.50	0.33
R-008362854-000T	0.72	0.26	3.93	0.09	3.49	0.00
R-008362830-000Y	4.59	0.12	4.90	0.04	3.48	0.03
R-008363016-000G	4.14	0.09	4.35	0.02	3.45	0.05
R-008362998-000G	4.29	0.18	4.05	0.12	3.45	0.01
R-008362674-000H	4.55	0.14	4.55	0.01	3.45	0.32
R-008362938-000C	4.27	0.10	5.01	0.22	3.44	0.27
R-008362788-000V	4.11	0.21	4.48	0.09	3.44	0.11
R-008362884-000V	4.11	0.08	4.90	0.13	3.44	0.11
R-008362896-000E	3.91	0.18	3.86	0.06	3.44	0.29
R-008363061-000A	3.84	0.17	4.34	0.01	3.43	0.14
R-008362782-000T	3.73	0.60	5.27	0.13	3.43	0.43
R-008362776-000K	4.08	0.15	4.33	0.15	3.43	0.12
R-008362764-000A	1.00	0.02	4.82	0.14	3.40	0.31
R-008362683-000S	0.85	0.00	4.80	0.12	3.39	0.32
R-008362869-000D	4.65	0.02	4.57	0.06	3.36	0.24
R-008309054-000S	0.88	0.01	4.27	0.08	3.36	0.12
R-008362746-000H	4.22	0.08	4.85	0.07	3.35	0.47
R-008362935-000B	4.51	0.01	5.00	0.14	3.33	0.15
R-008362995-000F	3.52	0.02	4.80	0.02	3.31	0.25
R-008362923-000S	4.16	0.16	4.15	0.08	3.31	0.09
R-008309099-000E	3.72	0.38	4.49	0.03	3.30	0.23
R-008362794-000C	3.97	0.05	3.81	0.05	3.30	0.12
R-008308556-000N	4.54	0.04	4.69	0.19	3.29	0.13
R-008309087-000V	4.04	0.06	4.19	0.14	3.28	0.01
R-008362893-000D	0.66	0.15	4.31	0.05	3.27	0.20
R-008362725-000P	4.20	0.22	4.54	0.23	3.26	0.05
R-008362863-000B	1.04	0.13	4.27	0.09	3.26	0.20
R-008362941-000J	3.93	0.42	4.38	0.16	3.24	0.34
R-008362929-000U	1.45	0.05	3.98	0.08	3.23	0.04
R-008363052-000S	0.43	0.13	4.30	0.07	3.23	0.03
R-008362857-000U	1.73	0.12	3.70	0.08	3.23	0.37
R-008362758-000T	0.70	0.16	4.19	0.10	3.22	0.41

TABLE 3a-continued

Primary screening data in HepG2 Cells, MK2D Cells and Huh7 Cells (n = 2), recorded as log 2(fold change) in CTNNB1 gene expression.

siNA Duplex ID	HEPG2 Mean ΔΔCt	HEPG2 SD ΔΔCt	MK2D Mean ΔΔCt	MK2D SD ΔΔCt	Huh7 Mean ΔΔCt	Huh7 SD ΔΔCt
R-008309048-000J	4.21	0.15	4.23	0.09	3.21	0.14
R-008363004-000X	3.76	0.12	4.55	0.07	3.20	0.43
R-008362719-000G	3.88	0.16	4.61	0.31	3.20	0.09
R-008362671-000G	4.56	0.19	4.71	0.19	3.20	0.06
R-008363049-000K	3.40	0.08	3.01	0.01	3.19	0.22
R-008362902-000Y	3.79	0.29	3.92	0.12	3.19	0.07
R-008363022-000P	4.32	0.21	4.06	0.12	3.14	0.43
R-008362848-000K	3.83	0.04	4.04	0.18	3.09	0.08
R-008362743-000G	4.46	0.16	5.28	0.10	3.09	0.69
R-008362737-000Z	4.41	0.09	4.88	0.24	3.09	0.19
R-008362881-000U	0.77	0.02	4.08	0.10	3.09	0.05
R-008308601-000T	4.21	0.54	4.56	0.02	3.08	0.17
R-008362983-000W	4.09	0.03	4.38	0.00	3.04	0.12
R-008362800-000W	4.42	0.15	4.69	0.06	3.02	0.38
R-008362971-000L	4.10	0.14	4.48	0.05	3.02	0.01
R-008308661-000X	3.68	0.27	4.68	0.21	3.00	0.09
R-008362956-000V	3.89	0.10	3.97	0.19	3.00	0.05
R-008363001-000W	3.97	0.05	4.25	0.06	2.99	0.02
R-008362680-000R	4.22	0.16	4.33	0.12	2.99	0.31
R-008309081-000T	3.97	0.11	4.21	0.01	2.99	0.35
R-008362860-000A	3.39	0.49	3.39	0.01	2.98	0.19
R-008362716-000F	3.87	0.10	4.27	0.19	2.96	0.20
R-008362809-000Z	0.82	0.00	3.79	0.06	2.95	0.18
R-008308562-000W	3.85	0.14	4.09	0.09	2.94	0.01
R-008362989-000Y	4.11	0.07	4.27	0.01	2.94	0.01
R-008309102-000X	3.95	0.05	3.89	0.20	2.90	0.11
R-008362773-000J	3.92	0.23	3.99	0.02	2.89	0.06
R-008362779-000L	4.30	0.20	4.46	0.02	2.85	0.86
R-008362962-000C	3.67	0.08	3.59	0.09	2.82	0.00
R-008362905-000Z	3.33	0.22	3.81	0.08	2.78	0.14
R-008362707-000X	3.53	0.49	4.13	0.15	2.78	0.03
R-008362977-000N	3.29	0.34	4.18	0.01	2.76	0.27
R-008362944-000K	3.56	0.19	3.31	0.13	2.75	0.19
R-008309018-000G	3.53	0.13	4.22	0.07	2.72	0.16
R-008362770-000H	3.92	0.15	3.97	0.01	2.72	0.12
R-008362749-000J	3.29	0.13	3.60	0.02	2.68	0.09
R-008308496-000Y	3.83	0.21	4.49	0.11	2.67	0.41
R-008362836-000A	0.49	0.02	3.94	0.05	2.67	0.81
R-008308667-000Z	4.42	0.01	4.60	0.03	2.65	0.45
R-008362926-000T	4.22	0.08	5.81	0.12	2.60	0.18
R-008362851-000S	4.01	0.80	4.57	0.01	2.53	0.95
R-008363007-000Y	3.23	0.05	2.93	0.15	2.51	0.19
R-008362701-000V	3.94	0.09	4.32	0.13	2.51	0.48
R-008362698-000C	4.10	0.03	4.15	0.13	2.50	0.24
R-008308625-000M	3.77	0.09	3.42	0.24	2.46	0.03
R-008362815-000G	4.27	0.20	4.14	0.09	2.46	0.51
R-008363067-000C	4.14	0.27	5.42	0.16	2.46	0.06
R-008362914-000H	3.78	0.03	3.66	0.06	2.41	0.25
R-008363028-000S	0.86	0.01	4.10	0.07	2.39	0.09
R-008362866-000C	3.42	0.03	3.68	0.01	2.38	0.07
R-008362695-000B	3.06	0.18	2.78	0.06	2.37	0.27
R-008363013-000F	3.56	0.24	3.93	0.11	2.37	0.16
R-008362908-000A	3.20	0.11	2.63	0.01	2.35	0.09
R-008362917-000J	3.01	0.04	3.23	0.05	2.34	0.15
R-008308508-000U	4.18	0.04	4.17	0.02	2.29	0.58
R-008308526-000L	0.59	0.04	3.87	0.09	2.27	0.15
R-008363034-000Z	0.78	0.17	3.95	0.02	2.27	0.30
R-008362827-000S	3.74	0.00	3.12	0.05	2.25	0.09
R-008362968-000E	4.00	0.02	3.46	0.12	2.24	0.62
R-008309006-000X	2.95	0.26	2.59	0.04	2.24	0.07
R-008362734-000Y	4.06	0.02	4.33	0.15	2.21	0.41
R-008362767-000B	4.22	0.05	4.19	0.13	2.13	0.41
R-008362806-000Y	0.73	0.04	2.89	0.02	2.08	0.56
R-008308724-000N	3.34	0.05	3.55	0.01	2.06	0.04
R-008362818-000H	1.49	0.14	3.44	0.05	2.05	0.18
R-008309051-000R	2.38	0.12	2.71	0.06	2.04	0.30
R-008362920-000R	2.82	0.31	3.00	0.13	1.98	0.03
R-008362965-000D	1.24	0.07	2.76	0.00	1.98	0.05
R-008308544-000D	0.53	0.03	3.67	0.07	1.97	0.04
R-008308523-000K	3.15	0.01	3.69	0.12	1.94	0.17
R-008362986-000X	3.24	0.08	3.50	0.13	1.92	0.01
R-008362731-000X	3.62	0.04	2.96	0.09	1.77	1.24

TABLE 3a-continued

Primary screening data in HepG2 Cells, MK2D Cells and Huh7 Cells (n = 2), recorded as log 2(fold change) in CTNNB1 gene expression.

siNA Duplex ID	HEPG2 Mean ΔΔCt	HEPG2 SD ΔΔCt	MK2D Mean ΔΔCt	MK2D SD ΔΔCt	Huh7 Mean ΔΔCt	Huh7 SD ΔΔCt
R-008363046-000J	2.67	0.02	3.94	0.05	1.75	0.07
R-008308733-000X	3.32	0.16	2.63	0.08	1.74	0.15
R-008362911-000G	0.75	0.04	2.74	0.10	1.73	0.26
R-008308706-000W	3.31	0.01	4.09	0.17	1.61	0.09
R-008308709-000X	3.29	0.13	3.95	0.00	1.54	0.30
R-008362890-000C	0.90	0.03	1.03	0.22	1.35	0.34
R-008363025-000R	2.95	0.06	3.05	0.08	1.32	0.81
R-008362953-000U	2.33	0.03	2.67	0.10	1.24	0.10
R-008362899-000F	1.50	0.17	2.77	0.03	1.24	0.13
R-008308697-000B	2.18	0.11	2.19	0.04	1.17	0.02
R-008308589-000S	2.17	0.22	3.42	0.03	1.12	0.08
R-008308634-000W	2.41	0.11	2.66	0.01	1.09	0.11
R-008362710-000D	0.71	0.10	2.17	0.11	1.06	0.18
R-008308493-000X	0.55	0.03	2.12	0.24	1.00	0.05
R-008308703-000V	0.87	0.02	1.69	0.02	0.95	0.13
R-008308568-000Y	2.84	0.14	2.85	0.23	0.63	0.41
R-008362887-000W	0.83	0.14	0.93	0.09	0.33	0.07
R-008362974-000M	0.80	0.07	0.96	0.02	0.23	0.02
R-008363037-000A	0.69	0.09	0.85	0.05	0.12	0.03
R-008363040-000G	−0.07	0.02	−0.22	0.05	−0.19	0.09
R-008362845-000J	−4.37	0.21	−1.50	0.07	−1.25	0.33
R-008362761-000Z	−2.03	0.11	−3.54	0.05	−1.88	0.24
R-008308586-000R	−1.64	0.18	−1.83	0.01	−2.27	0.31
R-008362803-000X	−4.04	0.51	−4.61	0.01	−4.03	0.44

A subset of siNAs from Table 3a having a large log 2(fold change) in the primary screen were rescreened in Huh7 cells. The results are shown in Table 3b.

TABLE 3b

Primary screening data in Huh7 Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	Huh7 Mean ΔΔCt	Huh7 SD ΔΔCt
R-008362791-000B	4.24	0.05
R-008362812-000F	4.17	0.02
R-008362689-000U	4.17	0.01
R-008362722-000N	4.17	0.04
R-008362932-000A	4.07	0.17
R-008363043-000H	4.05	0.02
R-008362875-000L	4.03	0.12
R-008308997-000F	3.99	0.35
R-008362947-000L	3.99	0.18
R-008362821-000P	3.95	0.11
R-008362686-000T	3.94	0.13
R-008363070-000J	3.91	0.08
R-008362824-000R	3.91	0.16
R-008362785-000U	3.88	0.06
R-008363031-000Y	3.88	0.10
R-008363073-000K	3.87	0.19
R-008362782-000T	3.86	0.04
R-008309033-000Y	3.85	0.00
R-008363064-000B	3.84	0.08
R-008362950-000T	3.84	0.05
R-008362959-000W	3.83	0.28
R-008363019-000H	3.82	0.02
R-008362842-000H	3.82	0.14
R-008363058-000U	3.75	0.11
R-008362713-000E	3.73	0.08
R-008362938-000C	3.72	0.05
R-008362755-000S	3.71	0.16
R-008362746-000H	3.59	0.22
R-008362830-000Y	3.56	0.16
R-008362704-000W	3.55	0.11
R-008362839-000B	3.48	0.23
R-008362992-000E	3.45	0.04

TABLE 3b-continued

Primary screening data in Huh7 Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	Huh7 Mean ΔΔCt	Huh7 SD ΔΔCt
R-008363055-000T	3.44	0.26
R-008363061-000A	3.38	0.07
R-008362995-000F	3.35	0.01

The CTNNB1 siNAs were designed and synthesized as described previously. Various siNAs were screened in MK2D cells. The log 2(fold change) in CTNNB1 gene expression data upon treatment with various CTNNB1 siNAs in human cells is shown in Table 3c. Each screen was performed at 24 hrs. Quantitative RT-PCR was used to assess the level of CTNNB1 mRNA and the data were normalized to the expression level of GAPDH (a ubiquitously expressed 'house-keeping' gene). Each treatment was then normalized against the non-CTNNB1 targeting control.

TABLE 3c

Primary screening data in MK2D Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	MK2D MEAN ΔΔCT	MK2D SD ΔΔCT
R-008395722-000P	4.06	0.06
R-008395725-000R	3.78	0.08
R-008395749-000K	4.20	0.02
R-008395752-000S	5.53	0.06
R-008395758-000U	2.41	0.01
R-008395761-000A	5.61	0.08
R-008395767-000C	3.00	0.00
R-008395770-000J	5.53	0.18
R-008395779-000M	4.93	0.16
R-008395785-000V	2.56	0.19
R-008395791-000C	6.76	0.23
R-008395800-000X	2.87	0.07
R-008395827-000T	2.89	0.14
R-008395863-000C	1.65	0.22
R-008395881-000V	3.94	0.05
R-008395887-000X	4.54	0.24
R-008395977-000P	5.63	0.47
R-008395980-000W	4.31	0.27
R-008395995-000G	4.83	0.12
R-008396004-000Y	3.16	0.01
R-008396022-000R	4.83	0.13
R-008396052-000T	4.08	0.08
R-008396061-000B	-0.99	0.08
R-008396067-000D	3.52	0.39
R-008396070-000K	4.84	0.03
R-008396079-000N	4.32	0.04
R-008396103-000Z	3.67	0.07
R-008396106-000A	5.34	0.03
R-008396109-000B	−1.10	0.03
R-008396112-000H	5.19	0.26
R-008396118-000K	3.23	0.01
R-008396136-000C	−2.56	
R-008396142-000K	−0.95	0.10
R-008396148-000M	3.84	0.24
R-008396151-000U	4.60	0.08
R-008396154-000V	4.77	0.07
R-008396172-000M	6.28	0.06
R-008396214-000K	2.82	0.29
R-008396220-000T	5.40	0.05
R-008396223-000U	4.57	0.06
R-008396226-000V	2.27	0.12
R-008396247-000N	3.32	0.08
R-008396250-000V	3.79	1.00
R-008396253-000W	6.42	0.03
R-008396259-000Y	2.14	0.03

TABLE 3c-continued

Primary screening data in MK2D Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	MK2D MEAN ΔΔCT	MK2D SD ΔΔCT
R-008396274-000P	5.39	0.18
R-008396292-000G	3.85	0.05
R-008396295-000H	2.57	0.08
R-008396298-000J	3.00	0.22
R-008396301-000B	2.10	0.24
R-008396304-000C	3.24	0.04
R-008396343-000N	2.49	0.07
R-008396349-000R	4.00	0.08
R-008396379-000T	4.29	0.22
R-008396382-000Z	−0.44	0.02
R-008396388-000B	3.90	0.18
R-008396391-000H	2.23	0.05
R-008396409-000F	3.96	0.26
R-008396415-000N	4.72	0.00
R-008396418-000P	4.48	0.20
R-008396421-000W	3.78	0.14
R-008396457-000A	3.89	0.01
R-008396478-000U	4.62	0.03
R-008396481-000A	4.29	0.14
R-008396529-000A	4.69	0.10
R-008396532-000G	4.46	0.05
R-008396538-000J	5.59	0.05
R-008396544-000S	5.04	0.20
R-008396550-000Z	3.79	0.18
R-008396553-000A	2.32	0.01
R-008396556-000B	2.85	0.07
R-008396559-000C	5.20	0.12
R-008396613-000R	4.92	0.10
R-008396616-000S	2.90	0.01
R-008396619-000T	4.67	0.37
R-008396622-000Z	4.09	0.08
R-008396631-000H	4.28	0.13
R-008396685-000E	4.01	0.10
R-008396694-000N	4.73	0.12
R-008396697-000P	1.56	0.16
R-008396730-000J	2.19	0.02
R-008396730-000J	3.24	0.03
R-008396733-000K	1.43	0.10
R-008396736-000L	5.14	0.04
R-008396742-000U	0.78	0.28
R-008396751-000C	3.62	0.13
R-008396754-000D	4.17	0.05
R-008396793-000P	2.68	0.01
R-008396796-000R	4.94	0.03
R-008396820-000B	4.70	0.08
R-008396826-000D	4.73	0.20
R-008396832-000L	3.63	0.10
R-008396835-000M	2.84	0.85
R-008396838-000N	3.40	0.20
R-008396868-000R	3.99	0.14
R-008396871-000X	4.62	0.12
R-008396874-000Y	4.01	0.02
R-008396898-000T	3.11	0.32
R-008396904-000L	2.46	0.06
R-008396910-000U	2.30	0.03
R-008396919-000X	4.06	0.23
R-008396934-000N	3.37	0.18
R-008396943-000X	3.77	0.01
R-008396949-000Z	3.40	0.07
R-008396958-000H	5.29	0.05
R-008396985-000J	5.25	0.09
R-008396994-000T	3.08	0.40
R-008397015-000U	4.41	0.08
R-008397018-000V	1.73	0.03
R-008397021-000B	5.50	0.05
R-008397024-000C	3.45	0.27
R-008397039-000N	4.21	0.04
R-008397060-000M	1.76	0.08
R-008397069-000R	3.16	0.14
R-008397072-000X	3.94	0.17
R-008397081-000F	3.02	0.02
R-008397108-000M	5.62	0.08
R-008397111-000U	4.08	0.10

TABLE 3c-continued

Primary screening data in MK2D Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	MK2D MEAN ΔΔCT	MK2D SD ΔΔCT
R-008397114-000V	3.50	0.03
R-008397132-000M	3.97	0.16
R-008397138-000P	6.60	0.17
R-008397141-000W	4.58	0.02
R-008397147-000Y	3.73	0.00
R-008397150-000E	6.44	0.11
R-008397153-000F	2.43	0.03
R-008397156-000G	4.04	0.31
R-008397165-000R	3.44	0.01
R-008397166-000S	3.29	0.15
R-008397180-000G	4.46	0.02
R-008397186-000J	5.22	0.06
R-008397237-000R	2.77	0.04
R-008397243-000Y	3.31	0.23
R-008397246-000Z	3.21	0.21
R-008397255-000H	3.77	0.05
R-008397258-000J	1.91	0.02
R-008397306-000P	3.04	0.05
R-008397309-000R	3.16	0.05
R-008397312-000X	5.97	0.13
R-008397315-000Y	4.19	0.33
R-008397342-000Z	3.04	0.06
R-008397345-000A	4.87	0.03
R-008397348-000B	3.62	0.04
R-008397351-000H	2.29	0.15
R-008397354-000J	4.81	0.09
R-008397372-000B	4.40	0.10
R-008397381-000K	3.38	0.08
R-008397384-000L	3.95	0.14
R-008397387-000M	6.11	0.04
R-008397390-000U	3.84	0.16
R-008397396-000W	6.69	0.24
R-008397408-000S	5.61	0.05
R-008397417-000A	3.92	0.49
R-008397420-000G	4.53	0.02
R-008397429-000K	2.91	0.05
R-008397450-000J	2.53	0.05
R-008397459-000M	4.75	0.00
R-008397462-000U	5.28	0.17
R-008397465-000V	4.45	0.18
R-008397468-000W	4.05	0.09
R-008397471-000C	3.22	0.12
R-008397474-000D	4.06	0.21
R-008397519-000C	3.67	0.03
R-008397531-000T	5.94	0.10
R-008397537-000V	4.20	0.07
R-008397540-000B	5.04	0.12
R-008397564-000W	5.95	0.12
R-008397576-000F	3.39	0.05
R-008397579-000G	2.94	0.02
R-008397582-000N	3.95	0.12
R-008397588-000R	4.25	0.07
R-008397591-000X	5.25	0.06
R-008397594-000Y	3.81	0.00
R-008397618-000D	4.58	0.03
R-008397630-000U	3.46	0.15
R-008398645-000E	3.71	0.07
R-008397657-000P	−1.50	0.14
R-008397660-000W	4.85	0.04
R-008397663-000X	2.62	0.03
R-008397666-000Y	3.68	0.09
R-008397669-000Z	2.80	0.78
R-008397702-000U	2.34	0.78
R-008397705-000V	5.13	0.20
R-008397732-000W	3.27	0.01
R-008397735-000X	2.92	0.03
R-008397738-000Y	3.97	0.06
R-008397768-000A	1.62	0.05
R-008397771-000G	4.45	0.17
R-008397774-000H	−1.15	0.02
R-008397777-000J	−1.16	0.09
R-008397783-000S	−1.16	0.03
R-008397807-000X	2.52	0.05

TABLE 3c-continued

Primary screening data in MK2D Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	MK2D MEAN ΔΔCT	MK2D SD ΔΔCT
R-008397828-000R	4.36	0.27
R-008397855-000S	1.94	0.01
R-008397858-000T	4.43	0.17
R-008397882-000T	5.26	0.10
R-008397885-000U	2.53	0.01
R-008397888-000V	3.55	0.03
R-008397933-000Z	4.19	0.22
R-008397966-000C	5.19	0.17
R-008397969-000D	3.35	0.11
R-008397987-000W	4.95	0.16
R-008397990-000C	4.69	0.09
R-008397993-000D	2.17	0.01
R-008397996-000E	−1.14	0.02
R-008398002-000V	3.74	0.10
R-008398020-000M	3.51	0.06
R-008398026-000P	5.64	0.06
R-008398050-000P	3.57	0.10
R-008398056-000S	4.46	0.13
R-008398086-000U	3.65	0.18
R-008398098-000D	3.93	0.04
R-008398119-000H	2.68	0.25
R-008398137-000A	5.16	0.02
R-008398140-000G	3.87	0.14
R-008398140-000G	4.86	0.03
R-008398143-000H	1.74	0.05
R-008398146-000J	3.95	0.12
R-008398149-000K	4.45	0.03
R-008398155-000T	4.37	0.25
R-008398161-000A	3.82	0.05
R-008398176-000L	3.83	0.14
R-008398182-000U	4.52	0.06
R-008398227-000T	6.28	0.06
R-008398239-000C	2.48	0.02
R-008398242-000J	3.81	0.03
R-008398245-000K	5.34	0.23
R-008398275-000M	1.53	0.08
R-008398278-000N	2.71	0.07
R-008398281-000V	4.31	0.14
R-008398326-000U	5.66	0.09
R-008398329-000V	3.83	0.26
R-008398332-000B	4.63	0.02
R-008398362-000D	2.98	0.17
R-008398365-000E	5.06	0.06
R-008398368-000F	4.37	0.03
R-008398374-000N	3.66	0.03
R-008398377-000P	−1.12	0.02
R-008398401-000A	4.57	0.18
R-008398413-000K	3.23	0.07
R-008398419-000M	3.78	0.10
R-008398422-000U	2.63	0.05
R-008398425-000V	3.31	0.02
R-008398428-000W	4.20	0.05
R-008398431-000C	4.82	0.02
R-008398434-000D	2.54	0.06
R-008398437-000E	5.38	0.09
R-008398479-000S	5.16	0.41
R-008398482-000Y	1.55	0.01
R-008398533-000E	3.60	0.01
R-008398539-000G	4.85	0.07
R-008398542-000N	3.64	0.01
R-008398563-000G	5.22	0.27
R-008398566-000H	2.69	0.13
R-008398575-000S	4.79	0.03
R-008398584-000A	2.93	0.04
R-008398590-000H	4.97	0.13
R-008398593-000J	4.52	0.03
R-008398617-000P	3.50	0.01
R-008396647-000S	4.34	0.23
R-008398650-000Y	4.26	0.01
R-008398653-000Z	3.27	0.22
R-008398656-000A	5.36	0.15
R-008398662-000H	5.03	0.42
R-008398665-000J	3.28	0.08

TABLE 3c-continued

Primary screening data in MK2D Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	MK2D MEAN ΔΔCT	MK2D SD ΔΔCT
R-008398668-000K	5.53	0.41
R-008398677-000U	4.94	0.03
R-008398686-000C	1.43	0.14
R-008398701-000E	4.38	0.10
R-008398740-000R	3.54	0.04
R-008398749-000U	2.72	0.18
R-008398782-000C	2.87	0.02
R-008398785-000D	−1.10	0.05
R-008398788-000E	5.61	0.09
R-008398815-000S	3.68	0.14
R-008398821-000Z	5.75	0.00
R-008398830-000H	4.45	0.21
R-008398833-000J	4.61	0.05
R-008398836-000K	3.83	0.01
R-008398863-000L	−1.22	0.03
R-008398866-000M	3.99	0.02
R-008398869-000N	4.06	0.32
R-008398872-000V	4.32	0.18
R-008398875-000W	3.28	0.08
R-008398902-000H	5.58	0.03
R-008398917-000U	2.05	0.13
R-008398923-000B	5.33	0.13
R-008398926-000C	2.22	0.07
R-008398956-000E	3.78	0.15
R-008398962-000M	1.67	0.04
R-008398965-000N	4.87	0.13
R-008398968-000P	3.76	0.21
R-008399031-000H	4.84	0.16
R-008399034-000J	5.71	0.05
R-008399037-000K	2.86	0.08
R-008399049-000V	3.77	0.01
R-008399058-000D	3.88	0.26
R-008399070-000U	5.31	0.00
R-008399091-000M	4.67	0.01
R-008399103-000H	3.75	0.18
R-008399109-000K	5.39	0.14
R-008399133-000K	3.73	0.05
R-008399145-000V	4.27	0.01
R-008399172-000W	3.39	0.07
R-008399175-000X	3.44	0.11
R-008399181-000E	3.37	0.06
R-008399184-000F	6.50	0.11
R-008399187-000G	4.29	0.10
R-008399202-000J	4.09	0.44
R-008399205-000K	2.85	0.21
R-008399208-000L	4.45	0.00
R-008399211-000T	4.08	0.08
R-008399214-000U	4.54	0.01
R-008399226-000D	2.02	0.05
R-008399262-000N	4.13	0.06
R-008399265-000P	3.87	0.03
R-008399268-000R	5.89	0.30
R-008399271-000X	4.44	0.18
R-008399274-000Y	1.24	0.07
R-008399334-000N	2.96	0.22
R-008399343-000X	3.86	0.02
R-008399370-000Y	1.45	0.92
R-008399373-000Z	3.64	0.17
R-008399376-000A	4.79	0.22
R-008399382-000H	4.33	0.06
R-008399394-000T	4.40	0.09
R-008399415-000X	3.21	0.15
R-008399418-000Y	3.33	0.13
R-008399421-000E	3.57	0.21
R-008399436-000R	−1.18	0.08
R-008399439-000S	3.23	0.13
R-008399442-000Y	4.12	0.04
R-008399445-000Z	−0.90	0.12
R-008399451-000G	2.57	0.66
R-008399454-000H	1.55	0.01
R-008399457-000J	2.95	0.00
R-008399481-000J	2.30	0.08
R-008399487-000L	2.81	0.26

TABLE 3c-continued

Primary screening data in MK2D Cells (n = 2), recorded as log 2 (fold change) in CTNNB1 gene expression.

siNA Duplex ID	MK2D MEAN ΔΔCT	MK2D SD ΔΔCT
R-008399526-000H	5.38	0.35
R-008399535-000S	3.24	0.04
R-008399538-000T	4.18	0.28
R-008399568-000V	3.85	0.13
R-008399571-000B	4.51	0.28
R-008399589-000N	2.43	0.07
R-008399592-000V	5.11	0.02
R-008399604-000R	−1.15	0.03
R-008399610-000Y	4.97	0.16
R-008399616-000A	2.18	0.03
R-008399628-000K	4.04	0.00
R-008399634-000T	3.53	0.23
R-008399640-000A	3.90	0.16
R-008399652-000K	4.94	0.03
R-008399655-000L	3.57	0.14
R-008399658-000M	3.74	0.42
R-008399661-000U	3.01	0.06
R-008399664-000V	3.84	0.16
R-008399670-000C	5.25	0.09
R-008399679-000F	3.51	0.29
R-008399682-000M	1.20	0.08

Select high ranking siNAs from Tables 3a & 3b were further analyzed for efficacy and potency in Huh7 cells use dose response curves. The results for these siNAs are shown in Table 4. The potency 50 is the calculated siNA transfection concentration that produces 50% target mRNA knockdown. The IC50 was determined after 24 hour exposure time.

TABLE 4

Dose response data for various siNAs in Huh 7 cells. Calculated maximum ΔΔCt is determined from the dose reponse curve.

siNA Duplex ID	Mean ΔΔCT	SD ΔΔCT	POTENCY 56 (nM)	IC50 (nM)
R-008362824-000R	4.18	0.09	0.02	0.02
R-008362821-000P	4.16	0.01	0.02	0.02
R-008363031-000Y	4.10	0.24	0.01	0.01
R-008362785-000U	4.00	0.31	0.03	0.03
R-008362686-000T	3.98	0.18	0.07	0.06
R-008365782-000T	3.95	0.55	0.05	0.04
R-008362875-000L	3.61	0.36	0.02	0.02
R-008308997-000F	3.59	0.14	0.02	0.02
R-008362722-000N	3.58	0.23	0.03	0.02
R-008362791-000B	3.51	0.89	0.02	0.01
R-008362932-000A	3.48	0.46	0.02	0.02
R-008362689-000U	3.39	0.81	0.02	0.02
R-008363043-000H	3.29	0.01	0.02	0.02
R-008363073-000K	3.21	0.45	0.10	0.08
R-008362812-000F	3.07	0.40	0.03	0.03
R-008362947-000L	3.07	0.28	0.02	0.01
R-008363070-000J	2.91	0.10	0.01	0.01

Additional siNAs from Tables 3a & 3b were further analyzed for efficacy and potency in MK2D cells using dose response curves. The results for these siNAs are shown in Table 5. The potency 50 is the calculated siNA transfection concentration that produces 50% target mRNA knockdown. The IC50 was determined after 24 hour exposure time.

TABLE 5

Dose response data for various siNAs in MK2D cells. Calculated maximum AACt is determined from the dose reponse curve.

siNA Duplex ID	Mean ΔΔCT	SD ΔΔCT	IC50 (nM)
R-008380929-000H002	6.8	0.03	0.004
R-008488882-000B001	5.8	0.01	0.004
R-008488885-000C001	6.1	0.03	0.007
R-008488887-000V001	6.6	0.02	0.004
R-008488889-000M001	6.4	0.23	0.005

Example 2

Determining In Vitro Serum Stability of siNAs

siNAs are reconstituted as 50 μM to 100 μM stock solution with H_2O and added to human serum pre-warmed to 37° C. to a final concentration of 20 μg/mL. The mixture is then incubated at 37° C. for 0, 1 and 2 hours. At the end of each time point, the reactions are stopped by mixing with equal volume of Phenomenex Lysis-Loading Buffer. Oligonucleotides are purified in 96-well format by Phenomenex Solid Phase Extraction and lyophilized until dry with Labconco Triad Lyo-00417. The lyophilized samples are reconstituted in 150 μL of 1 mM EDTA prepared with RNase-free H_2O. The sample solutions re then diluted 5 fold with 1 mM EDTA for liquid chromatography/mass spectrometry (LC/MS) analysis on ThermoFisher Orbitrap. Serum metabolites of the siNAs were determined based on the measured molecular weights.

Example 3

Testing of Cytokine Induction

To assess immunostimulative effects of various siNAs of the invention loaded in lipid nanoparticles (DLinDMA/Cholesterol/S-PEG-C-DMA/DSPC in a 40/48/2/10 ration), C57B1/6 mice are dosed with a single 3 mpk dose of LNP formulated siNAs through tail vein injection. Serum or plasma samples are collected at 3 and 24 hours post-dose. The cytokine and chemokine levels in these samples is measured with the SearchLight IR Cytokine Array from Aushon Biosciences according to the manufacturer's instruction. The cytokines and chemokines measured are IL-1α, IL-1β, IL-6, KC, IL-10, IFNγ, TNF, GMCSF, MIP-1β, MCP-I/JE, and RANTES.

Example 4

Efficacy Studies in Mouse

Mice are dosed IV via tail vein injections with LNP encapsulated siNAs or vehicle control using 2 different 3-week dosing schemes: one 1 mg/kg dose for 3 consecutive days or a single 6 mg/kg dose per week. In some experiments, the mice are co-dosed with sorafenib at a dose of 100 mg/kg BID every day for 3 weeks. Total tumor burden is measured by micro-CT scan imaging. The animals are sacrificed 5 days after the last siNA dose (Day 23), and normal liver and tumor tissues from each animal is collected for RNA purification. Total RNA is purified using RNeasy 96 kit (Qiagen, Cat#74182). cDNA is generated from total RNA using High Capacity cDNA Reverse Transcription Kit (Cat#: 4368813). Quantitative PCR reactions are performed with TaqMan Universal PCR Master Mix (Cat#: 4304437).

Human CTNNB1 TaqMan Gene Expression Assay (Hs00355045_ml) and human GAPDH TaqMan Gene Expression Assay is used to monitor the mRNA level of both transcripts in tumor tissue. Mouse CTNNB1 TaqMan Gene Expression Assay (Mm00483033_ml) and mouse GAPDH TaQMan Gene Expression Assay is used to monitor the mRNA level of both transcripts in liver tissue. The expression level of CTNNB1 is normalized against GAPDH to minimize technical variations.

Example 5

Pharmacodynamic Study in Non-Human Primates

Rhesus macaque monkeys are dosed with a single 2.5 mpk dose of siNA loaded lipid nanoparticles through intravenous infusion. To monitor target mRNA knockdown, liver biopsies are performed at various time points pre- and post-dose with 16T gauge Menghini needles for about 20 mg tissue per animal. Whole blood and serum/plasma is also collected at different time points pre- and post-dose to monitor potential toxicity associated with the treatments. All procedures adhere to the regulations outlined in the USDA Animal Welfare Act (9 CFR, Parts 1, 2 and 3) and the conditions specified in The Guide for Care and Use of Laboratory Animals (ILAR publication, 1996, National Academy Press). Total RNA from the liver biopsy tissue was purified using RNeasy 96 kit (Qiagen. Cat#74182). cDNA was generated from total RNA using High Capacity cDNA Reverse Transcription Kit (Cat#: 4368813). Quantitative PCR reactions were performed with TaqMan Universal PCR Master Mix (Cat#: 4304437). Human CTNNB1 TaqMan Gene Expression Assay (Hs00355045_ml) and rhesus GAPDH TaqMan Gene Expression Assay (Rh02621745_gl) is used to monitor the mRNA level of both transcripts in liver biopsy tissue. The expression level of CTNNB1 is normalized against GAPDH to minimize technical variations.

LNP formulations (DLinDMA/Cholesterol/S-PEG-C-DMA/DSPC in a 40/48/2/10 ratio) comprising the siNA are tested. Log 2(fold change) in CTNNB1 gene expression is determined on days 3, 7, 14, and 28 days post-dosing. Pre-dose CTNNB1 expression levels for the monkey is measured 7 days before the first dosing.

Example 6

Pharmacodynamic Studies in Mouse

Mice were dosed IV via tail vein injections with LNP encapsulated siNAs or vehicle control using a single 0.33 mg/kg. Five animals which received each treatment were sacrificed 2, 7, 14 and 21 days after the siNA dose, and liver tissues from each animal was collected for RNA purification. Total RNA was purified using RNeasy 96 kit (Qiagen, Cat#74182), cDNA was generated from total RNA using High Capacity cDNA Reverse Transcription Kit (Cat#: 4368813). Quantitative PCR reactions were performed with TaqMan Universal PCR Master Mix (Cat#:4304437). Mouse CTNNB1 TaqMan Gene Expression Assay (Mm00483033_ml) and mouse GAPDH TaqMan Gene Expression Assay was used to monitor the mRNA level of both transcripts. The expression level of CTNNB1 was normalized against GAPDH to minimize technical variations. Data is shown in Table 6.

TABLE 6

In vivo screening data in C57Bl/6 mice, recorded as log 2(fold change) in CTNNB1 gene expression.

	Day 2		Day 7		Day 14		Day 21	
	Mouse Mean ΔΔCT	Mouse SD ΔΔCT	Mouse Mean ΔΔCT	Mouse SD ΔΔCT	Mouse Mean ΔΔCT	Mouse SD ΔΔCT	Mouse Mean ΔΔCT	Mouse SD ΔΔCT
PBS	0.00	0.23	0.00	0.21	0.00	0.16	0.00	0.15
R-008380929-000H	2.95	0.27	2.76	0.14	2.33	0.09	1.95	0.33
R-008381104-000W	2.90	0.21	2.43	0.26	1.77	0.30	1.32	0.23
R-008488882-000B	3.21	0.37	2.86	0.33	2.34	0.14	1.93	0.18
R-008488885-000C	2.44	0.13	1.35	0.22	0.59	0.17	0.58	0.31
R-008488887-000V	2.11	0.31	1.76	0.14	0.94	0.42	1.05	0.32
R-008488889-000M	2.31	0.22	1.87	0.35	1.30	0.10	0.86	0.17

Example 7

Pharmacodynamic Study in Non-Human Primates

Rhesus macaque monkeys were dosed with a single 3.34 mg/m^2 of body surface area dose of siNA loaded lipid nanoparticles through intravenous infusion. To monitor target mRNA knockdown, liver biopsies were performed at various time points pre- and post-dose with 16T gauge Menghini needles for about 20 mg tissue per animal. Whole blood and serum/plasma is also collected at different time points pre- and post-dose to monitor potential toxicity associated with the treatments. All procedures adhered to the regulations outlined in the USDA Animal Welfare Act (9 CFR, Parts 1, 2 and 3) and the conditions specified in The Guide for Care and Use of Laboratory Animals (ILAR publication, 1996, National Academy Press). Total RNA from the liver biopsy tissue was purified using RNeasy 96 kit (Qiagen, Cat#74182), cDNA was generated from total RNA using High Capacity cDNA Reverse Transcription Kit (Cat#: 4368813). Quantitative PCR reactions were performed with TaqMan Universal PCR Master Mix (Cat#: 4304437). Human CTNNB1 TaqMan Gene Expression Assay (Hs00355045_ml) and rhesus GAPDH TaqMan Gene Expression Assay (Rh02621745_gl) was used to monitor the mRNA level of both transcripts in liver biopsy tissue. The expression level of CTNNB1 was normalized against GAPDH to minimize technical variations. Data is shown in

Table 7. LNP formulations (DLinDMA/Cholesterol/S-PEG-C-DMA/DSPC in a 40/48/2/10 ratio) comprising the siNA were tested. Log 2(fold change) in CTNNB1 gene expression was determined on days 2 and 7 post-dosing, Pre-dose CTNNB1 expression levels for the monkey is measured 6 days before the first dosing.

TABLE 7

In vivo screening data in rhesus, recorded as log 2(fold change) in CTNNB1 gene expression.

		Day −6		Day 2		Day 7	
LNP	siNA duplex	Rhesus Mean ΔΔCT	Rhesus SD ΔΔCT	Rhesus Mean ΔΔCT	Rhesus SD ΔΔCT	Rhesus Mean ΔΔCT	Rhesus SD ΔΔCT
	PBS	0.00	0.37	0.00	0.24	0.00	0.25
LNP-2	R-008488882-000B	−0.11	0.20	1.41	0.35	0.73	0.56
LNP-4	R-008488885-000C	−0.15	0.13	1.79	0.46	1.64	0.59
LNP-1	R-008488889-000M	0.02	0.29	1.59	0.43	1.44	0.60
LNP-3	R-008380929-000H	−0.10	0.25	1.89	0.17	1.60	0.04

Example 8

Short Interfering Nucleic Acid Lipid Nanoparticle (LNP) Formulations

A. General LNP Process Description for LNP Formulations:

The lipid nanoparticles were prepared by an impinging jet process. The particles were formed by mixing lipids dissolved in alcohol with siNA dissolved in a citrate buffer. The lipid solution contained a cationic lipid, a helper lipid (cholesterol), PEG (e.g. PEG-C-DMA, PEG-DMG) lipid, and DSPC at a concentration of 5-15 mg/mL with a target of 9-12 mg/mL in an alcohol (for example ethanol). The ratio of the lipids had a mole percent range of 25-98 for the cationic lipid with a target of 35-65, the helper lipid had a mole percent range from 0-75 with a target of 30-50, the PEG lipid has a mole percent range from 1-15 with a target of 1-6, and the DSPC had a mole percent range of 0-15 with a target of 0-12. The siNA solution contained one or more siNA sequences at a concentration range from 0.3 to 0.6 mg/mL with a target of 0.3-0.9 mg/mL in a sodium citrate buffered salt solution with pH in the range of 3.5-5. The two solutions were heated to a temperature in the range of 15-40° C., targeting 30-40° C., and then mixed in an impinging jet mixer instantly forming the LNP. The teeID had a range from 0.25 to 1.0 mm and a total flow rate from 10-600 mL/minute. The combination of flow rate and tubing ID had the effect of controlling the particle size of the LNPs between 30 and 200 nm. The LNP suspension was then mixed with a buffered solution at a higher pH with a mixing ratio in the range of 1:1 to 1:3 vol:vol, but targeting 1:2 vol:vol. This buffered solution was at a temperature in the range of 15-40° C., targeting 30-40° C. This LNP suspension was further mixed with a buffered solution at a higher pH and with a mixing ratio in the range of 1:1 to 1:3 vol:vol, but targeting 1:2 vol:vol. The buffered solution was at a temperature in the range of 15-40° C., targeting 30-40° C. The mixed LNPs were held from 30 minutes to 2 hrs prior to an anion exchange filtration step. The temperature during incubating was in the range of15-40° C., targeting 30-40° C. After incubating, the LNP suspension was filtered through a 0.8 um filter containing an anion exchange separation step. This process was tubing IDs ranging from 1 mm ID to 5 mm ID and a flow rate from 10 to 2000 mL/minute. The LNPs were concentrated and diafiltered via an ultrafiltration process where the alcohol was removed and the citrate buffer was exchanged for the final buffer solution such as phosphate buffered saline. The ultrafiltration process used a tangential flow filtration format (TFF). This process used a membrane nominal molecular weight cutoff range from 30-500 KD. The membrane format was hollow fiber or flat sheet cassette. The TFF processes with the proper molecular weight cutoff retained the LNP in the retentate and the filtrate or permeate contained the alcohol; citrate buffer; and final buffer wastes. The TFF process is a multiple step process with an initial concentration to a siNA concentration of 1-3 mg/mL. Following concentration, the LNP suspension was diafiltered against the final buffer for 10-20 volumes to remove the alcohol and perform buffer exchange. The material was then concentrated an additional 1-3 fold. The final steps of the LNP process were to sterile filter the concentrated LNP solution and vial the product.

Analytical Procedure:

1) siNA Concentration

The siNA duplex concentrations were determined by Strong Anion-Exchange High-Performance Liquid Chromatography (SAX-HPLC) using Waters 2695 Alliance system (Water Corporation, Milford, Mass.) with a 2996 PDA detector. The LNPs, otherwise referred to as RNAi Delivery Vehicles (RDVs), were treated with 0.5% Triton X-100 to free total siNA and analyzed by SAX separation using a Dionex BioLC DNAPac PA 200 (4×250 mm) column with UV detection at 254 nm. Mobile phase was composed of A: 25 mM $NaClO_4$, 10 mM Tris, 20% EtOH, pH 7.0 and B: 250 mM $NaClO_4$, 10 mM Tris, 20% EtOH, pH 7.0 with a liner gradient from 0-15 mm and a flow rate of 1 ml/minute. The siNA amount was determined by comparing to the siNA standard curve.

2) Encapsulation Rate

Fluorescence reagent SYBR Gold was employed for RNA quantitation to monitor the encapsulation rate of RDVs. RDVs with or without Triton X-100 were used to determine the free siNA and total siNA amount. The assay is performed using a SpectraMax M5e microplate spectrophotometer from Molecular Devices (Sunnyvale, Calif.). Samples were excited at 485 nm and fluorescence emission was measured at 530 nm. The siNA amount is determined by comparing to an siNA standard curve.

$$\text{Encapsulation rate} = (1 - \text{free siNA}/\text{total siNA}) \times 100\%$$

3) Particle Size and Polydispersity

RDVs containing 1 μg siNA were diluted to a final volume of 3 ml with 1×PBS. The particle size and polydispersity of the samples was measured by a dynamic light scattering method using Zeta PALS instrument (Brookhaven Instruments Corporation, Holtsville, N.Y.). The scattered intensity was measured with He—Ne laser at 25° C. with a scattering angle of 90°.

4) Zeta Potential Analysis

RDVs containing 1 μg siNA were diluted to a final volume of 2 ml with 1 mM Tris buffer (pH 7.4). Electrophoretic mobility of samples was determined using ZetaPALS instrument (Brookhaven Instruments Corporation, Holtsville, N.Y.) with electrode and He—Ne laser as a light source. The Smoluchowski limit was assumed in the calculation of zeta potentials.

5) Lipid Analysis

Individual lipid concentrations were determined by Reverse Phase High-Performance Liquid Chromatography (RP-HPLC) using Waters 2695 Alliance system (Water Corporation, Milford, Mass.) with a Corona charged aerosol detector (CAD) (ESA Biosciences, Inc, Chelmsford, Mass.). Individual lipids in RDVs were analyzed suing an Agilent Zorbax SB-C18 (50×4.6 mm, 1.8 μm particle size) column with CAD at 60° C. The mobile phase was composed of A: 0.1% TFA in H_2O and B: 0.1% TFA in IPA. The gradient changed from 60% mobile phase A and 40% mobile phase B from time 0 to 40% mobile phase A and 60% mobile phase B at 1.00 min; 40% mobile phase A and 60% mobile phase B from 1.00 to 5.00 min; 40% mobile phase A and 60% mobile phase B from 5.00 min to 25% mobile phase A and 75% mobile phase B at 10.00 min; 25% mobile phase A and 75% mobile phase B from 10.00 min to 5% mobile phase A and 95% mobile phase B at 15.00 min; and 5% mobile phase A and 95% mobile phase B from 15.00 to 60% mobile phase A and 40% mobile phase B at 20.00 min with a flow rate of 1 ml/minute. The individual lipid concentration was determined by comparing to the standard curve with all the lipid components in the RDVs with a quadratic curve fit. The molar percentage of each lipid was calculated based on its molecular weight.

B. General LNP Preparation for Various Formulations in Table 11

siNA nanoparticle suspensions in Table 11 were prepared by dissolving siNAs and/or carrier molecules in 20 mM sodium citrate buffer (pH 5.0) at a concentration of about 0.40 mg/mL. Lipid solutions were prepared by dissolving a mixture of cationic lipid (e.g., (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine, see structure in Table 12), DSPC, Cholesterol, and PEG-DMG (ratios shown in Table 11) in absolute ethanol at a concentration of about 8 mg/mL. The nitrogen to phosphate ratio was approximated to 6:1.

Nearly equal volumes of siNA/carrier and lipid solutions were delivered with two FPLC pumps at the same flow rates to a mixing T connector. A back pressure valve was used to adjust to the desired particle size. The resulting milky mixture was collected in a sterile glass bottle. This mixture was then diluted with an equal volume of citrate buffer, followed by equal volume of PBS (pH 7.4), and filtered through an ion-exchange membrane to remove any free siNA/carrier in the mixture. Ultra filtration against PBS (7.4)) was employed to remove ethanol and to exchange buffer. The final LNP was obtained by concentrating to the desired volume and sterile filtered through a 0.2 μm filter. The obtained LNPs were characterized in term of particle size, Zeta potential, alcohol content, total lipid content, nucleic acid encapsulated, and total nucleic acid concentration.

LNP Manufacture Process

In a non-limiting example, LNPs were prepared in bulk as follows. The process consisted of (1) preparing a lipid solution; (2) preparing an siNA/carrier solution; (3) mixing/particle formation; (4) incubation; (5) dilution; (6) ultrafiltration and concentration.

1. Preparation of Lipid Solution

2L glass reagent bottles and measuring cylinders were depyrogenated. The lipids were warmed to room temperature. Into the glass reagent bottle was transferred 8.0 g of (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine with a pipette and 1.2 g of DSPC, 3.5 g of Cholesterol, 0.9 g of PEG-DMG were added. To the mixture is added 1L of ethanol. The reagent bottle was placed in heated water bath, at a temperature not exceeding 50° C. The lipid suspension was stirred with a stir bar. A thermocouple probe was put into the suspension through one neck of the round bottom flask with a sealed adapter. The suspension was heated at 30-40° C. until it became clear. The solution was allowed to cool to room temperature.

2. Preparation of siNA/Carrier Solution

Into a sterile container (Corning storage bottle) was weighed 0.4 g times the water correction factor (approximately 1.2) of siNA powder. The siNA was transferred to a depyrogenated 2 L glass reagent bottle. The weighing container was rinsed 3× with citrate buffer (20 mM, pH 5.0) and the rinses were placed into the 2 L glass bottle, QS with citrate buffer to 1 L. The concentration of the siNA solution was determined with a UV spectrometer using the following procedure. 20 μL was removed from the solution, diluted 50 times to 1000 μL, and the UV reading recorded at A260 nm after blanking with citrate buffer. This was repeated. Note, if the readings for the two samples are consistent, an average can be taken and the concentration calculated based on the extinction coefficients of the siNAs. If the final concentration is out of the range of 0.40±0.01 mg/mL, the concentration can be adjusted by adding more siNA/carrier powder, or adding more citrate buffer. This process can be repeated for the second siNA, if applicable.

When the siNA/carrier solution comprised a single siNA duplex instead of a cocktail of two or more siNA duplexes and/or carriers, then the siNA/carrier was dissolved in 20 mM citrate buffer (pH 5.0) to give a final concentration of 0.4 mg/mL.

The lipid and ethanol solutions were then sterile filtered through a Pall Acropak 20 0.8/0.2 μm sterile filter PN 12203 into a depyrogenated glass vessel using a Master Flex Peristaltic Pump Model 7520-40 to provide a sterile starting material for the encapsulation process. The filtration process was run at an 80 mL scale with a membrane of 20 cm^2. The flow rate was 280 mL/minute. This process can be scaled by increasing the tubing diameter and the filtration area.

3. Particle Formation—Mixing Step

Using a two-barrel syringe driven pump (Harvard 33 Twin Syringe), the sterile lipid/ethanol solution and the sterile siNA/carrier or siNA/carrier cocktail/citrate buffer (20 mM citrate buffer, pH 5.0) solutions were mixed in a 0.5 mm ID T-mixer (Mixing Stage 1) at equal, or nearly equal, flow rates. The resulting outlet LNP suspension contained 40-50 vol % ethanol. To obtain a 45 vol % ethanol outlet suspension, the sterile lipid/ethanol and the sterile siNA/carrier or siNA/carrier cocktail/citrate buffer solutions were mixed at flow rates of 54 mL/min and 66 mL/min, respectively, such that the total flow rate of the mixing outlet is 120 mL/min.

4. Dilution

The outlet stream of Mixing Stage I was fed directly into a 4 mm ID T-mixer (Mixing Stage II), where it was diluted with a buffered solution at a higher pH (20 mM sodium citrate, 300 mM sodium chloride, pH 6.0) at a ratio of 1:1 vol:vol %. This buffered solution was at a temperature in the range of 30-40° C. and was delivered to the 4 mm T-mixer via a peristaltic pump (Cole Parmer MasterFlex L/S 600 RPM) at a flow rate of 120 mL/min.

The outlet stream of Mixing Stage II was fed directly into a 6 mm ID T-mixer (Mixing Stage III), where it was diluted with a buffered solution at higher pH (PBS, pH 7.4) at a ratio of 1:1 vol:vol %. This buffered solution was at a temperature in the range of 15-25° C., and was delivered to the 6 mm T-mixer via peristaltic pump (Cole Parmer MasterFlex L/S 600 RPM) at a flow rate of 240 mL/min.

5. Incubation and Free siNA Removal

The outlet stream of Mixing Stage III was held after mixing for 30 minute incubation. The incubation was conducted at temperature of 35-40° C. and the in-process suspension was protected from light. Following incubation, free (un-encapsulated) siNA was removed via anion exchange with Mustang Q chromatography filters (capsules). Prior to use, the chromatography filters were pretreated sequentially with flushes of 1N NaOH, 1M NaCl, and a final solution of 12.5 vol % ethanol in PBS. The pH of the final flush was checked to ensure pH<8. The incubated LNP stream was then filtered via Mustang Q filters via peristaltic pump (Cole Parmer MasterFlex L/S 600 RPM) at flow rate of approximately 100 mL/min. The filtered stream was received into a sterile glass container for ultrafiltration and concentration as follows.

6. Ultrafiltration, Concentration and Sterile Filtration

The ultrafiltration process is a timed process and the flow rates must be monitored carefully. This is a two step process: the first is a concentration step taking the diluted material and concentrating approximately 8-fold, to a concentration of approximately 0.3-0.6 mg/mL siNA.

In the first step, a ring-stand with a ultrafiltration membrane 100 kDa PES (Spectrum Labs) installed was attached to a peristaltic pump (Spectrum KrosFloII System). 9.2 L of sterile distilled water was added to the reservoir; 3 L was drained to waste and the remainder was drained through permeate to waste. 5.3 L of 0.25 N sodium hydroxide was added to the reservoir with 1.5 L drained to waste and 3.1 L drained through permeate to waste. The remaining sodium hydroxide was held in the system for sanitization (at least 10 minutes), and then the pump was drained. 9.2 L of 70 (v/v) % isopropyl alcohol was added to the reservoir with 1.5 L drained to waste and the remainder drained through permeate to waste. 6 L of conditioning buffer (12.5% ethanol in phosphate buffered saline was added with 1.5 L drained to waste and the remained drained through the permeate until the waste was of neutral pH (7-8). A membrane flux value was recorded, and the pump was then drained.

The diluted LNP solution was placed into the reservoir to the 1.1 L mark. The pump was turned on at 2.3 L/min. After 5 minutes of recirculation, the permeate pump was turned on at 62.5 mL/min and the liquid level was constant at approximately 950 mL in the reservoir. The diluted LNP solution was concentrated from 9.8 L to 1.1 L in 140 minutes, and the pump was paused when all the diluted LNP solution has been transferred to the reservoir.

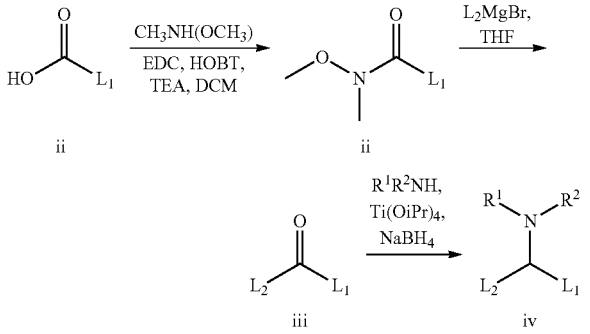
The second step was a diafiltration step exchanging the ethanol/aqueous buffer to phosphate buffered saline. During this step, approximately, 10-20 diafiltration volumes of phosphate buffered saline were used. Following diafiltration, a second concentration was undertaken to concentrate the LNP suspension 3-fold to approximately 1-1.5 mg/mL siRNA. The concentrated suspension was collected into sterile, plastic PETG bottles. The final suspension was then filtered sequentially via Pall 0.45 um PES and Pall 0.2 um PES filters for terminal sterilization prior to vial filling.

The obtained LNPs were characterized in terms of particle size. Zeta potential, alcohol content, total lipid content, nucleic acid encapsulated, and total nucleic acid concentration.

C. Synthesis of Novel Cationic Lipids

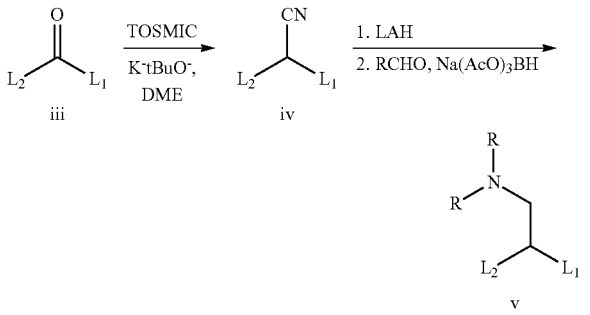
Synthesis of the novel cationic lipids is a linear process starting from lipid acid (i). Coupling to the N,O-dimethyl hydroxylamine gives the Weinreb amide ii. Grignard addition generates ketone iii. Titanium mediated reductive amination gives final products of type iv.

GENERAL SCHEME 1



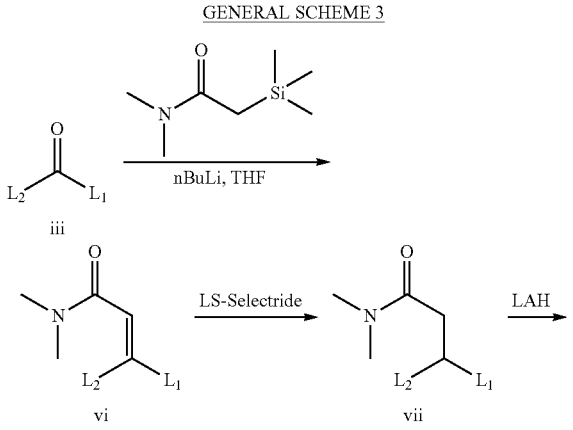
Synthesis of the single carbon homologated cationic lipids v is a linear process starting from lipid ketone (iii). Conversion of the ketone to the nitrile (iv) is accomplished via treatment with TOSMIC and potassium tert-butoxide. Reduction of the nitrile to the primary amine followed by reductive amination provides final cationic lipids v.

GENERAL SCHEME 2



Synthesis of two carbon homologated cationic lipids viii is a linear process starting from lipid ketone (iii). Conversion of the ketone to the α,β-unsaturated amide vi is accomplished under Peterson conditions. Conjugate reduction of the α,β-unsaturation is performed using LS-Selectride to give amide vii. Reduction of the amide with lithium aluminum hydride provides final cationic lipids viii.

GENERAL SCHEME 3



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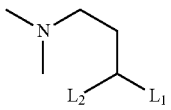
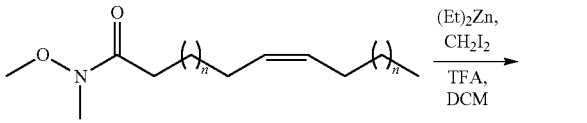


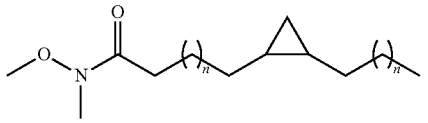
viii

Cyclopropyl containing lipids are prepared according to General Scheme 4. Unsaturated Weinreb amides ii are subjected to Simmons-Smith cyclopropanation conditions to give cyclopropyl containing Weinreb amides ix. These are carried on to final products as outlined in General Schemes 1-3.

GENERAL SCHEME 5



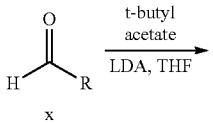
ii



ix

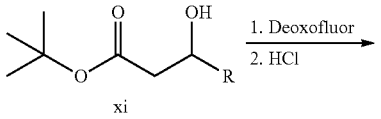
Synthesis of allylic amine cationic lipids xv is a linear process starting with aldehyde x. Addition of t-butyl aceate generates β-hydroxy ester xi. Conversion of the hydroxyl functionality to a fluoro group followed by acid treatment generates β-fluoro acid xii. Conversion of the acid to the Weinreb amide followed by Grignard addition gives the β-fluoro ketone xiv. Reductive amination results in simultaneous elimination to generate the desired allylic amine xv.

GENERAL SCHEME 5

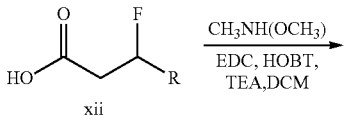


x

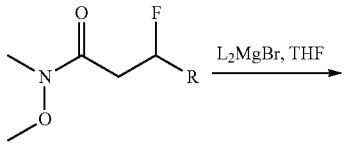
-continued



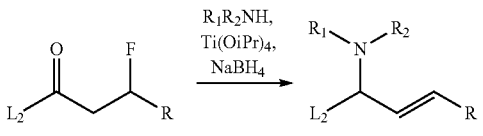
xi



xii

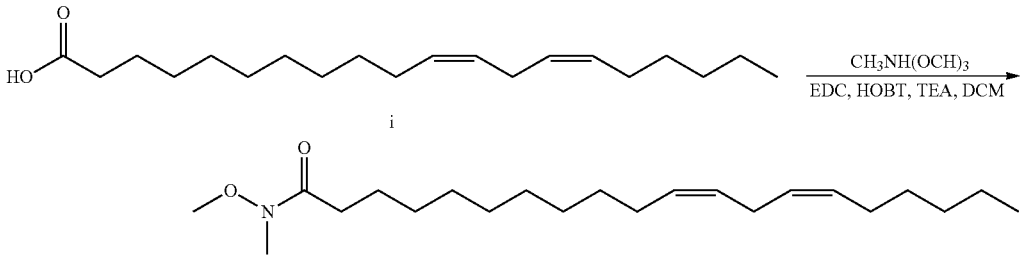


xiii



xiv xv

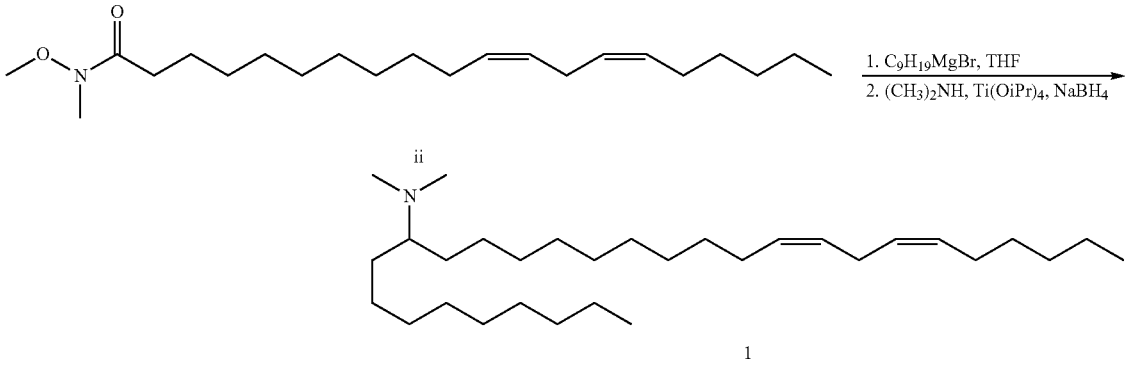
20,23 -nonacosadien-10-amine, N,N-dimethyl, (20Z,23Z) (Compound 1)



i ii

11,14-Eicosadienoic acid (11Z,14Z)-(50 g, 162 mmol), N,O-Dimethylhydroxylamine hydrochloride (31.6 g, 324 mmol), HOAt (44.1 g, 324 mmol). Et_3N (45.2 mL, 324 mmol), and EDC (62.1 g, 324 mmol) were mixed in DCM (810 mL) and stirred overnight at ambient temperature. Reaction was then washed 5×700 mL water, then washed 1× 600 mL 1M NaOH, dried with sodium sulfate, filtered through celite and evaporated to obtain 53.06 g (93%) 11,14-eicosadienamide, N-methoxy-N-methyl, (11Z,14Z) as a clear golden oil.

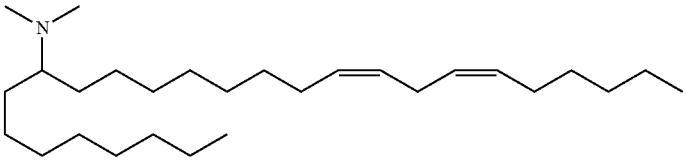
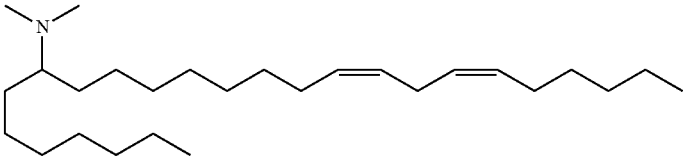
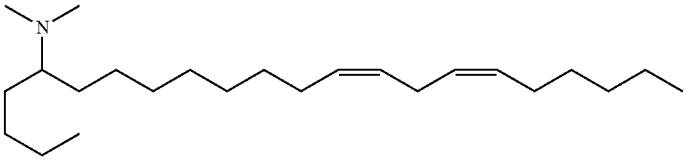
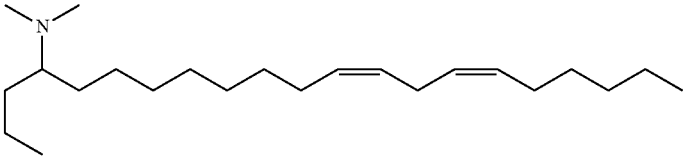
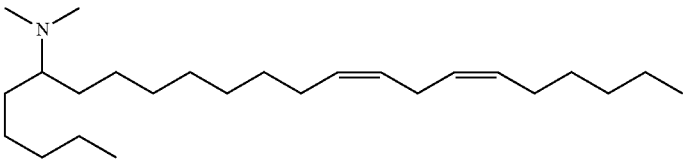
^{1}H NMR (400 MHz, $CDCl_3$) δ 5.35 (m, 4H), 3.68 (s, 3H), 3.18 (s, 3H), 2.77 (m, 2H), 2.41 (t, J=7 Hz, 2H), 2.05 (m, 4H), 1.63 (m, 2H), 1.40-1.26 (m, 18H), 0.89 (t, J=7 Hz, 3H).



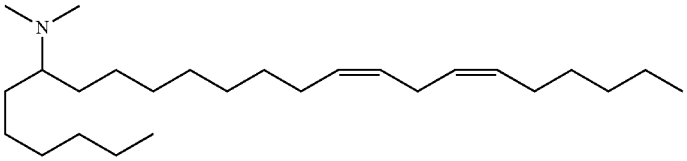
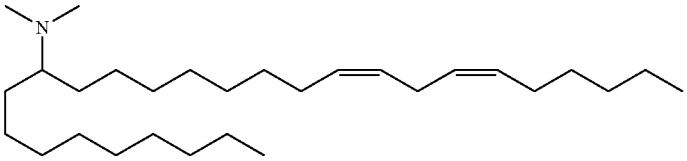
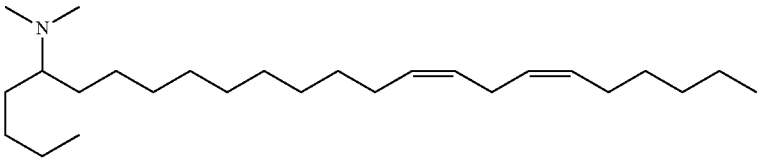
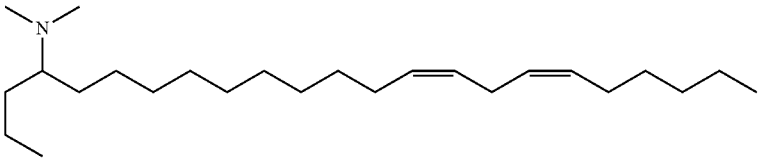
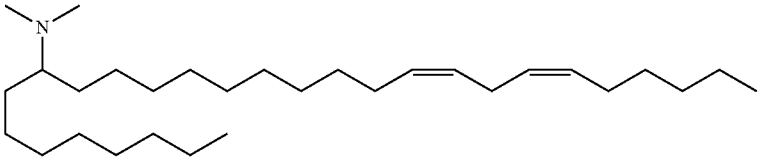
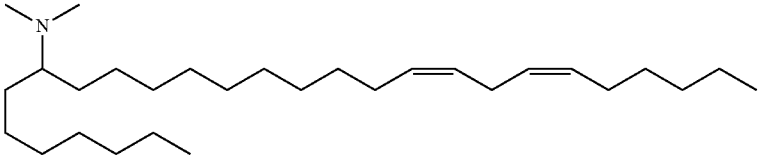
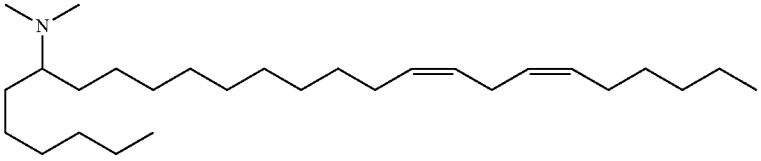
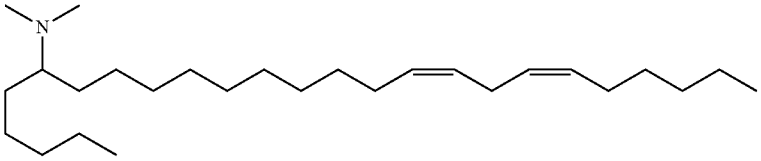
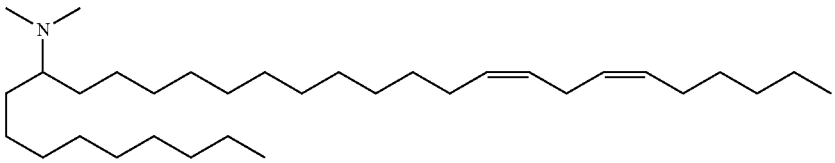
1

11,14-eicosadienamide, N-methoxy-N-methyl-, (11Z, 14Z)-1 (4 g, 11.38 mmol) was dissolved in dry THF (50.0 ml) in a 250 mL flask then 1 M nonylmagnesium bromide (22.76 ml, 22.76 mmol) was added under nitrogen at ambient temperature. After 10 min, the reaction was slowly quenched with excess sat. aq NH_4Cl. The reaction was washed into a separatory funnel with hexane and water, shaken, the lower aqueous layer discarded, the upper layer dried with sodium sulfate, filtered, and evaporated to give crude ketone as a golden oil. To the above crude ketone was added dimethylamine (2 M in THF) (14.22 ml, 28.4 mmol) followed by $Ti(O\text{-}i\text{-}Pr)_4$ (6.67 ml, 22.76 mmol) and let stir overnight. The next day, added EtOH (50 ml) followed by $NaBH_4$ (0.646 g, 17.07 mmol). After 5 min of stirring, directly injected entire reaction onto a 40 g silica column that was in line with a 330 g silica column. eluted 10 min 100% DCM, then 30 min 0-15% MeOH/DCM, collected 20,23-nonacosadien-10-amine, N,N-dimethyl-, (20Z,23Z) (1) (2.45 g, 5.47 mmol, 48.1% yield) as a faintly golden oil. ^1H NMR (400 MHz, $CDCl_3$) δ 5.35 (m, 4H), 2.78 (m, 2H), 2.23 (m, 1H), 2.21 (s, 6H), 2.05 (m, 4H), 1.45-1.16 (m, 38H), 0.89 (m, 6H). HRMS calcd for C31H61N 448.4877, found 448,4872.

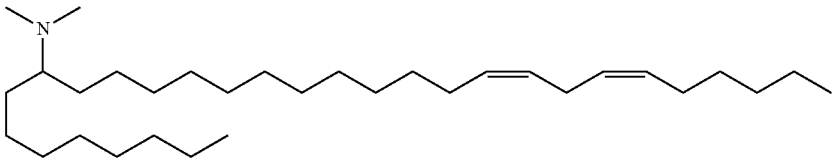
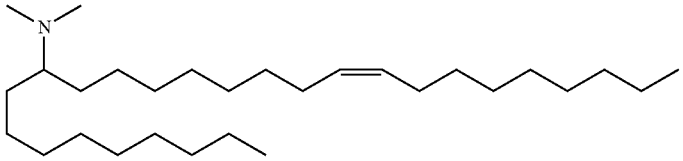
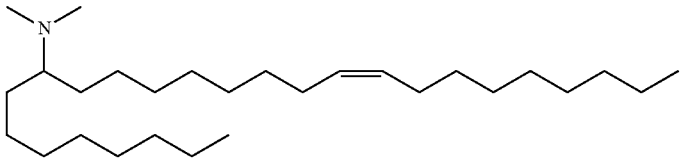
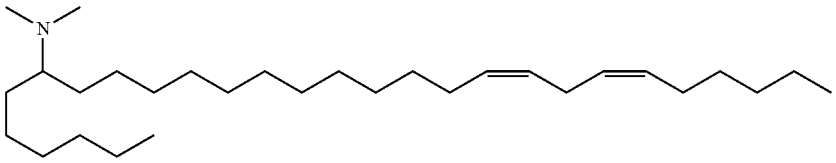
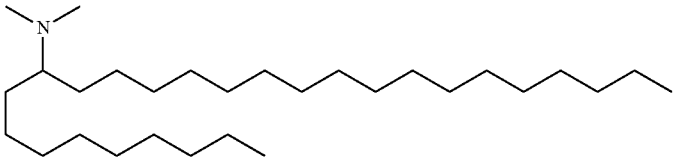
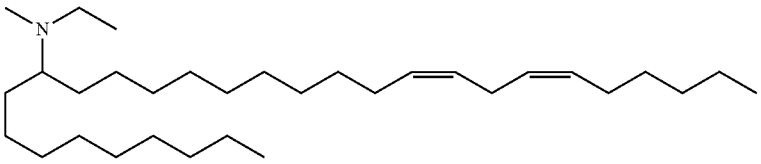
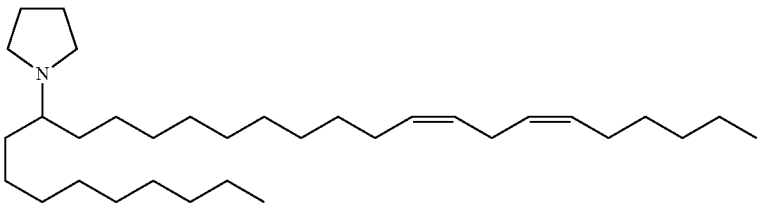
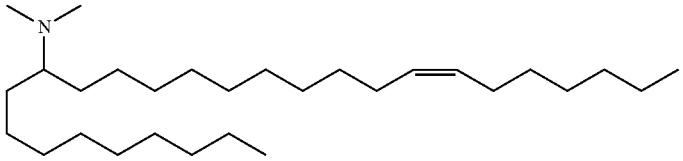
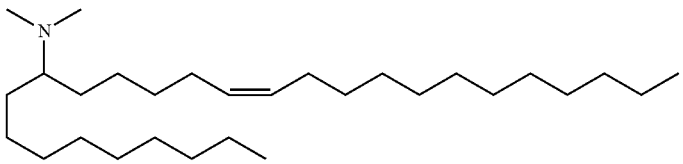
Compounds 2-30 are novel cationic lipids and were prepared according to the General Scheme I above.

Compound	Structure	HRMS
2		calcd C28H56N 406.4407, found 406.4405.
3		calcd C27H54N 392.4251, found 392.4250.
4		calcd C24H48N 350.3781, found 350.3770.
5		calcd C23H46N 336.3625, found 336.3613.
6		calcd C25H50N 364.3938, found 364.3941.

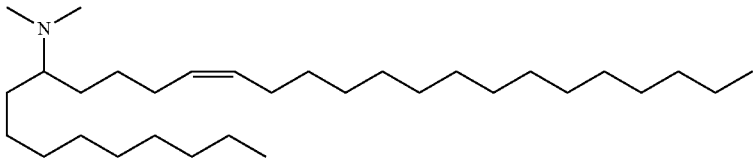
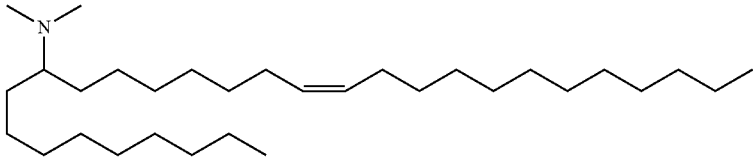
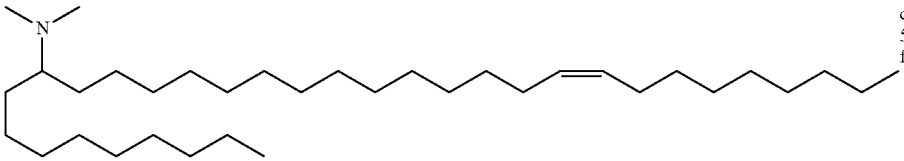
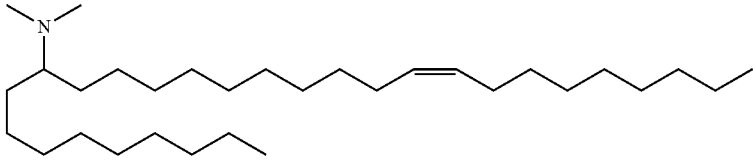
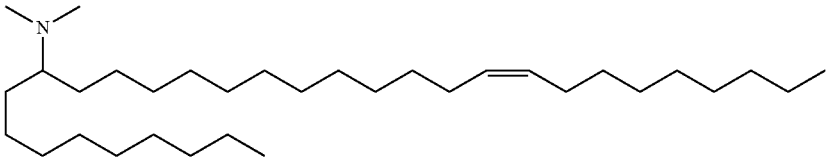
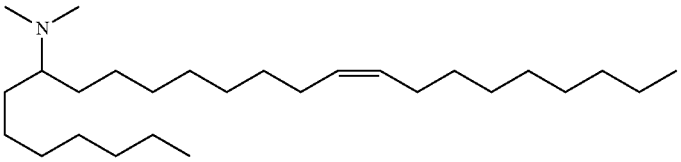
-continued

Compound	Structure	HRMS
7		calcd C26H52N 378.4094, found 378.4081.
8		calcd C29H58N 420.4564, found 420.4562.
9		calcd C26H52N 378.4094, found 378.4089.
10		calcd C25H50N 364.3938, found 364.3931.
11		calcd C30H60N 434.4720, found 434.4717.
12		calcd C29H58N 420.4564, found 420.4561.
13		calcd C28H56N 406.4407, found 406.4404.
14		calcd C27H54N 392.4251, found 392.4245.
15		calcd C33H66N 476.5190, found 476.5196.

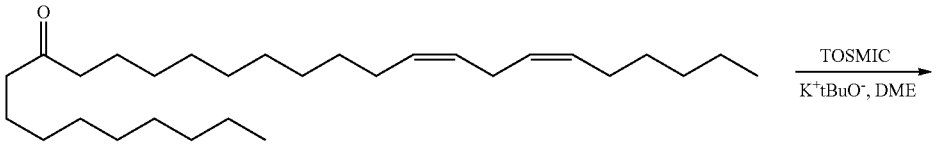
-continued

Compound	Structure	HRMS
16		calcd C32H64N 462.5033, found 462.5045.
17		calcd C29H59N 422.4720, found 422.4726.
18		calcd C28H57N 408.4564, found 408.4570.
19		calcd C30H59N 434.4720, found 434.4729.
20		calcd C29H61N 424.4877, found 424.4875.
21		calcd C32H64N 462.5033, found 462.5023.
22		calcd C33H64N 474.5033, found 474.5033.
23		calcd C29H60N 422.4720, found 422.4716.
24		calcd C29H60N 422.4720, found 422.4718.

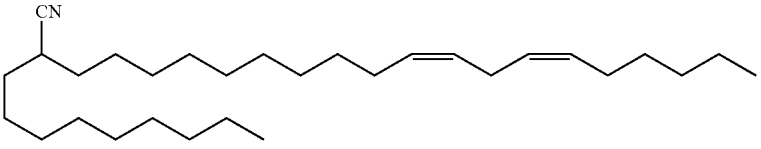
-continued

Compound	Structure	HRMS
25		calcd C31H64N 450.5033, found 450.5031.
26		calcd C31H64N 450.5033, found 450.5034.
27		calcd C35H72N 506.5659, found 506.5635.
28		calcd C31H64N 450.5033, found 450.5037.
29		calcd C33H68N 478.5346, found 478.5358.
30		calcd C27H56N 394.4407, found 394.4407.

(12Z,15Z)-N,N-dimethyl-2-nonylhenicosa-12,15-dien-1-amine (Compound 31)

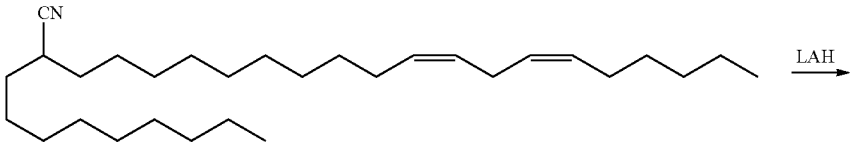


iii

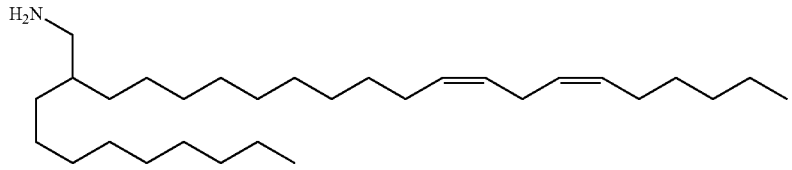


iv

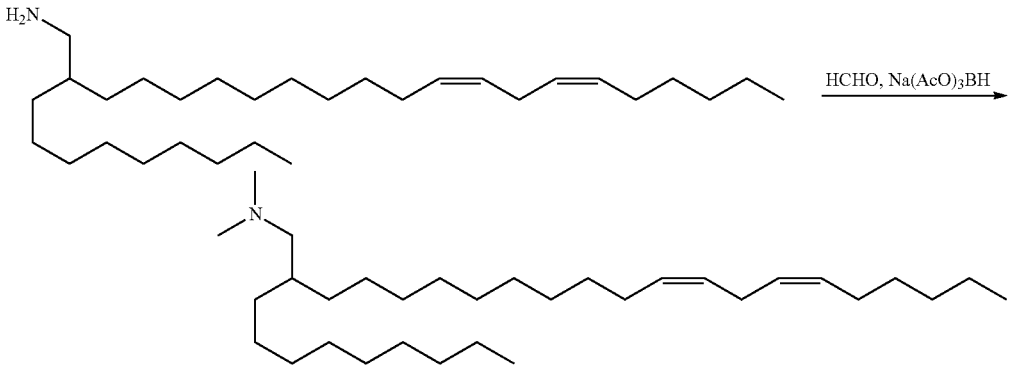
A solution of keton iii (4.0 g, 9.55 mmol), TOSMIC (2.4 g, 12.4 mmol) in dimethoxyethane (45 mL) was cooled to 0° C. and treated with potassium tert-butoxide (19.1 mmol, 19.1 mL of a 1M solution in tBuOH). After 90 minutes, the reaction was partitioned between hexanes and water. The organics were washed with water, dried over sodium sulfate, filtered and evaporated in vacuo. This material was purified by flash chromatography (0-5% EtOAc/hexanes) to give desired product (containing ~20% of s.m.). This mixture was carried into next step as is. LC/MS (M+H)=430.6.



iv



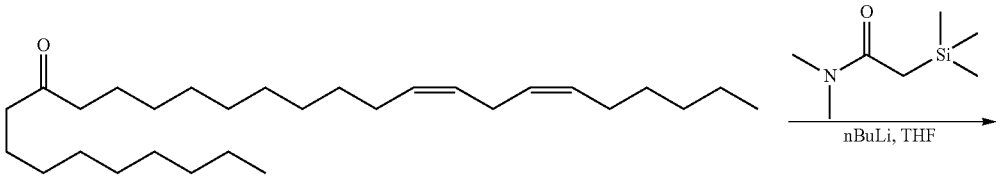
Lithium aluminum hydride (23.9 mmol, 23.9 mL or a 1M solution in THF) was added directly to nitrile iv (3.42 g, 8 mmol) at ambient temperature and the reaction was stirred for 20 minutes. The reaction was diluted with 100 mL THF, cooled to 0° C. and carefully quenched with sodium sulfate decahydrate solution. The solids were filtered off and washed with THF. The filtrate was evaporated in vacuo and carried directly into next reaction crude. LC/MS (M+H)=434.6.



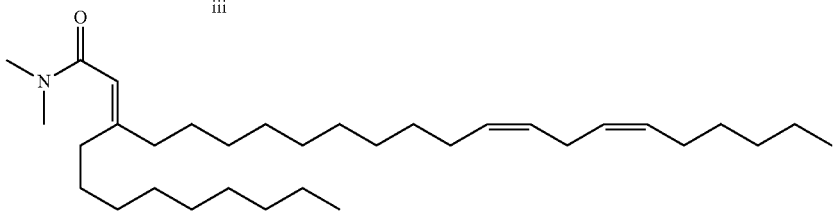
31

A solution of primary amine (3.45 g, 6.2 mmol) in dichloroethane (100 mL) was treated with formaldehyde (1.6 mL, 21.7 mmol) followed by sodium triacetoxyborohydride (6.6 g, 31 mmol). After 5 minutes, the reaction was partitioned between dichloromethane and 1N NaOH. The organics were dried over sodium sulfate, filtered and evaporated in vacuo. The crude mixture was purified by reverse phase preparative chromatography (C8 column) to provide (12Z,15Z)-N,N-dimethyl-2-nonylhenicosa-12,15-dien-1-amine. ^{1}H NMR HRMS calc'd 462.5033, found 462.5026. ^{1}H NMR (400 MHz, $CDCl_3$) δ 5.35 (m, 4H), 2.78 (2H, t, J=5.6 Hz), 2.18 (s, 6H), 2.05 (m, 6H), 1.3 (m, 39H), 0.89 (m, 6H).

(13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine (Compound 32)

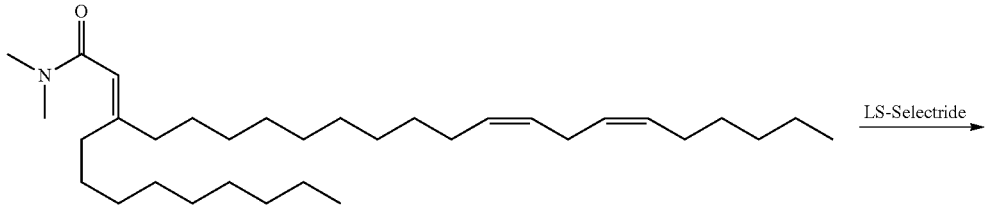


iii

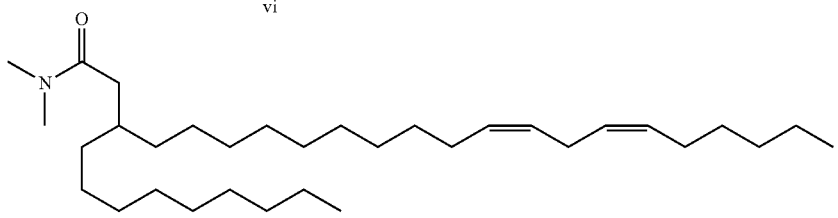


vi

The silyl amide Peterson reagent (3.1 g, 16.7 mmol) was dissolved in THF (35 mL) and cooled to −63° C. To this solution was added nBuLi (16.7 mmol. 6.7 mL of a 2.5 M solution). The reaction was warmed to ambient temperature for 30 minutes. The ketone (5.0 g, 11.9 mmol) was dissolved in THF (25 mL) in a second flask. The Peterson reagent was transferred to the ketone solution at −60° C. The reaction was warmed to −40° C. for 1 hour, then warmed to 0° C. for 30 minutes. The reaction was quenched with sodium bicarbonate, diluted with additional water and partitioned between water/hexanes. The organics were washed with brine, dried over sodium sulfate, filtered and evaporated in vacuo. Purification by flash chromatography (0-40% MTBE/hexanes) gave a α,β-unsatured amide vi. ^{1}H NMR (400 MHz, $CDCl_3$) δ 5.75 (s, 1H), 5.36 (m, 4H), 3.01 (s, 3H), 2.99 (s, 3H), 2.78 (t, 2H), 2.28 (t, 2H), 2.05 (m, 4H), 1.35 (m, 35H), 0.89 (m, 6H).

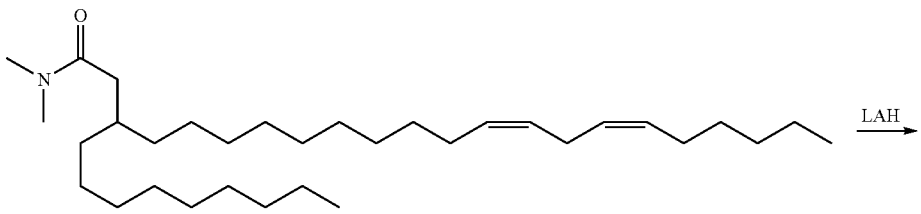


vi



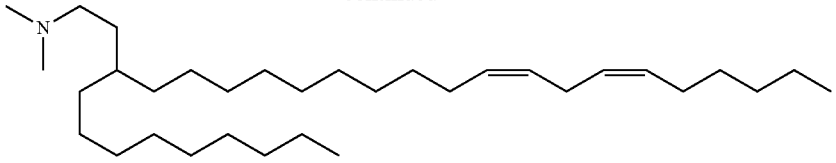
vii

α,β-unsatured amide vi (1 g, 2.1 mmol) and LS-Selectride (4.1 mmol, 4.1 mL of a 1M solution) were combined in a sealed tube and heated to 60° C. for 24 hours. The reaction was cooled to ambient temperature and partitioned between ammonium chloride solution and heptane. The organics were dried over sodium sulfate, filtered and evaporated in vacuo to give amide vii. This intermediate was carried directly into next reaction crude.



vii

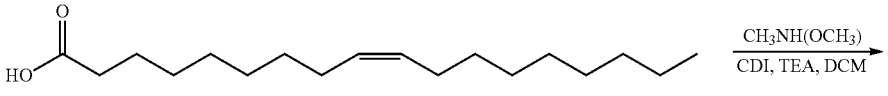
-continued



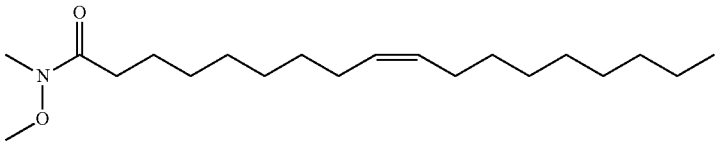
32

To a solution of amide vii (2.85 g, 5.8 mmol) was added lithium aluminum hydride (8.7 mmol, 8.7 mL of a 1M solution). The reaction was stirred at ambient temperature for 10 minutes then quenched by slow addition of sodium sulfate decahydrate solution. The solids were filtered and washed with THF and the filtrate evaporated in vacuo. The crude mixture was purified by reverse phase preparative chromatography (C8 column) to provide (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine (Compound 32) as an oil. HRMS (M+H) calc'd 476.5190 found 476.5189. ^{1}H NMR (400 MHz, $CDCl_3$) δ 5.37 (m, 4H), 2.78 (t, 2H), 2.42 (m, 8H), 2.05 (q, 4H), 1.28 (m, 41H), 0.89 (m, 6H).

N,N-dimethyl-1-(2-octylcyclopropyl)heptadecan-8-amine (Compound 33)

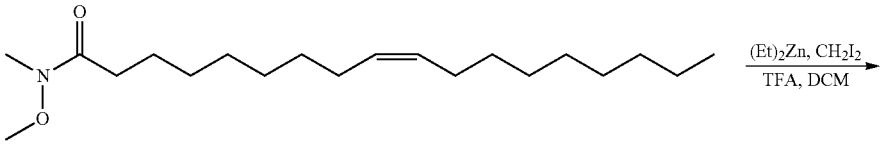


i

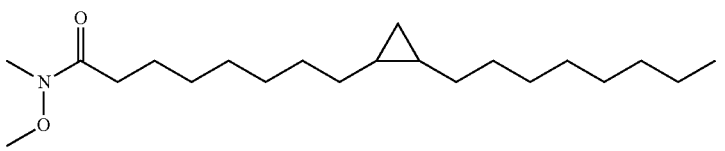


ii

To a solution of oleic acid (1 g, 3.5 mmol) in DCM (500 mL) cooled to 0° C. was added CDI (0.63 g, 3.9 mmol). The reaction was warmed to ambient temperature for 30 minutes before cooling to 0° C. and treating first with triethylamine (0.39 g, 3.9 mmol) and then dimethyl hydroxylamine hydrochloride (0.38 g, 3.9 mmol). After 1 hour the reaction was partitioned between water and heptane. The organics were dried over magnesium sulfate, filtered and evaporate in vacuo to give crude Weinreb amide ii which was carried directly into next reaction.

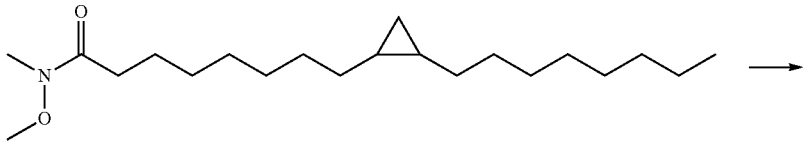


ii

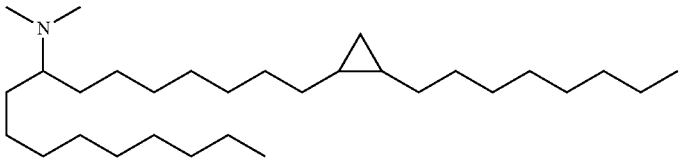


ix

A solution of diethylzinc (70.3 mmol, 70.3 mL of a 1M solution) in dichloromethane (130 mL) was cooled to −1° C. and treated dropwise with TFA (8.0 g, 70.3 mmol). After 30 minutes, diiodomethane (18.8 g, 70.3 mmol) was added and this was aged for 30 minutes in the ice bath. To this solution was added Weinreb amide ii (7.6 g, 23.4 mmol). The reaction was warmed to ambient temperature and stirred for 1 hour. The reaction was quenched with ammonium chloride solution (100 mL) and organic layer partitioned off, washed with 10% sodium thiosulfate, dried over magnesium sulfate, filtered and evaporated in vacuo. Purification was flash chromatography (0-30% MTBE/heptane) gave desired product ix. ^{1}H NMR (400 MHz, $CDCl_3$) δ 3.72 (s, 3H), 3.22 (s, 3H), 2.48 (t, 2H), 1.65 (m, 2H), 1.39 (m, 22H), 1.18 (m, 2H), 0.91 (t, 3H), 0.68 (m, 2H), 0.59 (m, 1H), −0.32 (m, 1H).



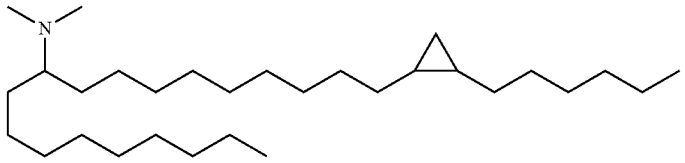
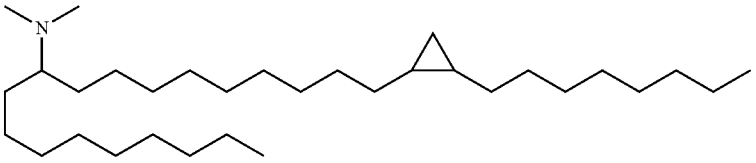
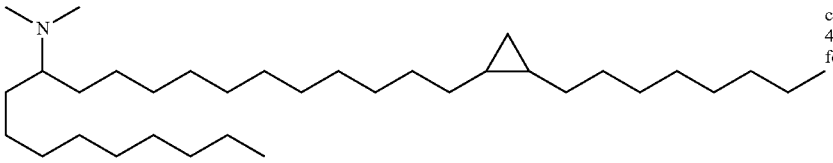
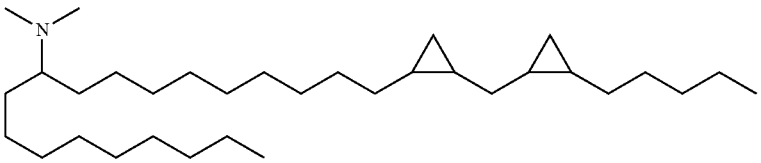
ix



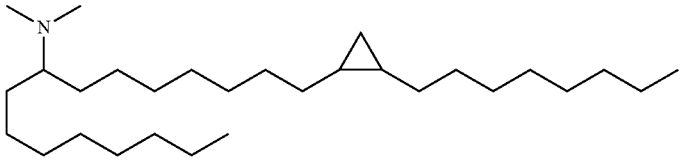
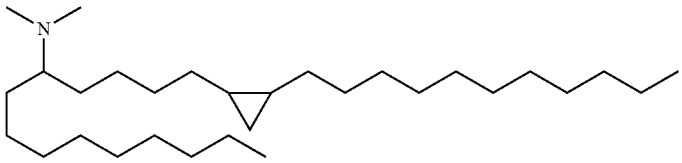
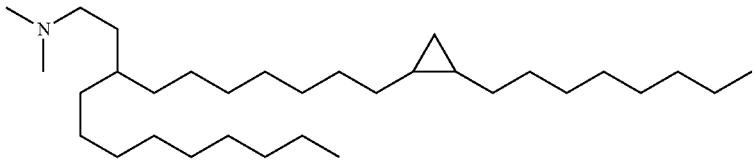
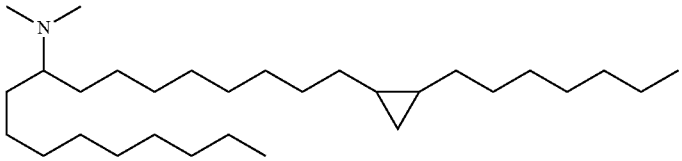
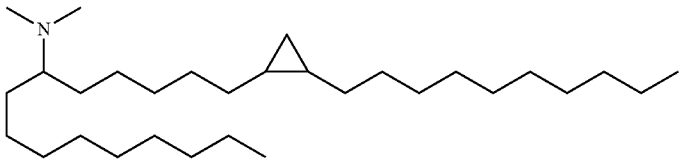
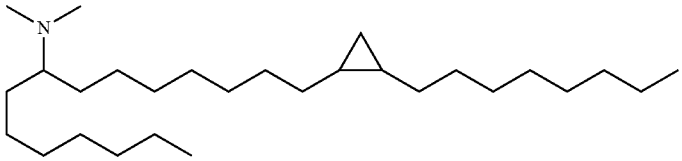
33

Conversion of Weinreb amide ix to Compound 33 was carried out in a manner analogous to that described for Compound 1 above (nonyl Grignard addition followed by reductive amination). LC/MS (M+H)=436.6. ^{1}H NMR (400 MHz, $CDCl_3$) δ 2.25 (s, 6H), 1.30 (m, 45H), 0.91 (m, 6H), 0.68 (m, 2H), 0.59 (m, 1H), −0.31 (m, 1H).

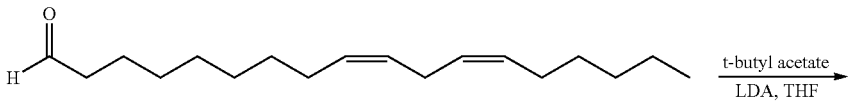
Compounds 34-43 are novel cationic lipids and were prepared according to General Schemes 1-4 above.

Compound	Structure	HRMS
34		calcd C30H62N 436.4877, found 436.4872.
35		calcd C32H66N 464.5190, found 464.5186.
36		calcd C34H70N 492.5503, found 492.5496.
37		calcd C33H66N 476.5190, found 476.5174.

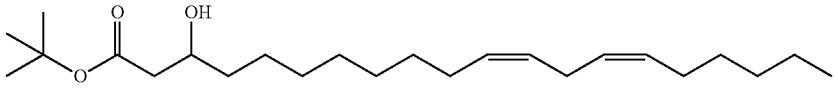
-continued

Compound	Structure	HRMS
38		calcd C29H60N 422.4720, found 422.4701.
39		calcd C30H62N 436.4877, found 436.4880.
40		calcd C32H66N 464.5190, found 464.5199.
41		calcd C30H62N 436.4877, found 436.4877.
42		calcd C30H62N 436.4877, found 436.4875.
43		LC/MS (M + H) 408.6

(11E,20Z,23Z)-N,N-dimethylnonacosa-11,20,23-trien-10-amine (Compound 44)

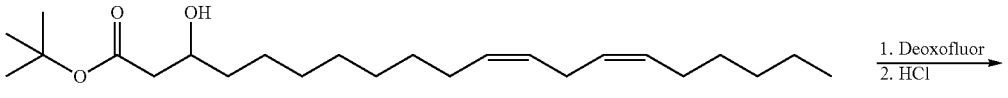


x

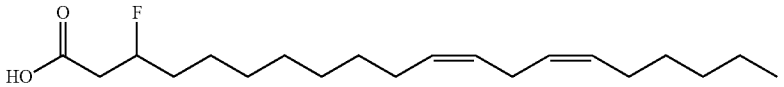


xi

To a solution of LDA (95 mmol, 47.5 mL of a 2M solution) in THF (127 mL) cooled to −78° C. was added t-butyl acetate. The reaction was stirred for 15 minutes followed by addition of aldehyde x. The reaction was immediately quenched with ammonium chloride solution, warmed to ambient temperature and partitioned between water/pentane. The organics were dried over sodium sulfate, filtered and evaporated in vacuo. LC/MS (M+H−tBu)=325.4.



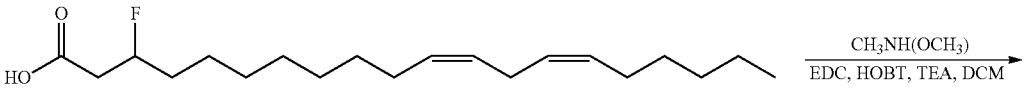
xi



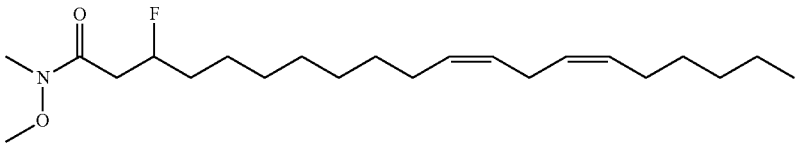
xii

Hydroxy ketone xi (7 g, 18.4 mmol) was dissolved in dichloromethane (150 mL) and cooled to 0° C. and treated with deoxofluor (7.3 g, 33.1 mmol). The reaction was warmed to ambient temperature with stirring for 16 hours followed by quenching with sodium bicarbonate solution. The reaction was partitioned and the organics dried over sodium sulfate, filtered and evaporate in vacuo. Flash column chromotagraphy (0-5% ethyl acetate/hexanes) gave the -fluoro ester.

Fluoro ester intermediate (6 g, 15.6 mmol) in dichloromethane was treated with hydrogen chloride (157 mmol, 39.2 mL or a 4M solution in dioxane) and the reaction was stirred at ambient temperature for 16 hours. The reaction was evaporated in vacuo to give desired β-fluoro acid xii. LC/MS (M+H)=327.3.

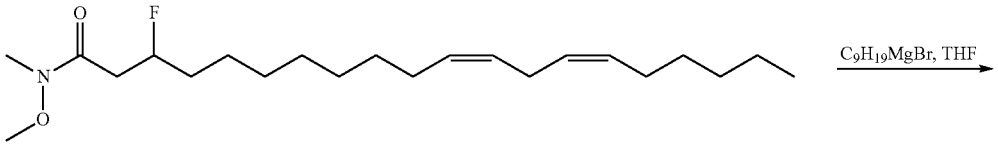


xii

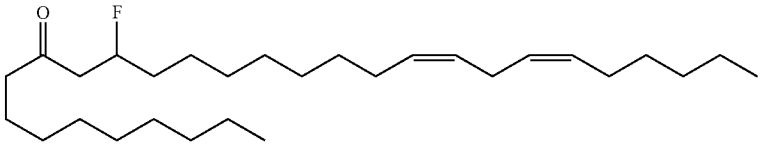


xiii

Fluoro carboxylic acid xii (5.1 g, 15.7 mmol), EDC (6.0 g, 31.4 mmol), N,O-dimethylhydroxylamine hydrochloride (3.1 g, 31.4 mmol), trimethylamine (4.0 g, 39.2 mmol), and HOAt (4.3 g, 31.4 mmol) were combined in DCM (78 mL) and stirred at ambient temperature for 16 hours. The reaction was partitioned between water/DCM and the organics were washed with water (3×) and NaOH solution (1×), dried over sodium sulfate, filtered and evaporated in vacuo. Crude material was purified by reverse phase preparative chromatography to give desired Weinreb amide xiii. LC/MS (M+H)=370.4.

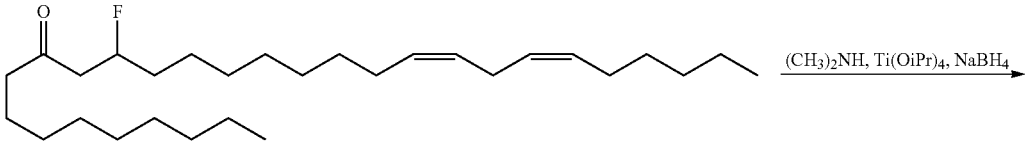


xiii

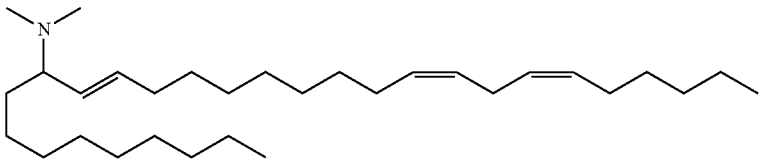


xiv

A solution of Weinreb amide xiii (4.3 g, 11.7 mmol) in THF (50 mL) was treated with nonylmagnesium bromide (23.4 mmol, 23.4 mL of a 1M solution) at ambient temperature. The reaction was quenched with ammonium chloride solution after 1 hour and partitioned between water and pentane. The organics were dried over sodium sulfate, filtered and evaporated in vacuo. This material was carried into next step crude.



xiv

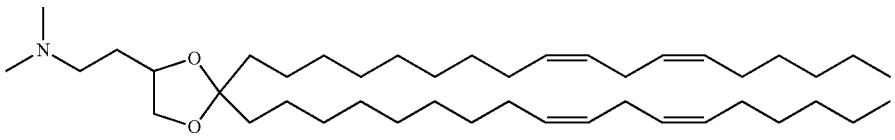


44

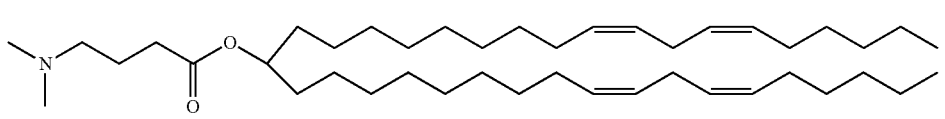
Ketone xiv (5.1 g, 11.7 mmol) was treated with dimethylamine (29.3 mmol, 14.7 mL of a 2M solution in THF) and titanium (IV) isopropoxide (6.7 g, 23.5 mmol) and the reaction was stirred at ambient temperature for 16 hours. To the reaction mixture was added ethanol (50 mL) followed by sodium borohydride (0.67 g, 17.6 mmol). The reaction was loaded directly onto a silica column and purified by flash chromatography (0-15% MeOH/DCM). The material required a second purification by preparative reverse phase chromatography to give (11E,20Z,23Z)-N,N-dimethylnonacosa-11,20,23-trien-10-amine. HRMS calc'd 446.4720, found 446.4724. ^{1}H NMR (400 MHz, $CDCl_3$) δ 5.48 (m, 1H), 5.37 (m, 4H), 5.23 (m, 1H), 2.78 (t, 2H), 2.58 (m, 1H), 2.22 (s, 6H), 2.04 (m, 4H), 1.56 (m, 1H), 1.30 (m, 31H), 0.89 (m, 6H).

Compound 45 is DLinKC2DMA as described in Nature Biotechnology, 2010, 28, 172-176, WO 2010/042877 A1, WO 2010/048536 A2, WO 2010/088537 A2, and WO 2009/127060 A1.

(45)



Compound 46 is MC3 as described in WO 2010/054401, and WO 2010/144740 A1.



(46)

D. Lipid Nanoparticle Compositions

The following lipid nanoparticle compositions (LNPs) of the instant invention are useful for the delivery of oligonucleotides, specifically siNA molecules of the invention:

Cationic Lipid/Cholesterol/PEG-DMG 56.6/38/5.4;
Cationic Lipid/Cholesterol/PEG-DMG 60/38/2;
Cationic Lipid/Cholesterol/PEG-DMG 67.3/29/3.7;
Cationic Lipid/Cholesterol/PEG-DMG 49.3/47/3.7;
Cationic Lipid/Cholesterol/PEG-DMG 50.3/44.3/5.4;
Cationic Lipid/Cholesterol/PEG-C-DMG/DSPC 40/48/2/10;
Cationic Lipid/Cholesterol/PEG-DMG/DSPC 40/48/2/10; and
Cationic Lipid/Cholesterol/PEG-DMG/DSPC 58/30/2/10.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein, as presently representative of preferred embodiments, are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

TABLE 8

CTNNB1 Accession Numbers
NM_001098210
Homo sapiens catenin (cadherin-associated protein), beta 1, 88 kDa, (CTNNB1), transcript variant 3, mRNA.
NM_001098210.1 GI:148227671
NM_007614
Mus museulus catenin (cadherin-associated protein), beta 1 (CTNNB1), transcript variant 1, mRNA
NM_007614.21 GI:31560726
XM_001115474
Macaca mulatia catenin (cadherin-associated protein), beta 1, 88 kDa, transcript variant (CTNNB1), mRNA.
XM_001115474.1 GI:109041278

TABLE 9

Non-limiting example of Stabilization Chemistries for chemically modified siNA constructs
Non-limiting example of Stabilization Chemistries for chemically modified siNA constructs

Chemistry	pyrimidine	purine	caps	p = S	Strand
"Stab 00"	Ribo	Ribo	TT at 3'-ends		S/AS
"Stab 1"	Ribo	Ribo	—	5 at 5'-end 1 at 3'-end	S/AS
"Stab 2"	Ribo	Ribo	—	All linkages	Usually AS
"Stab 3"	2'-fluoro	Ribo	—	4 at 5'-end 4 at 3'-end	Usually S
"Stab 4"	2'-fluoro	Ribo	5' and 3'-ends	—	Usually S
"Stab 5"	2'-fluoro	Ribo	—	1 at 3'-end	Usually AS
"Stab 6"	2'-O-Methyl	Ribo	5' and 3'-ends	—	Usually S
"Stab 7"	2'-fluoro	2'-deoxy	5' and 3'-ends	—	Usually S
"Stab 8"	2'-fluoro	2'-O-Methyl	—	1 at 3'-end	S/AS
"Stab 9"	Ribo	Ribo	5' and 3'-ends	—	Usually S
"Stab 10"	Ribo	Ribo	—	1 at 3'-end	Usually AS
"Stab 11"	2'-fluoro	2'-deoxy	—	1 at 3'-end	Usually AS
"Stab 12"	2'-fluoro	LNA	5' and 3'-ends		Usually S
"Stab 13"	2'-fluoro	LNA		1 at 3'-end	Usually AS
"Stab 14"	2'-fluoro	2'-deoxy		2 at 5'-end 1 at 3'-end	Usually AS Usually AS
"Stab 15"	2'-deoxy	2'-deoxy		2 at 5'-end 1 at 3'-end	Usually S
"Stab 16"	Ribo	2'-O-Methyl	5' and 3'-ends		Usually S
"Stab 17"	2'-O-Methyl	2'-O-Methyl	5' and 3'-ends		Usually S
"Stab 18"	2'-fluoro	2'-O-Methyl	5' and 3'-ends		S/AS
"Stab 19"	2'-fluoro	2'-O-Methyl	3'-end		Usually AS
"Stab 20"	2'-fluoro	2'-deoxy	3'-end		Usually AS
"Stab 21"	2'-fluoro	Ribo	3'-end		Usually AS
"Stab 22"	Ribo	Ribo	3'-end		Usually AS
"Stab 23"	2'-fluoro*	2'-deoxy*	5' and 3'-ends		Usually S
"Stab 24"	2'-fluoro*	2'-O-Methyl*	—	1 at 3'-end	S/AS

TABLE 9-continued

Non-limiting example of Stabilization Chemistries for chemically modified siNA constructs

Non-limiting example of Stabilization Chemistries for chemically modified siNA constructs

Chemistry	pyrimidine	purine	caps	p = S	Strand
"Stab 25"	2'-fluoro*	2'-O-Methyl*	—	1 at 3'-end	S/AS
"Stab 26"	2'-fluoro*	2'-O-Methyl*	—		S/AS
"Stab 27"	2'-fluoro*	2'-O-Methyl*	3'-end		S/AS
"Stab 28"	2'-fluoro*	2'-O-Methyl*	3'-end		S/AS
"Stab 29"	2'-fluoro*	2'-O-Methyl*		1 at 3'-end	S/AS
"Stab 30"	2'-fluoro*	2'-O-Methyl*			S/AS
"Stab 31"	2'-fluoro*	2'-O-Methyl*	3'-end		S/AS
"Stab 32"	2'-fluoro	2'-O-Methyl			S/AS
"Stab 33"	2'-fluoro	2'-deoxy*	5' and 3'-ends	—	Usually S
"Stab 34"	2'-fluoro	2'-O-Methyl*	5' and 3'-ends		Usually S
"Stab 35"	2'-fluoro*†	2'-O-Methyl*†			Usually AS
"Stab 36	2'-fluoro*†	2'-O-Methyl*†			Usually AS
"Stab04H"	2'-fluoro*‡	Ribo‡	5' and 3'-ends	1 at 3'-end	Usually S
"Stab06C"	2'-O-Methyl‡	Ribo‡	5' and 3'-ends		Usually S
"Stab07H"	2'-fluoro‡	2'-deoxy‡	5' and 3'-ends	1 at 3'-end	Usually S
"Stab07mU"	2'-fluoro‡	2'-deoxy‡	5' and 3'-ends		Usually S
"Stab09H"	Ribo‡	Ribo‡	5' and 3'-ends	1 at 3'-end	Usually S
"Stab16C"	Ribo‡	2'-O-Methyl‡	5' and 3'-ends		Usually S
"Stab16H"	Ribo‡	2'-O-Methyl‡	5' and 3'-ends	1 at 3'-end	Usually S
"Stab18C"	2'-fluoro‡	2'-O-Methyl‡	5' and 3'-ends		Usually S
"Stab18H"	2'-fluoro‡	2'-O-Methyl‡	5' and 3'-ends	1 at 3'-end	Usually S
"Stab52H"	2'-O-Methyl‡	Ribo‡	5' and 3'-ends	1 at 3'-end	Usually S
"Stab05C"	2'-fluoro‡	Ribo‡			Usually AS
"Stab05N"	2'-fluoro‡	Ribo‡		1 at 3'-end	Usually AS
"Stab10C"	Ribo‡	Ribo‡			Usually AS
"Stab10N"	Ribo‡	Ribo‡		1 at 3'-end	Usually AS
"Stab35G*"	2'-fluoro‡	2'-O-Methyl‡			Usually AS
"Stab35N*"	2'-fluoro‡	2'-O-Methyl‡		1 at 3'-end	Usually AS
"Stab35rev*"	2'-O-Methyl‡	2'-fluoro‡			Usually AS
"Stab50*"	Ribo‡	2'-O-Methyl‡			Usually AS
"Stab53*"	2'-O-Methyl‡	Ribo‡			Usually AS
"Stab53N*"	2'-O-Methyl‡	Ribo‡		1 at 3'-end	Usually AS
"Stab54"	Ribo‡	2'-fluoro‡			Usually AS

TABLE 10

Exemplary Solid Pahse Oligonucleotied Synthsis Conditions

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time* RNA
A. 2.5 μmol Synthesis Cycle ABI 394 Instrument					
Phosphoramidites	6.5	163 μL	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 μL	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 μL	5 sec	5 sec	5 sec
N-CTNNB1-hyllmidazole	186	233 μL	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 μL	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA
B. 0.2 μmol Synthesis Cycle ABI 394 Instrument					
Phosphoramidites	15	31 μL	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 μL	45 sec	233 min	465 sec
Acetic Anhydride	655	124 μL	5 sec	5 sec	5 sec
N-CTNNB1-hyllmidazole	1245	124 μL	5 sec	5 sec	5 sec
TCA	700	732 μL	10 sec	10 sec	10 sec
Iodine	20.6	244 μL	15 sec	15 sec	15 sec

TABLE 10-continued

Exemplary Solid Pahse Oligonucleotied Synthsis Conditions

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time* RNA
Beaucage	7.7	232 μL	100 sec	300 sec	300 sec
Acetonitrile	NA	2.64 mL	NA	NA	NA

TABLE 11

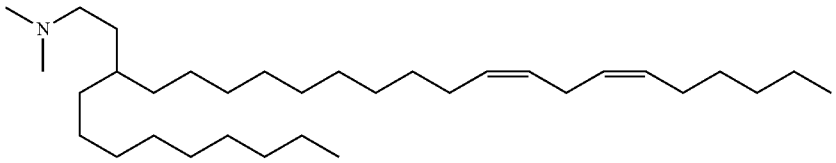
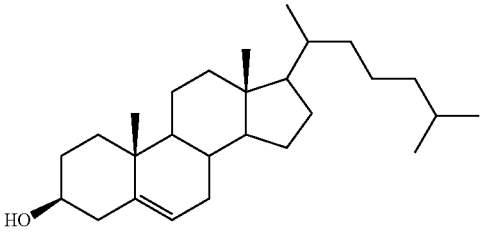
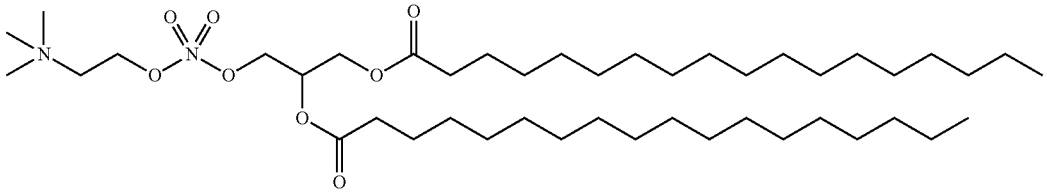
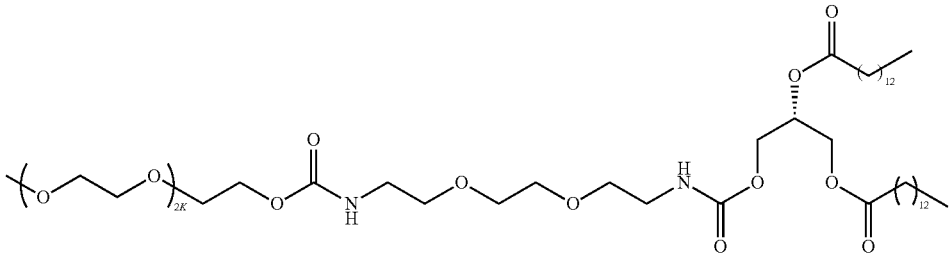
Composition of Select Lipid Nanoparticle Formulations

LNP Identifier	Lipid Components and Molar Ratios				siNA Duplex	N/P
LNP-1	Compound 32 (50%)	Cholesterol (30%)	DSPC (10%)	PEG-DMG (2%)	R-008488889-000M	6
LNP-2	Compound 32 (50%)	Cholesterol (30%)	DSPC (10%)	PEG-DMG (2%)	R-008488882-000B	6
LNP-3	Compound 32 (50%)	Cholesterol (30%)	DSPC (10%)	PEG-DMG (2%)	R-008380929-000H	6
LNP-4	Compound 32 (50%)	Cholesterol (30%)	DSPC (10%)	PEG-DMG (2%)	R-008488885-000C	6

N/P ratio = Nitrogen:Phosphorous ratio between cationic lipid and nucleic acid

TABLE 12

Chemical Structures of Lipids in Formulations of Table 11

Lipid	Chemical Structure
Compound 32	
Cholesterol	
DSPC	
PEG-DMG	

SEQUENCE LISTING

The patent contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US09447420B2). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What we claim is:

1. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB1), wherein

(a) the siNA comprises a sense strand and an antisense strand;

(b) each strand is independently 19-24 nucleotides in length; and

(c) at least one strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides of SEQ NO: 194.

2. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB1), wherein

(a) the siNA comprises a sense strand and an antisense strand;

(b) each strand is independently 19-24 nucleotides in length; and

(c) the antisense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides 5'-ACGACUAGUUCAGUUGCUU-3' (SEQ ID NO: 194).

3. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB1), wherein

(a) the siNA comprises a sense strand and an antisense strand;

(b) each strand is independently 19-24 nucleotides in length; and

(c) the antisense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides of 5'-AAGCAACUGAACUAGUCGU-3' (SEQ ID NO: 5107).

4. The double-stranded short interfering nucleic acid (siNA) molecule of claim **3**, wherein the sense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides of 5'-ACGACUAGUUCA-GUUGCUU-3' (SEQ ID NO: 194); and wherein one of more of the nucleotides are chemically modified.

5. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-3**, wherein at least one nucleotide is a chemically modified nucleotide.

6. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, further comprising at least one non-nucleotide.

7. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, wherein at least one nucleotide comprises a universal base.

8. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, comprising at least one phosphorothioate internucleotide linkage.

9. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, comprising a cap on the 3'-end, 5'-end or both 3' and 5' ends of at least one strand.

10. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, comprising one or more 3'-overhang nucleotides on one or both strands.

11. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, wherein the 5' end of the antisense strand is phosphorylated.

12. The double-stranded short interfering nucleic acid (siNA) molecule of claim **10**, wherein the 3'-overhang nucleotides on at least one strand are 2'-O-methyl nucleotides.

13. The double-stranded short interfering nucleic acid (siNA) molecule of claim **12**, wherein the 2'-O-methyl nucleotides are linked with a phosphorothioate internucleotide linkage.

14. The double-stranded short interfering nucleic acid (siNA) molecule of claim **5**, wherein the chemically modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide.

15. The double-stranded short interfering nucleic acid (siNA) molecule of claim **5**, wherein the chemically modified nucleotide is a 2'-deoxy nucleotide.

16. The double-stranded short interfering nucleic acid (siNA) molecule of claim **5**, wherein the chemically modified nucleotide is a 2'-O-alkyl nucleotide.

17. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, wherein five or more pyrimidine nucleotides in one or both strands are 2'-deoxy-2'-fluoro pyrimidine nucleotides.

18. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, wherein five or more pyrimidine nucleotides in one or both strands are 2'-O-methyl pyrimidine nucleotides.

19. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, wherein five or more purine nucleotides in one or both strands are 2'-deoxy-2'-fluoro purine nucleotides.

20. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, wherein five or more purine nucleotides in one or both strands are 2'-O-methyl purine nucleotides.

21. The double-stranded short interfering nucleic acid (siNA) molecule of claim **17**, wherein five or more purine nucleotides in one or both strands are 2'-O-methyl purine nucleotides.

22. The double-stranded short interfering nucleic acid (siNA) molecule of claim **18**, wherein five or more purine nucleotides in one or both strands are 2'-deoxy-2'-fluoro nucleotides.

23. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB1), comprising SEQ ID NOS: 6372 and 6374.

24. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB1), comprising SEQ ID NOS: 6372 and 6373.

25. A composition comprising:

(a) a double-stranded short interfering nucleic acid (siNA) molecule having SEQ ID NOS:6372 and 6374;

(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;

(c) cholesterol;

(d) DSPC; and

(e) PEG-DMG.

26. A composition comprising:

(a) a double-stranded short interfering nucleic acid (siNA) molecule having SEQ ID NOS: 6372 and 6373;

(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;

(c) cholesterol;

(d) DSPC; and

(e) PEG-DMG.

27. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB 1), comprising SEQ ID NOS: 6372 and 6371.

28. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB 1), comprising SEQ ID NOS: 1912 and 1913.

29. A double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of cadherin-associated protein, beta 1 (CTNNB 1), comprising SEQ ID NOS: 1840 and 1841.

30. A composition comprising:

(a) a double-stranded short interfering nucleic acid (siNA) molecule having SEQ ID NOS: 6372 and 6371;

(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;

(c) cholesterol;

(d) DSPC; and

(e) PEG-DMG.

31. A composition comprising:

(a) a double-stranded short interfering nucleic acid (siNA) molecule having SEQ ID NOS: 1912 and 1913;

(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;

(c) cholesterol;

(d) DSPC; and

(e) PEG-DMG.

32. A composition comprising:

(a) a double-stranded short interfering nucleic acid (siNA) molecule having SEQ ID NOS: 1840 and 1841;

(b) (13Z,16Z)-N,N-dimethyl-3-nonyldocosa-13,16-dien-1-amine;

(c) cholesterol;
(d) DSPC; and
(e) PEG-DMG.

33. The double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **23**, **24**, and **27-29**, comprising one or more phosphorothioate internucleotide linkages.

34. A composition comprising the double-stranded short interfering nucleic acid (siNA) molecule according to any one of claims **1-4**, **23**, **24**, and **27-29** in a pharmaceutically acceptable carrier or diluent.

35. The composition according to any one of claims **25**, **26**, and **30-32**, wherein the (13Z,16Z)-N,N-dimethyl-3-nonyldocosa -13,16-dien-1-amine, cholesterol, DSPC, and PEG-DMG have a molar ratio of 50:30: 10:2 respectively.

36. The composition according to any one of claims **25**, **26**, and **30-32**, further comprising sucrose, trehalose, or any combination thereof.

37. A method of treating a human subject suffering from a condition which is mediated by the action, or by loss of action, of cadherin-associated protein, beta 1 (CTNNB 1), comprising administering to said subject an effective amount of the double-stranded short interfering nucleic acid (siNA) molecule of any one of claims **1-4**, **23**, **24**, and **27-29**.

38. The method according to claim **37**, wherein the condition is cancer.

39. The method of claim **37**, wherein the subject is a human.

* * * * *